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(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

MSTMFADTLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR  
QQKKKIERQEELKNNNRDLMSVRMKSMAIGFCFTALMGMFNSIFDGRVVAKLPTPLSYIQ  
GLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPSGKFS

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE  
SAME

FIELD OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNA and to the  
5 recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

Extracellular proteins play important roles in, among other things, the formation, differentiation and  
10 maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration,  
differentiation, or interaction with other cells, is typically governed by information received from other cells  
and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance,  
mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which  
are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted  
15 polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of  
action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics,  
biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons,  
interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins.  
Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts  
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are  
focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel  
secreted proteins. Examples of screening methods and techniques are described in the literature [see, for  
example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation,  
25 differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation,  
migration, differentiation, or interaction with other cells, is typically governed by information received from  
other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides  
(for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and  
hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.  
30 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor  
kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesin molecules like  
selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is  
regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze  
that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

5

Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

#### SUMMARY OF THE INVENTION

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In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity,

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alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid

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sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid

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sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

30

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%

nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein,  
5 the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid  
10 sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90%  
15 nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively  
20 at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-  
25 inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide  
30 that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length,  
35 alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length,

5 alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the

10 referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are

15 contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

20 In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid

25 sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other

30 specifically defined fragment of the full-length amino acid sequence as disclosed herein.

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In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid

sequence identity, alternatively at least about 82 % amino acid sequence identity, alternatively at least about 83 % amino acid sequence identity, alternatively at least about 84 % amino acid sequence identity, alternatively at least about 85 % amino acid sequence identity, alternatively at least about 86 % amino acid sequence identity, alternatively at least about 87 % amino acid sequence identity, alternatively at least about 88 % amino acid sequence identity, alternatively at least about 89 % amino acid sequence identity, alternatively at least about 90 %  
5 amino acid sequence identity, alternatively at least about 91 % amino acid sequence identity, alternatively at least about 92 % amino acid sequence identity, alternatively at least about 93 % amino acid sequence identity, alternatively at least about 94 % amino acid sequence identity, alternatively at least about 95 % amino acid sequence identity, alternatively at least about 96 % amino acid sequence identity, alternatively at least about 97 % amino acid sequence identity, alternatively at least about 98 % amino acid sequence identity and alternatively at  
10 least about 99 % amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein  
15 those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.  
20

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small  
25 molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.  
30

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.  
35

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

5 In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

10 In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

15 In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

20 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO177 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16438-1387".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

25 Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO3574 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA19360-2552".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

30 Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO1280 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA33455-1548".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO4984 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA37155-2651".

35 Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO4988 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA38269-2654".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

5 Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO305 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA40619-1220".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO1866 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA44174-2513".

10 Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO4996 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA44675-2662".

15 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO4406 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA45408-2615".

Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

20 Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO1120 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA48606-1479".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

25 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO4990 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNAS2753-2656".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO738 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA53915-1258".

30 Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO3577 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA53991-2553".

35 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO1879 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA54009-2517".

Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO1471 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA56055-1643".

5 Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO1114 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA57033-1403".

10 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO1076 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA57252-1453".

15 Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO1483 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA58799-1652".

20 Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO4985 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA59770-2652".

25 Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO5000 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA59774-2665".

30 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO1881 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA60281-2518".

35 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO4314 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA60736-2559".

40 Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO4987 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA61875-2653".

45 Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO4313 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA62312-2558".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

5 Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO4799 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA62849-1604".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

10 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO4995 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA66307-2661".

10 Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO1341 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA66677-2535".

15 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO1777 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA71235-1706".

Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

20 Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO3580 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA71289-2547".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

25 Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO1779 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA73775-1707".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1754 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA76385-1692".

30 Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO1906 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA76395-2527".

35 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1870 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA77622-2516".

Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO4329 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA77629-2573".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ 5 ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO4979 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA77645-2648".

Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

10 Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO1885 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA79302-2521".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

15 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO1882 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA79865-2519".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO4989 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA80135-2655".

20 Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO4323 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA80794-2568".

25 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO1886 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA80796-2523".

Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

30 Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO4395 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA80840-2605".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

35 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO1782 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA80899-2501".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO4338 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA81228-2580".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

5 Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO4341 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA81761-2583".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO5990 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA96042-2682".

10 Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO3438 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA82364-2538".

15 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO4321 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA82424-2566".

Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

20 Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO4304 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA82430-2557".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

25 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA83500-2506".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO4403 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA83509-2612".

30 Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO4324 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA83560-2569".

35 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO4303 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA84139-2555".

Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO4305 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA84141-2556".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ 5 ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO4404 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA84142-2613".

Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ 10 ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1884 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA84318-2520".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO4349 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA84909-2590".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO4401 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA84912-2610".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1867 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA84925-2514".

Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ 25 ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO4319 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA84928-2564".

Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO4991 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA84932-2657".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO4398 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA86592-2607".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO4346 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA86594-2587".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO4350 cDNA, 5 wherein SEQ ID NO:125 is a clone designated herein as "DNA86647-2591".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO4318 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA87185-2563".

10 Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO4340 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA87656-2582".

15 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO4400 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA87974-2609".

Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

20 Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO4320 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA88001-2565".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

25 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO4409 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA88004-2575".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO4399 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA89220-2608".

30 Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO4418 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA89947-2618".

35 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO4330 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA90842-2574".

Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO4339 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA91775-2581".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ 5 ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO4326 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA91779-2571".

Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

10 Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO6014 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA92217-2697".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

15 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO3446 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA92219-2541".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4322 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA92223-2567".

20 Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO4381 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA92225-2603".

25 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO4348 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA92232-2589".

Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

30 Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO4371 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA92233-2599".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

35 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO3742 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA92243-2549".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO5773 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA92253-2671".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO5774 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA92254-2672".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO4343 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA92255-2584".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO4325 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA92269-2570".

Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO4347 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA92288-2588".

Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO3743 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA92290-2550".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO4426 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA93012-2622".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO4500 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA93020-2642".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO4389 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA94830-2604".

Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO4337 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA94833-2579".

Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO4992 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA94838-2658".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO5996 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA94844-2686".

Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO4345 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA94854-2586".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA95930".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO5780 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA96868-2677".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO5992 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA96871-2683".

Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO4428 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA96880-2624".

Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO4994 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA96986-2660".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO5995 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA96988-2685".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO6094 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA96995-2709".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

5 Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO4317 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA97004-2562".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

10 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO5997 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA97005-2687".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

15 Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO5005 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA97009-2668".

Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO5004 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA97013-2667".

20 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO6001 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA98380-2690".

25 Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO6013 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA98561-2696".

30 Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO4502 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA98575-2644".

35 Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO6007 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA98593-2694".

Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

40 Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO6028 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA98600-2703".

Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO100 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA99333".

5 Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO4327 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA99391-2572".

10 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO4315 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA99393-2560".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

15 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO5993 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA100276-2684".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

20 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO4503 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA100312-2645".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

25 Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO4976 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA100902-2646".

Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO5798 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA102899-2679".

30 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO6242 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA104875-2720".

35 Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO6095 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA105680-2710".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO6093 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA105779-2708".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

5 Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO6012 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA105794-2695".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO6027 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA105838-2702".

10 Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO6181 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA107698-2715".

15 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO6097 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA107701-2711".

Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

20 Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO6090 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA107781-2707".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

25 Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO7171 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA108670-2744".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO6258 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA108688-2725".

30 Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO9820 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA108769-2765".

35 Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO6243 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA108935-2721".

Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO6182 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA110700-2716".

5 Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO6079 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA111750-2706".

Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

10 Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO7434 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA123430-2755".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

15 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO9865 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA125154-2785".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO9828 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA142238-2768".

20 Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO196 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA22779-1130".

25 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO197 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA22780-1078".

Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

30 Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO195 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA26847-1395".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

35 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO187 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA27864-1155".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO182 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA27865-1091".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO188 cDNA, 5 wherein SEQ ID NO:277 is a clone designated herein as "DNA28497-1130".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO183 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA28498".

10 Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO184 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA28500".

15 Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO185 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA28503".

Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

20 Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO200 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA29101-1122".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

25 Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO202 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA30869".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

Figure 289 shows a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO214 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA32286-1191".

30 Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figure 289.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO215 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA32288-1132".

35 Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO219 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA32290-1164".

Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO211 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA32292-1131".

5 Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO220 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA32298-1132".

10 Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO366 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA33085-1110".

15 Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO216 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA33087-1158".

20 Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO221 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA33089-1132".

25 Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO228 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA33092-1202".

30 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO217 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA33094-1131".

35 Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO222 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA33107-1135".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

40 Figure 311 shows a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO224 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA33221-1133".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figure 311.

Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO230 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA33223-1136".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

5 Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO198 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA33457-1078".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO226 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA33460-1166".

10 Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO261 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA33473-1176".

15 Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO242 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA33785-1143".

Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

20 Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO227 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA33786-1132".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

25 Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO237 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA34353-1428".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO241 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA34392-1170".

30 Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO231 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA34434-1139".

35 Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO235 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA35558-1167".

Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO323 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA35595-1228".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ 5 ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO245 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA35638-1216".

Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

10 Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO246 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA35639-1172".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

15 Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO288 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA35663-1129".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO248 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA35674-1142".

20 Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO257 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA35841-1173".

25 Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO172 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA35916-1161".

Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

30 Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO258 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA35918-1174".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

35 Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO265 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA36350-1158".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

Figure 351 shows a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO326 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA37140-1234".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figure 351.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO266 cDNA, 5 wherein SEQ ID NO:353 is a clone designated herein as "DNA37150-1178".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO269 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA38260-1180".

10 Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO285 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA40021-1154".

15 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO328 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA40587-1231".

Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

20 Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO344 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA40592-1242".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

25 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO272 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA40620-1183".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO301 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA40628-1216".

30 Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO331 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA40981-1234".

35 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO332 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA40982-1235".

Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO353 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA41234-1242".

5 Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO310 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA43046-1225".

Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

10 Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO337 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA43316-1237".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

15 Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO346 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA44167-1243".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO350 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA44175-1314".

20 Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO526 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA44184-1319".

25 Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO381 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA44194-1317".

Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

30 Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO846 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA44196-1353".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

35 Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO363 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA45419-1252".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO365 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA46777-1253".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO1310 cDNA, 5 wherein SEQ ID NO:391 is a clone designated herein as "DNA47394-1572".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO731 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA48331-1329".

10 Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO322 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA48336-1309".

15 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO536 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA49142-1430".

Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

20 Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO719 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA49646-1327".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

25 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO619 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA49821-1562".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO771 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA49829-1346".

30 Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO1083 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA50921-1458".

35 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO862 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA52187-1354".

Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO733 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA52196-1348".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ 5 ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO1188 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA52598-1518".

Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ 10 ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO770 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA54228-1366".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ 15 ID NO:413 shown in Figure 413.

Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO1080 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA56047-1456".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ 20 ID NO:415 shown in Figure 415.

Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO1017 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA56112-1379".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ 25 ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO1016 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA56113-1378".

Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ 25 ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO792 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56352-1358".

Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ 30 ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO938 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56433-1406".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ 35 ID NO:423 shown in Figure 423.

Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO1012 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA56439-1376".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ 35 ID NO:425 shown in Figure 425.

Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO1008 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57530-1375".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

5 Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO1075 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57689-1385".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1007 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57690-1374".

10 Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO1056 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA57693-1424".

15 Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO791 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA57838-1337".

Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

20 Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1111 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA58721-1475".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

25 Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO812 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59205-1421".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO1066 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59215-1425".

30 Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1185 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59220-1514".

35 Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1031 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA59294-1381".

Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1360 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA59488-1603".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ 5 ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1309 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA59588-1571".

Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

10 Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1107 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA59606-1471".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

15 Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO836 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA59620-1463".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO1132 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA59767-1489".

20 Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA59777-1480".

25 Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1130 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA59814-1486".

Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

30 Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO844 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA59839-1461".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

35 Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1154 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA59846-1503".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1181 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA59847-1511".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

5 Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1126 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA60615-1483".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1186 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA60621-1516".

10 Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO1198 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA60622-1525".

15 Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO1159 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA60627-1508".

Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

20 Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO1265 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA60764-1533".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

25 Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO1250 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA60775-1532".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO1475 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA61185-1646".

30 Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO1312 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA61873-1574".

35 Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO1308 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA62306-1570".

Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO1326 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA62808-1582".

5 Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO1192 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA62814-1521".

Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

10 Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO1246 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA64885-1529".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

15 Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO1356 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA64886-1601".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO1275 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA64888-1542".

20 Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO1274 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA64889-1541".

25 Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO1358 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA64890-1612".

Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

30 Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO1286 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA64903-1553".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

35 Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO1294 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA64905-1558".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO1273 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA65402-1540".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

5 Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO1279 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA65405-1547".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO1195 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA65412-1523".

10 Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO1271 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA66309-1538".

15 Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO1338 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA66667-1596".

Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

20 Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA66675-1587".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

25 Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO1434 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA68818-2536".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO1418 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA68864-1629".

30 Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO1387 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA68872-1620".

35 Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO1384 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA71159-1617".

Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO1565 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA73727-1673".

5 Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figure 525 shows a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO1474 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA73739-1645".

Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figure 525.

10 Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO1917 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA76400-2528".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

15 Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO1787 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA76510-2504".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO1556 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA76529-1666".

20 Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO1561 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA76538-1670".

25 Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO1693 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA77301-1708".

Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

30 Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO1868 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA77624-2515".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

35 Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO1890 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA79230-2525".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO1887 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA79862-2522".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO4353 cDNA, 5 wherein SEQ ID NO:543 is a clone designated herein as "DNA80145-2594".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA83500-2506".

10 Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO4357 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA84917-2597".

15 Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO4302 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA92218-2554".

Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

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#### DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

##### I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers 25 to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to 30 each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides 35 disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be

isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence  
5 polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue  
10 for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of  
15 the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such  
20 polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of  
25 the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (*e.g.*, Nielsen et al., *Prot. Eng.* 10:1-6 (1997) and von Heinje et al., *Nucl. Acids. Res.* 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature  
30 polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as  
35 disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for

instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly

available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

10

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence

comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

5 In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

10 100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino 15 acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

\*PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide 20 sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid 25 sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at 30 least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain 35 of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-

length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic

acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, %

5 nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value  
10 is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which  
15 may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

20 Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res., 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected  
25 occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid  
30 sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to

## C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

5 "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least  
10 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

15 An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-  
20 encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not

substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')<sub>2</sub>, and Fv fragments; diabodies; linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')<sub>2</sub> fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V<sub>H</sub>-V<sub>L</sub> dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')<sub>2</sub> antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and

IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V<sub>H</sub> and V<sub>L</sub> domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V<sub>H</sub> and V<sub>L</sub> domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) in the same polypeptide chain (V<sub>H</sub>-V<sub>L</sub>). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The

components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and  
5 in a routine manner, in relation to the stated purpose.

**Table 1**

40

45

50

55

Table 1 (cont')

```

/*
 */
#include <stdio.h>
#include <ctype.h>

5   #define MAXJMP      16    /* max jumps in a diag */
#define MAXGAP      24    /* don't continue to penalize gaps larger than this */
#define JMPS        1024   /* max jmps in an path */
#define MX          4     /* save if there's at least MX-1 bases since last jmp */

10  #define DMAT        3     /* value of matching bases */
#define DMIS        0     /* penalty for mismatched bases */
#define DINS0       8     /* penalty for a gap */
#define DINS1       1     /* penalty per base */
15  #define PINS0       8     /* penalty for a gap */
#define PINS1       4     /* penalty per residue */

20  struct jmp {
    short           n[MAXJMP]; /* size of jmp (neg for delay) */
    unsigned short  x[MAXJMP]; /* base no. of jmp in seq x */
    }; /* limits seq to 2^16 - 1 */

25  struct diag {
    int             score; /* score at last jmp */
    long            offset; /* offset of prev block */
    short           ijmp;  /* current jmp index */
    struct jmp     jp;    /* list of jmps */
    };

30  struct path {
    int             spc; /* number of leading spaces */
    short           nJMPS; /* size of jmp (gap) */
    int             xJMPS; /* loc of jmp (last elem before gap) */
    };

35  char            *ofile; /* output file name */
char            *namex[2]; /* seq names: getseqs() */
char            *prog; /* prog name for err msgs */
char            *seqx[2]; /* seqs: getseqs() */
40  int              dmax; /* best diag: nw() */
int              dmax0; /* final diag */
int              dna; /* set if dna: main() */
int              endgaps; /* set if penalizing end gaps */
45  int              gpx, gpy; /* total gaps in seqs */
int              len0, lcn1; /* seq lens */
int              ngpx, ngpy; /* total size of gaps */
int              smax; /* max score: nw() */
int              *xbm; /* bitmap for matching */
50  long             offset; /* current offset in jmp file */
struct diag     *dx; /* holds diagonals */
struct path      pp[2]; /* holds path for seqs */

55  char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_malloc();

```

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *   where file1 and file2 are two dna or two protein sequences.
 *   The sequences can be in upper- or lower-case and may contain ambiguity
 *   Any lines beginning with ';' or '>' are ignored
 *   Max file length is 65535 (limited by unsigned short x in the jmp struct)
 *   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 *   Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
{
    int      ac;
    char    *av[];
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '>' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0;          /* 1 to penalize endgaps */
    ofile = "align.out";  /* output file */

    nw();                /* fill in the matrix, get the possible jmps */
    readjmps();           /* get the actual jmps */
    print();              /* print stats, alignment */

    cleanup(0);           /* unlink any tmp files */
}

```

**Table 1 (cont')**

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 5   a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw0
{
10    char      *px, *py;          /* seqs and ptrs */
    int       *ndely, *dely;     /* keep track of dely */
    int       ndelx, delx;      /* keep track of delx */
    int       *tmp;
    int       mis;              /* score for each type */
15    int       ins0, ins1;      /* insertion penalties */
    register id;              /* diagonal index */
    register ij;              /* jmp index */
    register *col0, *coll;     /* score for curr, last row */
    register xx, yy;          /* index into seqs */
20
    dx = (struct diag *)g_malloc("to get diags", len0+len1+1, sizeof(struct diag));
    ndely = (int *)g_malloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_malloc("to get dely", len1+1, sizeof(int));
25    col0 = (int *)g_malloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_malloc("to get coll", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;
30
    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
35        }
        col0[0] = 0;           /* Waterman Bull Math Biol 84 */
    }
    else
40        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
     */
45    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
         */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
50                col1[0] = delx = col0[0] - ins1;
                ndelx = xx;
        }
        else {
55            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
60

```

Table 1 (cont?)

```

...nw

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */
}

```

55

60

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely(yy))
    col1[yy] = mis;
5
else if (delx >= dely(yy)) {
    col1[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dma || (ndelx >= MAXJMP
&& xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = ndelx;
    dx[id].jp.x[ij] = xx;
20
    dx[id].score = delx;
}
else {
    col1[yy] = dely(yy);
    ij = dx[id].ijmp;
25
    if (dx[id].jp.n[0] && (!dma || (ndely(yy) >= MAXJMP
&& xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
    }
    dx[id].jp.n[ij] = -ndely(yy);
    dx[id].jp.x[ij] = xx;
    dx[id].score = dely(yy);
}
35
if (xx == len0 && yy < len1) {
    /* last col
    */
    if (endgaps)
        col1[yy] -= ins0+ins1*(len1-yy);
    if (col1[yy] > smax) {
        smax = col1[yy];
        dmax = id;
    }
40
}
50
if (endgaps && xx < len0)
    col1[yy-1] -= ins0+ins1*(len0-xx);
if (col1[yy-1] > smax) {
    smax = col1[yy-1];
    dmax = id;
}
55
tmp = col0; col0 = col1; col1 = tmp;
}
60
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);
}

```

**Table 1 (cont')**

```

/*
 *
 * print() - only routine visible outside this module
 *
5   * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10  * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() - -put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE   256      /* maximum output line */
#define P_SPC    3         /* space between name or num and seq */

20 extern _day[26][26];
int   olen;           /* set output line length */
FILE  *fx;            /* output file */

25 print()                                print
{
    int     lx, ly, firstgap, lastgap;    /* overlap */

30   if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "< first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "< second sequence: %s (length = %d)\n", namex[1], len1);
35   olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
40   if (dmax < len1 - 1) {             /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45     pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) {             /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
50   }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
55   }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5   getmat(lx, ly, firstgap, lastgap)           getmat
      int     lx, ly;                      /* "core" (minus endgaps) */
      int     firstgap, lastgap;          /* leading/trailing overlap */
{
10   int         nm, i0, i1, siz0, siz1;
    char        outrx[32];
    double      pct;
    register    n0, n1;
    register char *p0, *p1;

15   /* get total matches, score
 */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20   n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while (*p0 && *p1) {
25     if (siz0) {
          p1++;
          n1++;
          siz0--;
        }
30     else if (siz1) {
          p0++;
          n0++;
          siz1--;
        }
35     else {
          if (xbm[*p0-'A']&xm[*p1-'A'])
            nm++;
          if (n0++ == pp[0].n[i0])
            siz0 = pp[0].n[i0++];
          if (n1++ == pp[1].n[i1])
            siz1 = pp[1].n[i1++];
          p0++;
          p1++;
        }
45   }

/* pct homology:
 * if penalizing endgaps, base is the shorter seq
 * else, knock off overhangs and take shorter core
 */
50   if (endgaps)
      lx = (len0 < len1)? len0 : len1;
    else
55   lx = (lx < ly)? lx : ly;
    pct = 100.* (double)nm / (double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
            nm, (nm == 1)? "" : "es", lx, pct);

```

Table 1 (cont')

```

        fprintf(fx, "< gaps in first sequence: %d", gapx); ...getmat
5       if (gapx) {
          (void) sprintf(outx, " (%d %s%s)", ngapx, (dna)? "base": "residue", (ngapx == 1)? ":" : "s");
          fprintf(fx, "%s", outx);

        fprintf(fx, "< gaps in second sequence: %d", gapy);
10      if (gapy) {
          (void) sprintf(outx, " (%d %s%s)", ngapy, (dna)? "base": "residue", (ngapy == 1)? ":" : "s");
          fprintf(fx, "%s", outx);
        }

15      if (dma)
          fprintf(fx,
                  "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
                  smax, DMAT, DMIS, DINSO, DIN1);
      else
          fprintf(fx,
                  "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
                  smax, PINS0, PINS1);

20      if (endgaps)
          fprintf(fx,
                  "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
                  firstgap, (dma)? "base" : "residue", (firstgap == 1)? ":" : "s",
                  lastgap, (dma)? "base" : "residue", (lastgap == 1)? ":" : "s");
      else
          fprintf(fx, "<endgaps not penalized\n");

30      }

35      static nm;           /* matches in core -- for checking */
      static lmax;          /* lengths of stripped file names */
      static ij[2];         /* jmp index for a path */
      static nc[2];          /* number at start of current line */
      static ni[2];          /* current elem number -- for gapping */
      static siz[2];
      static char *ps[2];    /* ptr to current element */
      static char *po[2];    /* ptr to next output char slot */
40      static char out[2][P_LINE]; /* output line */
      static char star[P_LINE]; /* set by stars() */

      /*
       * print alignment of described in struct path pp[]
       */
45      static pr_align()
      {
        int nn;           /* char count */
        int more;
50        register i;

        for (i = 0, lmax = 0; i < 2; i++) {
          nn = stripname(hamex[i]);
          if (nn > lmax)
            lmax = nn;

          nc[i] = 1;
          ni[i] = 1;
          siz[i] = ij[i] = 0;
          ps[i] = seqx[i];
          po[i] = out[i];
        }
      }

```

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

5           more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
15      else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
20      else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;
            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
            }
30            ni[i]++;
        }
35      }
40      if (++nn == olen || !more && nn) {
            dumpblock();
            for (i = 0; i < 2; i++)
                po[i] = out[i];
            nn = 0;
        }
50      }

        /*
         * dump a block of lines, including numbers, stars: pr_align()
         */
55      static
dumpblock()
{
    register i;
    for (i = 0; i < 2; i++)
        *po[i] = '\0';
}

```

**dumpblock**

Table 1 (cont')

```

...dumpblock

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' '))
        if (i == 0)
            nums(i);
        if (i == 0 && *out[1])
            stars();
    putline(i);
    if (i == 0 && *out[1])
        fprintf(fx, star);
    if (i == 1)
        nums(i);
}
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
{
    int      ix;      /* index in out[] holding seq line */
    char      nline[P_LINE];
    register   i, j;
    register char  *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
int      ix;
{

```

Table 1 (cont')

```

...putline
5
int          i;
register char *px;
for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);
10
/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
15
for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
    (void) putc('\n', fx);
}
20
/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
25 stars()
{
    int          i;
    register char *p0, *p1, cx, *px;
30
if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
    !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
    return;
px = star;
for (i = lmax+P_SPC; i; i--)
    *px++ = ' ';
35
for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
    if (isalpha(*p0) && isalpha(*p1)) {
40
        if (xbm[*p0-'A']&xbm[*p1-'A']) {
            cx = '*';
            nm++;
        }
        else if (!dn && day[*p0-'A'][*p1-'A'] > 0)
            cx = '.';
        else
            cx = ' ';
    }
    else
        cx = ' ';
50
    *px++ = cx;
}
*px++ = '\n';
*px = '\0';
55 }

```

**Table 1 (cont')**

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5    stripname(pn)
      char    *pn;     /* file name (may be path) */
{
      register char    *px, *py;

10   py = 0;
      for (px = pn; *px; px++)
          if (*px == '/')
              py = px + 1;
15   if (py)
          (void) strcpy(pn, py);
      return(strlen(pn));
}
20

25

30

35

40

45

50

55

60
```

**Table 1 (cont')**

```

/*
 * cleanup() - cleanup any tmp file
 * getseq() - read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 5   * readjmps() -- get the good jmps, from tmp file if necessary
 * writejmps() -- write a filled array of jmps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

10  char  *jname = "/tmp/homgXXXXXX";           /* tmp file for jmps */
FILE  *fj;

15  int   cleanup();                         /* cleanup tmp file */
long  lseek();

/*
 * remove any tmp file if we blow
 */
20  cleanup(i)
{
    int   i;
    if (fj)
        (void) unlink(jname);
25  exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30  char  *
getseq(file, len).                               cleanup
35  char  *file;    /* file name */
int   *len;     /* seq len */
{
    char   line[1024], *pseq;
    register char  *px, *py;
40  int   natgc, tlen;
FILE  *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
45  exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
50  for (px = line; *px != '\n'; px++)
        if (isupper(*px) || islower(*px))
            tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
55  pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

**Table 1 (cont')**

```

...getseq
py = pseq + 4;
*len = tlen;
rewind(fp);
5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
20
(void) fclose(fp);
dna = natgc > (tlen/3);
return(pseq+4);
}

25 char *
g_calloc(msg, nx, sz)
{
    char *msg; /* program, calling routine */
    int nx, sz; /* number and size of elements */
30
    char *px, *calloc();
    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_malloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
35
            exit(1);
        }
    }
    return(px);
}
40
/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps0
45
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50
    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
            for (j = dx[dmax].jmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
60
                ;
    }
}

```

Table 1 (cont')**...readjmps**

```

if (j < 0 && dx[dmax].offset && f) {
    (void) lseek(fd, dx[dmax].offset, 0);
    (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
    (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
    dx[dmax].ijmp = MAXJMP-1;
}
else
    break;
}
if (i >= JMPS) {
    fprintf(stderr, "%s: too many gaps in alignment\n", prog);
    cleanup(1);
}
if (j >= 0) {
    siz = dx[dmax].jp.n[j];
    xx = dx[dmax].jp.x[j];
    dmax += siz;
    if (siz < 0) { /* gap in second seq */
        pp[1].n[i1] = -siz;
        xx += siz;
        /* id = xx - yy + len1 - 1
         */
        pp[1].x[i1] = xx - dmax + len1 - 1;
        gapy++;
        ngapy -= siz;
    /* ignore MAXGAP when doing endgaps */
    siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
    i1++;
}
else if (siz > 0) { /* gap in first seq */
    pp[0].n[i0] = siz;
    pp[0].x[i0] = xx;
    gapx++;
    ngapx += siz;
}
/* ignore MAXGAP when doing endgaps */
siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
i0++;
}
}
else
    break;
}

/* reverse the order of jmps
 */
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5   writejmps(ix)
      int      ix;
{
      char    *mktemp();
10  if (!fj) {
          if (mktemp(jname) < 0) {
              fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
              cleanup(1);
          }
15  if ((fj = fopen(jname, "w")) == 0) {
              fprintf(stderr, "%s: can't write %s\n", prog, jname);
              exit(1);
          }
20  (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
      (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}
25

30

35

40

45

50

55

60

```

Table 2

PRO	XXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

15	PRO	XXXXXXXXXXX	(Length = 10 amino acids)
	Comparison Protein	XXXXXXYYYYYYZZY	(Length = 15 amino acids)

% amino acid sequence identity =

20 (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

Table 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNNNNNNNNN	(Length = 16 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 6 divided by 14 = 42.9%

Table 5

15	PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
	Comparison DNA	NNNNNNVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

20 (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired 5 termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial 10 changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
20	Ala (A)	val; leu; ile	val
25	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
	Gln (Q)	asn	asn
30	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe; norleucine	leu
35	Leu (L)	norleucine; ile; val; met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
40	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
45	Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 5      (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- (3) acidic: asp, glu;
- (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- 10     (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London Ser A, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

### C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-

octane and agents such as methyl-3-[(*p*-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, 5 pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation 10 by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid 15 sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by 20 chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically 25 or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety 30 of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide 35 which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to

be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., **8**:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, **5**:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, **3**(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, **6**:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, **255**:192-194 (1992)]; an  $\alpha$ -tubulin epitope peptide [Skinner et al., J. Biol. Chem., **266**:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, **87**:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27, 1995.

#### D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., **85**:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

30

##### 1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., 5 supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled 10 ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across 15 the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

20

## 2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting 25 transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl<sub>2</sub>, CaPO<sub>4</sub>, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells 30 without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the 35

method of Van Solingen et al., *J. Bact.*, 130:946 (1977) and Hsiao et al., *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., *Methods in Enzymology*, 185:527-537 (1990) and Mansour et al., *Nature*, 336:348-352 (1988).

- 5 Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include  
10 Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescens*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting.  
15 Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli*  
20 W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan'*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.  
25 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, *Nature*, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., *Bio/Technology*, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., *J. Bacteriol.*, 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilicola* (ATCC 36,906; Van den Berg et al., *Bio/Technology*, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., *J. Basic Microbiol.*, 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., *Proc. Natl. Acad. Sci. USA*, 76:5259-5263 [1979]); *Schwanniomyces*  
30 such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., *Biochem. Biophys. Res. Commun.*, 112:284-289 [1983]; Tilburn et al.,

Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotrophic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

5 Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila S2* and *Spodoptera Sf9*, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (WI38, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

15 3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

25 The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, 30 penicillinase, Ipp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces*  $\alpha$ -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the 35 protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the  $2\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

5

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

10

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

15

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the tac promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

20

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

25

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytchrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

30

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July

1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

5 Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the 10 replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

15 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

20

#### 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an 25 appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

30 Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on 35 the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

5 It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns  
10 to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

15

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

20 The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, 25 including radionucleotides such as <sup>32</sup>P or <sup>35</sup>S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

30

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense 5 oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. 10 The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences. 15 Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increase affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target 20 nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO<sub>4</sub>-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic 25 acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide 30 sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase. 35

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

5 The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The 10 nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where 15 the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or 20 a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic 25 animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that 30 contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced 35 into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of

the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral

(typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

10 The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

15 The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

20 The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

25 The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; 30 antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, 35 PLURONIC™ or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

5 Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling  
10 in toxicokinetics" In Toxicokinetics and New Drug Development, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

15 When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1  $\mu$ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos.  
20 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

25 Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN- ), interleukin-2, and MN rgp120. Johnson et al., Nat. Med., 2:795-799 (1996); Yasuda, Biomed. Ther., 27:1221-1223 (1993); Hora et al., Bio/Technology, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

30 The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

35 This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides

encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

5 All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

20 If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lacZ reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for  $\beta$ -galactosidase. A complete kit (MATCHMAKER<sup>TM</sup>) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein

domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time 5 allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture 10 containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, 15 antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, 20 ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means 25 including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is 30 resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro- sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

35 In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988)). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

5

#### F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

##### 1. Polyclonal Antibodies

10 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate 15 the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

20

##### 2. Monoclonal Antibodies

25 The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

30 The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or 35 survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of

HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, **133**:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, **107**:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent

heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

*In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

5

### 3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and

Boerner et al., J. Immunol., **147**(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology **10**, 779-783 (1992); Lonberg et al., Nature **368** 856-859 (1994); Morrison, Nature **368**, 812-13 (1994); Fishwild et al., Nature Biotechnology **14**, 845-51 (1996); Neuberger, Nature Biotechnology **14**, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. **13** 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

#### 4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, **305**:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., **10**:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, **121**:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain.

In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

5 Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

10 15 Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic 20 activity of human cytotoxic lymphocytes against human breast tumor targets.

25 Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

30 35 Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule

on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc $\gamma$ R), such as Fc $\gamma$ RI (CD64), Fc $\gamma$ RII (CD32) and Fc $\gamma$ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

#### 5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptopbutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., **176**: 1191-1195 (1992) and Shope, J. Immunol., **148**: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, **53**: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, **3**: 219-230 (1989).

#### 30 7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins

(PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, saponaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the trichothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include <sup>212</sup>Bi, <sup>131</sup>I, <sup>131</sup>In, <sup>90</sup>Y, and <sup>186</sup>Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridylthiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionucleotide).

#### 8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

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#### 9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that

specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco *et al.*, Proc. Natl. Acad. Sci. USA, **90**: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, supra.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and  $\gamma$  ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT <sup>TM</sup> (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

#### G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC

Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

20

## EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

25

### EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST 30 databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA 35 sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were

often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to Sall hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRKSB is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

#### EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

##### 1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the Sall/NotI linker cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

##### 2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, linker with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL<sup>+</sup>, SUC<sup>+</sup>, GAL<sup>+</sup>. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles 15 in sec71, sec72, sec62, with truncated sec71 being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

20 Transformation was performed based on the protocol outlined by Gietz et al., Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser et al., Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2 x 10<sup>6</sup> cells/ml (approx. OD<sub>600</sub>=0.1) into fresh YEPD broth (500 ml) and regrown to 1 x 10<sup>7</sup> 25 cells/ml (approx. OD<sub>600</sub>=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA 30 pH 7.5, 100 mM Li<sub>2</sub>OOCCH<sub>3</sub>), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 µg, vol. < 10 µl) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 µl, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li<sub>2</sub>OOCCH<sub>3</sub>, pH 7.5) was added. This mixture was 35 gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 µl, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells

were then diluted into TE (1 ml) and aliquots (200  $\mu$ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al., *Anal. Biochem.*, 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

#### 4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30  $\mu$ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5  $\mu$ l) was used as a template for the PCR reaction in a 25  $\mu$ l volume containing: 0.5  $\mu$ l KlenTaq (Clontech, Palo Alto, CA); 4.0  $\mu$ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5  $\mu$ l KlenTaq buffer (Clontech); 0.25  $\mu$ l forward oligo 1; 0.25  $\mu$ l reverse oligo 2; 12.5  $\mu$ l distilled water. The sequence of the forward oligonucleotide 1 was:

25 5'-TGTAAAACGACGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:553)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:554)

PCR was then performed as follows:

a.		Denature	92°C, 5 minutes
b.	3 cycles of:	Denature	92°C, 30 seconds
		Anneal	59°C, 30 seconds
		Extend	72°C, 60 seconds
c.	3 cycles of:	Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
d.	25 cycles of:	Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds

e. Hold 4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 µl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

#### EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

#### EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
DNA16438-1387	209771	April 14, 1998
DNA19360-2552	203654	February 9, 1999
DNA33455-1548	PTA-127	May 25, 1999
DNA37155-2651	PTA-429	July 27, 1999
DNA38269-2654	PTA-432	July 27, 1999
DNA40619-1220	209525	December 10, 1997

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA44174-2513	203577	January 12, 1999
	DNA44675-2662	PTA-430	July 27, 1999
	DNA45408-2615	PTA-203	June 8, 1999
5	DNA48606-1479	203040	July 1, 1998
	DNA52753-2656	PTA-611	August 31, 1999
	DNA53915-1258	209593	January 21, 1998
	DNA53991-2553	203649	February 9, 1999
	DNA54009-2517	203574	January 12, 1999
10	DNA56055-1643	PTA-129	May 25, 1999
	DNA57033-1403	209905	May 27, 1998
	DNA57252-1453	203585	January 12, 1999
	DNA58799-1652	203665	February 9, 1999
	DNA59770-2652	PTA-427	July 27, 1999
15	DNA59774-2665	PTA-615	August 31, 1999
	DNA60281-2518	203582	January 12, 1999
	DNA60736-2559	203838	March 9, 1999
	DNA61875-2653	PTA-428	July 27, 1999
	DNA62312-2558	203836	March 9, 1999
20	DNA62849-1604	PTA-205	June 8, 1999
	DNA66307-2661	PTA-431	July 27, 1999
	DNA66677-2535	203659	February 9, 1999
	DNA71235-1706	203584	January 12, 1999
	DNA71289-2547	PTA-126	May 25, 1999
25	DNA73775-1707	PTA-128	May 25, 1999
	DNA76385-1692	203664	February 9, 1999
	DNA76395-2527	203578	January 12, 1999
	DNA77622-2516	203554	December 22, 1998
	DNA77629-2573	203850	March 16, 1999
30	DNA77645-2648	PTA-45	May 11, 1999
	DNA79302-2521	203545	December 22, 1998
	DNA79865-2519	203544	December 22, 1998
	DNA80135-2655	PTA-234	June 15, 1999
	DNA80794-2568	203848	March 16, 1999
35	DNA80796-2523	203555	December 22, 1998
	DNA80840-2605	203949	April 20, 1999
	DNA80899-2501	203539	December 15, 1998
	DNA81228-2580	203871	March 23, 1999
	DNA81761-2583	203862	March 23, 1999
40	DNA82358-2738	PTA-510	August 10, 1999
	DNA82364-2538	203603	January 20, 1999
	DNA82424-2566	203813	March 2, 1999
	DNA82430-2557	203812	March 2, 1999
	DNA83500-2506	203391	October 29, 1998
45	DNA83509-2612	203965	April 27, 1999
	DNA83560-2569	203816	March 2, 1999
	DNA84139-2555	203814	March 2, 1999
	DNA84141-2556	203810	March 2, 1999
	DNA84142-2613	PTA-22	May 4, 1999
50	DNA84318-2520	203580	January 12, 1999
	DNA84909-2590	203889	March 30, 1999
	DNA84912-2610	203964	April 27, 1999
	DNA84925-2514	203548	December 22, 1998
	DNA84928-2564	203817	March 2, 1999
55	DNA84932-2657	PTA-235	June 15, 1999

Table 7 (cont')

<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
5 DNA86592-2607 DNA86594-2587 DNA86647-2591 DNA87185-2563 DNA87656-2582	203968	April 27, 1999
	203894	March 30, 1999
	203893	March 30, 1999
	203811	March 2, 1999
	203867	March 23, 1999
	203963	April 27, 1999
10 DNA88001-2565 DNA88004-2575 DNA89220-2608 DNA89947-2618 DNA90842-2574	203815	March 2, 1999
	203890	March 30, 1999
	PTA-130	May 25, 1999
	203970	April 27, 1999
	203845	March 16, 1999
15 DNA91775-2581 DNA91779-2571 DNA92217-2697 DNA92219-2541	203861	March 23, 1999
	203844	March 16, 1999
	PTA-513	August 10, 1999
	203663	February 9, 1999
20 DNA92223-2567 DNA92225-2603 DNA92232-2589 DNA92233-2599	203851	March 16, 1999
	203950	April 20, 1999
	203895	March 30, 1999
	PTA-134	May 25, 1999
	203852	March 16, 1999
25 DNA92243-2549 DNA92253-2671 DNA92254-2672 DNA92255-2584	PTA-258	June 22, 1999
	PTA-259	June 22, 1999
	203866	March 23, 1999
	203853	March 16, 1999
30 DNA92269-2570 DNA92288-2588 DNA92290-2550 DNA93012-2622	203892	March 30, 1999
	203847	March 16, 1999
	PTA-21	May 4, 1999
	PTA-121	May 25, 1999
	203951	April 20, 1999
35 DNA94830-2604 DNA94833-2579 DNA94838-2658 DNA94844-2686	203869	March 23, 1999
	PTA-232	June 15, 1999
	PTA-385	July 20, 1999
	203864	March 23, 1999
	PTA-262	June 22, 1999
40 DNA96868-2677 DNA96871-2683 DNA96880-2624 DNA96986-2660	PTA-381	July 20, 1999
	PTA-15	May 4, 1999
	PTA-239	June 15, 1999
	PTA-384	July 20, 1999
	PTA-475	August 3, 1999
45 DNA97004-2562 DNA97005-2687 DNA97009-2668 DNA97013-2667	203854	March 16, 1999
	PTA-378	July 20, 1999
	PTA-257	June 22, 1999
	PTA-231	June 15, 1999
	PTA-388	July 20, 1999
50 DNA98380-2690 DNA98561-2696 DNA98575-2644 DNA98593-2694	PTA-620	August 31, 1999
	PTA-118	May 25, 1999
	PTA-477	August 3, 1999
	PTA-488	August 3, 1999
	203849	March 16, 1999
55 DNA99391-2572 DNA99393-2560 DNA100276-2684 DNA100312-2645	203837	March 9, 1999
	PTA-380	July 20, 1999
	PTA-44	May 11, 1999
	PTA-42	May 11, 1999
	PTA-123	May 25, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA104875-2720	PTA-482	August 3, 1999
	DNA105680-2710	PTA-483	August 3, 1999
	DNA105779-2708	PTA-485	August 3, 1999
5	DNA105794-2695	PTA-480	August 3, 1999
	DNA105838-2702	PTA-476	August 3, 1999
	DNA107698-2715	PTA-472	August 3, 1999
	DNA107701-2711	PTA-487	August 3, 1999
	DNA107781-2707	PTA-484	August 3, 1999
10	DNA108670-2744	PTA-546	August 17, 1999
	DNA108688-2725	PTA-515	August 10, 1999
	DNA108769-2765	PTA-861	October 19, 1999
	DNA108935-2721	PTA-518	August 10, 1999
	DNA110700-2716	PTA-512	August 10, 1999
15	DNA111750-2706	PTA-489	August 3, 1999
	DNA123430-2755	PTA-614	August 31, 1999
	DNA125154-2785	PTA-957	November 16, 1999
	DNA142238-2768	PTA-819	October 5, 1999
	DNA22779-1130	209280	September 18, 1997
20	DNA26847-1395	209772	April 14, 1998
	DNA27864-1155	209375	October 16, 1997
	DNA27865-1091	209296	September 23, 1997
	DNA28497-1130	209279	September 18, 1997
	DNA29101-1122	209653	March 5, 1998
25	DNA32286-1191	209385	October 16, 1997
	DNA32288-1132	209261	September 16, 1997
	DNA32290-1164	209384	October 16, 1997
	DNA32292-1131	209258	September 16, 1997
	DNA32298-1132	209257	September 16, 1997
30	DNA33085-1110	209087	May 30, 1997
	DNA33087-1158	209381	October 16, 1997
	DNA33089-1132	209262	September 16, 1997
	DNA33092-1202	209420	October 28, 1997
	DNA33094-1131	209256	September 16, 1997
35	DNA33107-1135	209251	September 16, 1997
	DNA33221-1133	209263	September 16, 1997
	DNA33223-1136	209264	September 16, 1997
	DNA33460-1166	209376	October 16, 1997
	DNA33473-1176	209391	October 17, 1997
40	DNA33785-1143	209417	October 28, 1997
	DNA33786-1132	209253	September 16, 1997
	DNA34353-1428	209855	May 12, 1998
	DNA34392-1170	209526	December 10, 1997
	DNA34434-1139	209252	September 16, 1997
45	DNA35558-1167	209374	October 16, 1997
	DNA35595-1228	209528	December 10, 1997
	DNA35638-1216	209265	September 16, 1997
	DNA35639-1172	209396	October 17, 1997
	DNA35663-1129	209201	August 18, 1997
50	DNA35674-1142	209416	October 28, 1997
	DNA35841-1173	209403	October 17, 1997
	DNA35916-1161	209419	October 28, 1997
	DNA35918-1174	209402	October 17, 1997
	DNA36350-1158	209378	October 16, 1997
55	DNA37140-1234	209489	November 21, 1997

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
5	DNA37150-1178	209401	October 17, 1997
	DNA38260-1180	209397	October 17, 1997
	DNA40021-1154	209389	October 17, 1997
	DNA40587-1231	209438	November 7, 1997
	DNA40592-1242	209492	November 21, 1997
	DNA40620-1183	209388	October 17, 1997
10	DNA40628-1216	209432	November 7, 1997
	DNA40981-1234	209439	November 7, 1997
	DNA40982-1235	209433	November 7, 1997
	DNA41234-1242	209618	February 5, 1998
	DNA43046-1225	209484	November 21, 1997
	DNA43316-1237	209487	November 21, 1997
15	DNA44167-1243	209434	November 7, 1997
	DNA44184-1319	209704	March 26, 1998
	DNA44194-1317	209808	April 28, 1998
	DNA44196-1353	209847	May 6, 1998
	DNA45419-1252	209616	February 5, 1998
	DNA46777-1253	209619	February 5, 1998
20	DNA47394-1572	203109	August 11, 1998
	DNA48331-1329	209715	March 31, 1998
	DNA48336-1309	209669	March 11, 1998
	DNA49142-1430	203002	June 23, 1998
	DNA49646-1327	209705	March 26, 1998
	DNA49821-1562	209981	June 16, 1998
25	DNA49829-1346	209749	April 7, 1998
	DNA50921-1458	209859	May 12, 1998
	DNA52187-1354	209845	May 6, 1998
	DNA52196-1348	209748	April 7, 1998
	DNA52598-1518	203107	August 11, 1998
	DNA54228-1366	209801	April 23, 1998
30	DNA56047-1456	209948	June 9, 1998
	DNA56112-1379	209883	May 20, 1998
	DNA56113-1378	203049	July 1, 1998
	DNA56352-1358	209846	May 6, 1998
	DNA56433-1406	209857	May 12, 1998
	DNA56439-1376	209864	May 14, 1998
35	DNA57530-1375	209880	May 20, 1998
	DNA57689-1385	209869	May 14, 1998
	DNA57690-1374	209950	June 9, 1998
	DNA57693-1424	203008	June 23, 1998
	DNA57838-1337	203014	June 23, 1998
	DNA58721-1475	203110	August 11, 1998
40	DNA59205-1421	203009	June 23, 1998
	DNA59215-1425	209961	June 9, 1998
	DNA59220-1514	209962	June 9, 1998
	DNA59294-1381	209866	May 14, 1998
	DNA59488-1603	203157	August 25, 1998
	DNA59588-1571	203106	August 11, 1998
45	DNA59606-1471	209945	June 9, 1998
	DNA59620-1463	209989	June 16, 1998
	DNA59767-1489	203108	August 11, 1998
	DNA59777-1480	203111	August 11, 1998
	DNA59814-1486	203359	October 20, 1998
	DNA59839-1461	209988	June 16, 1998

Table 7 (cont')

<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
5	DNA59846-1503	209978 June 16, 1998
	DNA59847-1511	203098 August 4, 1998
	DNA60615-1483	209980 June 16, 1998
	DNA60621-1516	203091 August 4, 1998
	DNA60622-1525	203090 August 4, 1998
	DNA60627-1508	203092 August 4, 1998
10	DNA60764-1533	203452 November 10, 1998
	DNA60775-1532	203173 September 1, 1998
	DNA61185-1646	203464 November 17, 1998
	DNA61873-1574	203132 August 18, 1998
	DNA62306-1570	203254 September 9, 1998
	DNA62808-1582	203358 October 20, 1998
15	DNA62814-1521	203093 August 4, 1998
	DNA64885-1529	203457 November 3, 1998
	DNA64886-1601	203241 September 9, 1998
	DNA64888-1542	203249 September 9, 1998
	DNA64889-1541	203250 September 9, 1998
	DNA64890-1612	203131 August 18, 1998
20	DNA64903-1553	203223 September 15, 1998
	DNA64905-1558	203233 September 15, 1998
	DNA65402-1540	203252 September 9, 1998
	DNA65405-1547	203476 November 17, 1998
	DNA65412-1523	203094 August 4, 1998
	DNA66309-1538	203235 September 15, 1998
25	DNA66667-1596	203267 September 22, 1998
	DNA66675-1587	203282 September 22, 1998
	DNA68818-2536	203657 February 9, 1999
	DNA68864-1629	203276 September 22, 1998
	DNA68872-1620	203160 August 25, 1998
	DNA71159-1617	203135 August 18, 1998
30	DNA73727-1673	203459 November 3, 1998
	DNA73739-1645	203270 September 22, 1998
	DNA76400-2528	203573 January 12, 1999
	DNA76510-2504	203477 November 17, 1998
	DNA76529-1666	203315 October 6, 1998
	DNA76538-1670	203313 October 6, 1998
35	DNA77301-1708	203407 October 27, 1998
	DNA77624-2515	203553 December 22, 1998
	DNA79230-2525	203549 December 22, 1998
	DNA79862-2522	203550 December 22, 1998
	DNA80145-2594	PTA-204 June 8, 1999
	DNA83500-2506	203391 October 29, 1998
40	DNA84917-2597	203863 March 23, 1999
	DNA92218-2554	203834 March 9, 1999
	DNA96042-2682	PTA-382 July 20, 1999

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of

the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

5       The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

10

**EXAMPLE 5: Use of PRO as a hybridization probe**

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe. DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

15

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

20       DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

**EXAMPLE 6: Expression of PRO in *E. coli***

25

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

30

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

35       The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant

colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

5

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

10

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate•2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO<sub>4</sub>) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

20

*E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

25

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the

solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile  
5 since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using  
10 a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

15 **EXAMPLE 7: Expression of PRO in mammalian cells**

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector.  
20 Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg  
25 DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl<sub>2</sub>. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO<sub>4</sub>, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are  
30 then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml <sup>35</sup>S-cysteine and 200 µCi/ml <sup>35</sup>S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.  
35

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 75:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRKS-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRKS-PRO can be transfected into CHO cells using known reagents such as CaPO<sub>4</sub> or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as <sup>35</sup>S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRKS vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni<sup>2+</sup>-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res., 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Qiagen), Dospel® or Fugene® (Boehringer

Mannheim). The cells are grown as described in Lucas et al., *supra*. Approximately  $3 \times 10^7$  cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2  $\mu$ m filtered PS20 with 5% 0.2  $\mu$ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with  $3 \times 10^5$  cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at  $1.2 \times 10^6$  cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22  $\mu$ m filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 mL/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalting into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 mL G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 mL Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 mL fractions into tubes containing 275  $\mu$ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalting into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme

sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described 5 above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the 10 fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

15 The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence 20 encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfected the above plasmid and BaculoGold™ virus 25 DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by 30 Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is 35 loaded onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM

phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A<sub>280</sub> baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni<sup>2+</sup>-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged PRO are pooled and dialyzed against loading buffer.

5        Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

**EXAMPLE 10: Preparation of Antibodies that Bind PRO**

10      This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

15      Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be  
20      boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

25      After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

30      The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

35      The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

5 Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a 10 chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

15 Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

20 A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 12: Drug Screening

25 This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened 30 against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

35 Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment

and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable  
5 binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening  
10 techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any  
15 peptide which shares one or more antigenic determinants with PRO polypeptide.

#### EXAMPLE 13: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or  
20 inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, *Bio/Technology*, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically,  
25 by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved  
30 activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, *J. Biochem.*, 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent  
35 drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then

be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

**EXAMPLE 14: Identification of PRO Polypeptides That Stimulate TNF- $\alpha$  Release In Human Blood (Assay 128)**

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- $\alpha$  in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- $\alpha$  would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- $\alpha$  release would be beneficial. Specifically, 200  $\mu$ l of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 $\mu$ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50 $\mu$ l of plasma is collected from each well and tested for the presence of TNF- $\alpha$  by ELISA assay. A positive in the assay is a higher amount of TNF- $\alpha$  in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay: PRO195, PRO202, PRO215, PRO221, PRO217, PRO222, PRO198, PRO245, PRO172, PRO265, PRO266, PRO344, PRO337, PRO322, PRO1286, PRO1279, PRO1338 and PRO1343.

**EXAMPLE 15: Detection of Polypeptides That Affect Glucose or FFA Uptake in Skeletal Muscle (Assay 106)**

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as being capable of affecting glucose and/or FFA uptake by skeletal muscle in this assay: PRO182, PRO366, PRO198, PRO172 and PRO719.

EXAMPLE 16: Chondrocyte Re-differentiation Assay (Assay 110)

This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of the test PRO polypeptide, 5 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200 µl/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

The following polypeptide tested positive in this assay: PRO182, PRO366, PRO198 and PRO1868.

EXAMPLE 17: Chondrocyte Proliferation Assay (Assay 111)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day and the cells are reseeded to 25,000 cells/cm<sup>2</sup> every five days. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37°C, 20 µl of Alamar blue is added to each well and the plates are incubated for an additional 3 hours at 37°C. The fluorescence is then measured in each well (Ex:530 nm; Em: 590 nm). The fluorescence of a plate containing 200 µl of the serum-free medium is measured to obtain the background. A positive result in the assay is obtained when the fluorescence of the PRO polypeptide treated sample is more like that of the positive control than the negative control.

The following PRO polypeptides tested positive in this assay: PRO202, PRO224, PRO172 and PRO1312.

EXAMPLE 18: Detection of PRO Polypeptides That Affect Glucose or FFA Uptake by Primary Rat Adipocytes (Assay 94)

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by adipocyte cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by adipocytes

would be beneficial including, for example, obesity, diabetes or hyper- or hypo-insulinemia.

In a 96 well format, PRO polypeptides to be assayed are added to primary rat adipocytes, and allowed to incubate overnight. Samples are taken at 4 and 16 hours and assayed for glycerol, glucose and FFA uptake. After the 16 hour incubation, insulin is added to the media and allowed to incubate for 4 hours. At this time, a sample is taken and glycerol, glucose and FFA uptake is measured. Media containing insulin without the PRO polypeptide is used as a positive reference control. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as being capable of affecting glucose and/or FFA uptake in this assay: PRO202, PRO211, PRO344 and PRO1338.

10

EXAMPLE 19: Gene Expression in Bovine Pericytes (Assay 105)

This assay is designed to identify PRO polypeptides which activate gene expression in pericytes. Such polypeptides would be expected to be useful as growth factors and/or for situations where the activation of gene expression is desired or beneficial. Bovine pericytes are plated on 60mm culture dishes in growth media for 1 week. On day 1, various PRO polypeptides are diluted (1%) and incubated with the pericytes for 1, 4 and 24 hr. timepoints. The cells are harvested and the RNA isolated using TRI-Reagent following the included instructions. The RNA is then quantified by reading the 260/280 OD using a spectrophotometer. The gene expression analysis is done by TaqMan reactions using Perkin Elmer reagents and specially designed bovine probes and primers. Expression of the following genes is analyzed: GAPDH, beta-integrin, connective tissue growth factor (CTGF), ICAM-1, monocyte chemoattractant protein-1 (MCP-1), osteopontin, transforming growth factor-beta (TGF-beta), TGF-beta receptor, tissue inhibitor of metalloproteinase (TIMP), tissue factor (TF), VEGF- $\alpha$ , thrombospondin, VEGF- $\beta$ , angiopoietin-2, and collagenase. Replicates are then averaged and the SD determined. The gene expression levels are then normalized to GAPDH. These are then normalized to the expression levels obtained with a protein (PIN32) which does not significantly induce gene expression in bovine pericytes when compared to untreated controls. Any PRO polypeptide that gives a gene expression level 2-fold or higher over the PIN32 control is considered a positive hit.

The following PRO polypeptides tested positive in this assay: PRO366.

EXAMPLE 20: Identification of PRO Polypeptides That Activate Pericytes (Assay 125)

This assay shows that certain polypeptides of the invention act to activate proliferation of pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Such PRO polypeptides also would be expected to be useful as growth factors and/or for situations where the induction of cell proliferation is desired or beneficial. Activation of pericyte proliferation also correlates with the induction of angiogenesis and, as such, PRO polypeptides capable of inducing pericyte proliferation would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received

from VEC Technologies, and all but 5 ml media is removed from the flask. On day 2, the pericytes are trypsinized, washed, spun and plated on 96 well plates. On day 7, the media is removed and the pericytes are treated with 100  $\mu$ l of either the specific PRO polypeptide or control treatments (positive control = DME+5% +/- PDGF @ 500ng/ $\mu$ l; negative control = PIN32, a polypeptide determined to have no significant effect on pericyte proliferation). C-fos and GAPDH gene expression levels are then determined and the replicates are averaged and the SD is determined. The c-fos values are normalized to GAPDH and the results are expressed as fold increase over PIN32. Anything providing at least a 2-fold or higher response as compared to the negative control is considered positive for the assay.

5 The following polypeptides tested positive in this assay: PRO366.

10 **EXAMPLE 21: Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)**

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

15 The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO<sub>2</sub> in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100U/ml penicillin and 100 $\mu$ g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 20 18 ng/ml interleukin-1 $\alpha$ , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, *Biochem. Biophys. Acta* 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

25 When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 $\alpha$  and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The 30 polypeptides testing positive in this assay are : PRO216.

**EXAMPLE 22: Proliferation of Rat Utricular Supporting Cells (Assay 54)**

This assay shows that certain polypeptides of the invention act as potent mitogens for inner ear supporting cells which are auditory hair cell progenitors and, therefore, are useful for inducing the regeneration 35 of auditory hair cells and treating hearing loss in mammals. The assay is performed as follows. Rat UEC-4 utricular epithelial cells are aliquoted into 96 well plates with a density of 3000 cells/well in 200  $\mu$ l of serum-containing medium at 33°C. The cells are cultured overnight and are then switched to serum-free medium at

37°C. Various dilutions of PRO polypeptides (or nothing for a control) are then added to the cultures and the cells are incubated for 24 hours. After the 24 hour incubation,  $^3\text{H}$ -thymidine ( $1 \mu\text{Ci}/\text{well}$ ) is added and the cells are then cultured for an additional 24 hours. The cultures are then washed to remove unincorporated radiolabel, the cells harvested and Cpm per well determined. Cpm of at least 30% or greater in the PRO polypeptide treated cultures as compared to the control cultures is considered a positive in the assay.

5       The following polypeptides tested positive in this assay: PRO172.

**EXAMPLE 23: Stimulatory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 24)**

This example shows that certain polypeptides of the invention are active as a stimulator of the proliferation of stimulated T-lymphocytes. Compounds which stimulate proliferation of lymphocytes are useful 10 therapeutically where enhancement of an immune response is beneficial. A therapeutic agent may take the form of antagonists of the polypeptide of the invention, for example, murine-human chimeric, humanized or human antibodies against the polypeptide.

The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, 15 Published by John Wiley & Sons, Inc.

More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37°C, 5% CO<sub>2</sub>) and then 20 washed and resuspended to  $3 \times 10^6$  cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

The assay is prepared by plating in triplicate wells a mixture of:

100:1 of test sample diluted to 1% or to 0.1%.

25       50 :1 of irradiated stimulator cells, and

50 :1 of responder PBMC cells.

100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37°C, 5% CO<sub>2</sub> for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mC/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

30       In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells 35 to  $1 \times 10^7$  cells/ml of assay media. The assay is then conducted as described above.

Positive increases over control are considered positive with increases of greater than or equal to 180% being preferred. However, any value greater than control indicates a stimulatory effect for the test protein.

The following PRO polypeptides tested positive in this assay: PRO344.

**EXAMPLE 24: Pericyte c-Fos Induction (Assay 93)**

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100 µl of PRO polypeptide test samples and controls (positive control = DME +5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading versus frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM +5% FBS.

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The following polypeptides tested positive in this assay: PRO301, PRO619, PRO1066 and PRO1265.

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**EXAMPLE 25: Cytokine Release Assay (Assay 120)**

This assay is designed to determine whether PRO polypeptides of the present invention are capable of inducing the release of cytokines from peripheral blood mononuclear cells (PBMCs). PRO polypeptides capable of inducing the release of cytokines from PBMCs are useful from the treatment of conditions which would benefit from enhanced cytokine release and will be readily evident to those of ordinary skill in the art. Specifically, 1x10<sup>6</sup> cells/ml of peripheral blood mononuclear cells (PBMC) are cultured with 1% of a PRO polypeptide for 3 days in complete RPMI media. The supernatant is then harvested and tested for increased concentrations of various cytokines by ELISA as compared to a human IgG treated control. A positive in the assay is a 10-fold or greater increase in cytokine concentration in the PRO polypeptide treated sample as compared to the human IgG treated control.

25

30

The following polypeptides tested positive in this assay: PRO526 and PRO1343.

**EXAMPLE 26: Inhibition of A-Peptide Binding to Factor VIIA (Assay 118)**

This assay is designed to identify PRO polypeptides which are capable of inhibiting the binding of A-peptide to factor VIIA, thereby affecting the blood coagulation cascade. PRO polypeptides testing positive in this assay are expected to be useful for the treatment of conditions where alteration of the blood coagulation cascade would be beneficial including, for example, stroke, heart attack and various coagulation disorders. These PRO polypeptides are also useful for the identification of agonist and antagonist molecules which would

also be useful for treatment of those conditions.

Specifically, 384 well plates are coated with soluble factor VIIA and are incubated overnight at 4°C. The wells are then decanted and are blocked by the addition of 0.5% BSA for 1 hour. The wells are then washed and 20 $\mu$ l of biotinylated A-peptide and either various concentration of the PRO polypeptide (test) or nothing (negative control) are added to each well. The plates are then incubated for 1 hour at room temperature. The wells are again washed and then 40 $\mu$ l of streptavidin-europium is added to each well. The plates are then incubated for 30 minutes at room temperature and then washed. 40 $\mu$ l of a fluorescence enhancement solution is then added to each well, the plates incubated for 5 minutes at room temperature and each well is then read on Wallac Victor reader under europium delayed fluorescence settings. Percent inhibition of binding of the A-peptide to the factor VIIA is then determined (as compared to the negative control), wherein a positive in the assay is a percent inhibition of 30% or greater.

The following PRO polypeptides tested positive in this assay: PRO182.

**EXAMPLE 27: Inhibition of Adipocyte Differentiation Assay (Assay 66)**

This assay is designed to identify PRO polypeptides which are capable of inhibiting insulin-induced differentiation of adipocytes. PRO polypeptides testing positive in this assay would be expected to be useful for the treatment of conditions associated with obesity, diabetes, etc.

Specifically, 3T3-L1 cells are seeded into the wells of 96 well plates at 6x10<sup>4</sup> cells/well and allowed to grow to confluence for 7 days. At day 7, the cells are treated with various concentrations of the PRO polypeptide (or nothing for the negative control) in the presence of 1 $\mu$ g/ml insulin, 0.25x10<sup>-6</sup> M dexamethasone and 0.5mM IBMX. The samples are then incubated at 37°C in 7% CO<sub>2</sub> for 2 days. After the incubation, the media is removed by aspiration and the cells are washed with PBS and re-exposed to the PRO polypeptide (or nothing for the negative control) and 1 $\mu$ g/ml insulin. After 5 days, the media is removed and replaced with fresh PRO polypeptide (or nothing for the negative control) and insulin. After 5 days, the cells are lysed and the cell lysate is assayed using Sigma's Triglyceride [INT] kit (Sigma procedure #336). A positive in the assay is 20% greater inhibition of adipocyte differentiation in the PRO polypeptide treated samples as compared to the negative control.

The following PRO polypeptides tested positive in this assay: PRO185 and PRO198.

**EXAMPLE 28: HUVEC Stimulation by PRO Polypeptides (Assay 131)**

This assay is designed to identify PRO polypeptides which are capable of stimulating the proliferation of HUVEC cells. PRO polypeptides testing positive in this assay would be expected to be useful for inducing angiogenesis for the treatment of conditions where angiogenesis would be beneficial including, for example, wound healing, and the like. Antagonists of these PRO polypeptides would be expected to be useful for inhibiting angiogenesis for the treatment of, for example, tumors, and the like.

Specifically, COSTAR® flat bottom black plates are treated with fibronectin for 20 minutes and then washed twice with PBS. HUVEC cells are then plated at 2000 cells/well in an appropriate growth medium. The plates are then incubated overnight and then the PRO polypeptide (1% final concentration), nothing (negative

control) or IL1 $\beta$  (3.3 ng/ml final concentration; positive control) is added. The plates are again incubated overnight, stained with ICAM1-Cy5 and read on FMAT. A positive in the assay is a 2-fold or greater increase in fluorescence as compared to the positive control.

The following PRO polypeptides tested positive in this assay: PRO222.

5      **EXAMPLE 29: Promotion of Chondrocyte Redifferentiation (Assay 129)**

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

10     Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4  $\mu$ g/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100  $\mu$ l of the same media without serum and 100  $\mu$ l of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200  $\mu$ l/well. After 5 days at 37°C, 22  $\mu$ l of media containing 100  $\mu$ g/ml Hoechst 33342 and 50  $\mu$ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the > 50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

15     The following PRO polypeptides tested positive in this assay: PRO301.

20      **EXAMPLE 30: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors**

25     Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be 30 arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease 35 condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and

hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In 5 one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. 10 mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not 15 only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio 20 was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, 25 but also serve as therapeutic targets for the treatment of those tumors.

Table 8

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
30	PRO177	breast tumor	universal normal control
	PRO177	liver tumor	universal normal control
	PRO177	lung tumor	universal normal control
	PRO3574	breast tumor	universal normal control
	PRO3574	colon tumor	matched normal colon control
	PRO1280	breast tumor	universal normal control
35	PRO1280	lung tumor	universal normal control
	PRO4984	lung tumor	universal normal control
	PRO4988	colon tumor	universal normal control
	PRO4988	lung tumor	universal normal control
	PRO305	lung tumor	universal normal control
40	PRO305	colon tumor	universal normal control
	PRO1866	prostate tumor	universal normal control

Table 8 (cont')

Molecule	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO1866	lung tumor	universal normal control
PRO1866	colon tumor	universal normal control
PRO4996	breast tumor	universal normal control
5 PRO4996	lung tumor	universal normal control
PRO4406	lung tumor	universal normal control
PRO4406	colon tumor	universal normal control
PRO1120	colon tumor	universal normal control
10 PRO1120	breast tumor	universal normal control
PRO1120	rectal tumor	universal normal control
PRO4990	lung tumor	universal normal control
PRO738	cervical tumor	universal normal control
PRO738	lung tumor	universal normal control
15 PRO738	breast tumor	universal normal control
PRO3577	lung tumor	universal normal control
PRO1879	breast tumor	universal normal control
PRO1879	lung tumor	universal normal control
PRO1879	colon tumor	universal normal control
20 PRO1471	lung tumor	universal normal control
PRO1076	prostate tumor	universal normal control
PRO1483	lung tumor	universal normal control
PRO4985	rectal tumor	universal normal control
PRO4985	colon tumor	universal normal control
25 PRO4985	breast tumor	universal normal control
PRO4985	lung tumor	universal normal control
PRO5000	lung tumor	universal normal control
PRO1881	liver tumor	universal normal control
PRO1881	lung tumor	universal normal control
30 PRO1881	breast tumor	universal normal control
PRO4314	lung tumor	universal normal control
PRO4314	breast tumor	universal normal control
PRO4987	lung tumor	universal normal control
PRO4313	lung tumor	universal normal control
35 PRO4313	breast tumor	universal normal control
PRO4799	colon tumor	universal normal control
PRO4995	liver tumor	universal normal control
PRO4995	colon tumor	universal normal control
PRO4995	colon tumor	universal normal control
40 PRO1341	prostate tumor	matched normal colon control
PRO1341	lung tumor	universal normal control
PRO1341	colon tumor	universal normal control
PRO1341	colon tumor	universal normal control
PRO1777	lung tumor	universal normal control
45 PRO1777	colon tumor	matched normal colon control
PRO3580	lung tumor	universal normal control
PRO3580	prostate tumor	universal normal control
PRO1779	lung tumor	universal normal control
PRO1779	colon tumor	universal normal control
50 PRO1779	cervical tumor	universal normal control
PRO1754	breast tumor	universal normal control
PRO1754	lung tumor	universal normal control
PRO1906	breast tumor	universal normal control
PRO1906	colon tumor	universal normal control
PRO1906	prostate tumor	universal normal control
55 PRO1870	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4329	lung tumor	universal normal control
	PRO4979	colon tumor	universal normal control
	PRO1885	rectal tumor	universal normal control
5	PRO1885	colon tumor	universal normal control
	PRO1885	colon tumor	matched normal colon control
	PRO1882	prostate tumor	universal normal control
	PRO1882	lung tumor	universal normal control
	PRO1882	colon tumor	universal normal control
10	PRO1882	breast tumor	universal normal control
	PRO1882	cervical tumor	universal normal control
	PRO4989	rectal tumor	universal normal control
	PRO4989	breast tumor	universal normal control
	PRO4989	colon tumor	matched normal colon control
15	PRO4989	colon tumor	universal normal control
	PRO4323	lung tumor	universal normal control
	PRO4323	liver tumor	universal normal control
	PRO1886	breast tumor	universal normal control
	PRO1886	lung tumor	universal normal control
20	PRO1886	rectal tumor	universal normal control
	PRO4395	colon tumor	universal normal control
	PRO4395	prostate tumor	universal normal control
	PRO4395	lung tumor	universal normal control
	PRO4395	cervical tumor	universal normal control
25	PRO1782	colon tumor	universal normal control
	PRO1782	lung tumor	universal normal control
	PRO4388	lung tumor	universal normal control
	PRO4341	breast tumor	universal normal control
	PRO4341	lung tumor	universal normal control
30	PRO3438	lung tumor	universal normal control
	PRO4321	breast tumor	universal normal control
	PRO4321	lung tumor	universal normal control
	PRO4321	colon tumor	universal normal control
	PRO4304	breast tumor	universal normal control
35	PRO4304	lung tumor	universal normal control
	PRO4403	colon tumor	universal normal control
	PRO4403	breast tumor	universal normal control
	PRO4403	lung tumor	universal normal control
	PRO4324	lung tumor	universal normal control
40	PRO4324	breast tumor	universal normal control
	PRO4303	cervical tumor	universal normal control
	PRO4303	lung tumor	universal normal control
	PRO4303	breast tumor	universal normal control
	PRO4303	colon tumor	universal normal control
45	PRO4303	prostate tumor	universal normal control
	PRO4305	breast tumor	universal normal control
	PRO4305	lung tumor	universal normal control
	PRO4305	colon tumor	universal normal control
	PRO4305	liver tumor	universal normal control
50	PRO4404	lung tumor	universal normal control
	PRO4404	breast tumor	universal normal control
	PRO4404	rectal tumor	universal normal control
	PRO1884	lung tumor	universal normal control
	PRO4349	colon tumor	universal normal control
55	PRO4349	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4401	colon tumor	universal normal control
	PRO4401	lung tumor	universal normal control
	PRO1867	lung tumor	universal normal control
5	PRO1867	liver tumor	universal normal control
	PRO4319	breast tumor	universal normal control
	PRO4319	lung tumor	universal normal control
	PRO4991	lung tumor	universal normal control
	PRO4991	colon tumor	universal normal control
10	PRO4398	lung tumor	universal normal control
	PRO4346	lung tumor	universal normal control
	PRO4350	colon tumor	universal normal control
	PRO4350	prostate tumor	universal normal control
	PRO4350	lung tumor	universal normal control
15	PRO4318	prostate tumor	universal normal control
	PRO4318	lung tumor	universal normal control
	PRO4340	breast tumor	universal normal control
	PRO4340	lung tumor	universal normal control
	PRO4400	breast tumor	universal normal control
20	PRO4400	lung tumor	universal normal control
	PRO4320	lung tumor	universal normal control
	PRO4409	lung tumor	universal normal control
	PRO4409	cervical tumor	universal normal control
	PRO4409	colon tumor	universal normal control
25	PRO4399	lung tumor	universal normal control
	PRO4399	breast tumor	universal normal control
	PRO4418	lung tumor	universal normal control
	PRO4418	breast tumor	universal normal control
	PRO4330	cervical tumor	universal normal control
30	PRO4330	colon tumor	matched normal colon control
	PRO4339	breast tumor	universal normal control
	PRO4339	colon tumor	universal normal control
	PRO4326	lung tumor	universal normal control
	PRO4326	colon tumor	universal normal control
35	PRO6014	breast tumor	universal normal control
	PRO3446	colon tumor	universal normal control
	PRO3446	lung tumor	universal normal control
	PRO4322	lung tumor	universal normal control
	PRO4322	rectal tumor	universal normal control
40	PRO4322	colon tumor	matched normal colon control
	PRO4381	breast tumor	universal normal control
	PRO4381	lung tumor	universal normal control
	PRO4381	colon tumor	universal normal control
	PRO4348	lung tumor	universal normal control
45	PRO4348	prostate tumor	universal normal control
	PRO4371	breast tumor	universal normal control
	PRO3742	colon tumor	universal normal control
	PRO3742	lung tumor	universal normal control
	PRO5773	lung tumor	universal normal control
50	PRO5773	colon tumor	universal normal control
	PRO5773	prostate tumor	universal normal control
	PRO5774	colon tumor	universal normal control
	PRO4343	colon tumor	universal normal control
	PRO4325	lung tumor	universal normal control
55	PRO4347	lung tumor	universal normal control

Table 8 (cont')

Molecule	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO4347	colon tumor	universal normal control
PRO4347	rectal tumor	universal normal control
PRO3743	colon tumor	universal normal control
5 PRO3743	lung tumor	universal normal control
PRO3743	prostate tumor	universal normal control
PRO4426	colon tumor	universal normal control
PRO4500	colon tumor	universal normal control
PRO4389	breast tumor	universal normal control
10 PRO4389	lung tumor	universal normal control
PRO4337	colon tumor	universal normal control
PRO4337	breast tumor	universal normal control
PRO4337	lung tumor	universal normal control
PRO4992	lung tumor	universal normal control
15 PRO5996	lung tumor	universal normal control
PRO4345	lung tumor	universal normal control
PRO4345	colon tumor	universal normal control
PRO5780	lung tumor	universal normal control
PRO5780	breast tumor	universal normal control
20 PRO5992	lung tumor	universal normal control
PRO5992	colon tumor	universal normal control
PRO5992	breast tumor	universal normal control
PRO4428	prostate tumor	universal normal control
PRO4994	lung tumor	universal normal control
25 PRO5995	lung tumor	universal normal control
PRO5995	colon tumor	universal normal control
PRO6094	lung tumor	universal normal control
PRO6094	colon tumor	universal normal control
PRO4317	lung tumor	universal normal control
30 PRO4317	colon tumor	universal normal control
PRO4317	liver tumor	universal normal control
PRO4317	colon tumor	matched normal colon control
PRO5997	colon tumor	universal normal control
35 PRO5997	lung tumor	universal normal control
PRO5005	lung tumor	universal normal control
PRO5005	colon tumor	universal normal control
PRO5004	colon tumor	universal normal control
PRO6001	breast tumor	universal normal control
PRO6013	colon tumor	universal normal control
40 PRO4502	lung tumor	universal normal control
PRO4502	colon tumor	universal normal control
PRO6007	breast tumor	universal normal control
PRO6028	breast tumor	universal normal control
PRO6028	colon tumor	universal normal control
45 PRO4327	prostate tumor	universal normal control
PRO4315	colon tumor	universal normal control
PRO5993	lung tumor	universal normal control
PRO5993	colon tumor	universal normal control
PRO4503	colon tumor	universal normal control
50 PRO4976	lung tumor	universal normal control
PRO5798	lung tumor	universal normal control
PRO5798	colon tumor	universal normal control
PRO6242	colon tumor	universal normal control
PRO6242	colon tumor	matched normal colon control
55 PRO6242	breast tumor	universal normal control

Table 8 (cont')

Molecule	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO6242	liver tumor	universal normal control
PRO6242	rectal tumor	universal normal control
PRO6095	breast tumor	universal normal control
5 PRO6095	lung tumor	universal normal control
PRO6093	colon tumor	universal normal control
PRO6093	breast tumor	universal normal control
PRO6093	lung tumor	universal normal control
10 PRO6093	colon tumor	matched normal colon control
PRO6012	colon tumor	universal normal control
PRO6027	lung tumor	universal normal control
PRO6027	colon tumor	universal normal control
PRO6027	rectal tumor	universal normal control
15 PRO6181	prostate tumor	universal normal control
PRO6181	lung tumor	universal normal control
PRO6181	colon tumor	universal normal control
PRO6097	colon tumor	universal normal control
PRO6097	lung tumor	universal normal control
20 PRO6090	lung tumor	universal normal control
PRO7171	lung tumor	universal normal control
PRO7171	colon tumor	universal normal control
PRO7171	breast tumor	universal normal control
PRO6258	prostate tumor	universal normal control
25 PRO6258	breast tumor	universal normal control
PRO6258	cervical tumor	universal normal control
PRO6258	liver tumor	universal normal control
PRO6258	colon tumor	universal normal control
PRO9820	prostate tumor	universal normal control
PRO6243	lung tumor	universal normal control
30 PRO6182	lung tumor	universal normal control
PRO6079	lung tumor	universal normal control
PRO6079	colon tumor	universal normal control
PRO6079	breast tumor	universal normal control
35 PRO6079	prostate tumor	universal normal control
PRO7434	lung tumor	universal normal control
PRO9865	colon tumor	universal normal control
PRO9828	colon tumor	universal normal control
PRO196	colon tumor	universal normal control
40 PRO196	lung tumor	universal normal control
PRO196	breast tumor	universal normal control
PRO197	colon tumor	universal normal control
PRO197	lung tumor	universal normal control
PRO197	breast tumor	universal normal control
45 PRO195	colon tumor	universal normal control
PRO195	lung tumor	universal normal control
PRO195	breast tumor	universal normal control
PRO187	lung tumor	universal normal control
PRO187	liver tumor	universal normal control
PRO182	colon tumor	universal normal control
50 PRO182	lung tumor	universal normal control
PRO182	breast tumor	universal normal control
PRO188	rectal tumor	universal normal control
PRO183	colon tumor	universal normal control
PRO183	lung tumor	universal normal control
55 PRO183	breast tumor	universal normal control

Table 8 (cont')

Molecule	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO183	rectal tumor	universal normal control
PRO184	lung tumor	universal normal control
PRO184	breast tumor	universal normal control
5 PRO185	lung tumor	universal normal control
PRO200	colon tumor	universal normal control
PRO200	lung tumor	universal normal control
PRO200	breast tumor	universal normal control
10 PRO200	rectal tumor	universal normal control
PRO202	colon tumor	universal normal control
PRO202	lung tumor	universal normal control
PRO202	breast tumor	universal normal control
PRO202	rectal tumor	universal normal control
15 PRO214	colon tumor	universal normal control
PRO214	lung tumor	universal normal control
PRO215	colon tumor	universal normal control
PRO215	lung tumor	universal normal control
PRO215	breast tumor	universal normal control
20 PRO219	colon tumor	universal normal control
PRO219	lung tumor	universal normal control
PRO219	breast tumor	universal normal control
PRO219	liver tumor	universal normal control
PRO211	lung tumor	universal normal control
25 PRO211	breast tumor	universal normal control
PRO220	colon tumor	universal normal control
PRO220	lung tumor	universal normal control
PRO220	breast tumor	universal normal control
PRO366	colon tumor	universal normal control
30 PRO366	lung tumor	universal normal control
PRO366	breast tumor	universal normal control
PRO216	lung tumor	universal normal control
PRO221	colon tumor	universal normal control
PRO221	lung tumor	universal normal control
35 PRO221	breast tumor	universal normal control
PRO228	lung tumor	universal normal control
PRO228	breast tumor	universal normal control
PRO217	lung tumor	universal normal control
PRO217	breast tumor	universal normal control
40 PRO222	colon tumor	universal normal control
PRO222	lung tumor	universal normal control
PRO222	breast tumor	universal normal control
PRO224	colon tumor	universal normal control
PRO224	lung tumor	universal normal control
45 PRO224	breast tumor	universal normal control
PRO224	prostate tumor	universal normal control
PRO224	rectal tumor	universal normal control
PRO230	colon tumor	universal normal control
PRO230	lung tumor	universal normal control
50 PRO230	breast tumor	universal normal control
PRO230	prostate tumor	universal normal control
PRO198	colon tumor	universal normal control
PRO198	lung tumor	universal normal control
PRO198	breast tumor	universal normal control
55 PRO198	liver tumor	universal normal control

Table 8 (cont')

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO226	lung tumor	universal normal control
PRO226	breast tumor	universal normal control
PRO261	lung tumor	universal normal control
5 PRO242	colon tumor	universal normal control
PRO242	lung tumor	universal normal control
PRO242	breast tumor	universal normal control
PRO227	colon tumor	universal normal control
10 PRO227	lung tumor	universal normal control
PRO237	colon tumor	universal normal control
PRO237	lung tumor	universal normal control
PRO237	breast tumor	universal normal control
PRO237	prostate tumor	universal normal control
15 PRO241	colon tumor	universal normal control
PRO241	lung tumor	universal normal control
PRO241	breast tumor	universal normal control
PRO231	colon tumor	universal normal control
20 PRO231	lung tumor	universal normal control
PRO231	breast tumor	universal normal control
PRO235	rectal tumor	universal normal control
PRO235	colon tumor	universal normal control
PRO235	lung tumor	universal normal control
25 PRO235	breast tumor	universal normal control
PRO323	liver tumor	universal normal control
PRO323	lung tumor	universal normal control
PRO323	breast tumor	universal normal control
PRO245	rectal tumor	universal normal control
30 PRO245	colon tumor	universal normal control
PRO245	lung tumor	universal normal control
PRO245	breast tumor	universal normal control
PRO245	cervical tumor	universal normal control
PRO246	liver tumor	universal normal control
35 PRO246	colon tumor	universal normal control
PRO246	lung tumor	universal normal control
PRO288	breast tumor	universal normal control
PRO288	lung tumor	universal normal control
PRO288	breast tumor	universal normal control
PRO248	lung tumor	universal normal control
40 PRO248	rectal tumor	universal normal control
PRO257	colon tumor	universal normal control
PRO257	lung tumor	universal normal control
PRO257	prostate tumor	universal normal control
PRO172	colon tumor	universal normal control
45 PRO172	lung tumor	universal normal control
PRO172	breast tumor	universal normal control
PRO258	colon tumor	universal normal control
PRO258	lung tumor	universal normal control
PRO258	breast tumor	universal normal control
PRO265	lung tumor	universal normal control
50 PRO265	breast tumor	universal normal control
PRO265	rectal tumor	universal normal control
PRO326	colon tumor	universal normal control
PRO326	lung tumor	universal normal control
PRO326	breast tumor	universal normal control
55 PRO326	liver tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO266	colon tumor	universal normal control
	PRO266	lung tumor	universal normal control
	PRO266	breast tumor	universal normal control
5	PRO269	lung tumor	universal normal control
	PRO269	rectal tumor	universal normal control
	PRO285	colon tumor	universal normal control
	PRO285	lung tumor	universal normal control
	PRO285	breast tumor	universal normal control
10	PRO328	colon tumor	universal normal control
	PRO328	lung tumor	universal normal control
	PRO328	breast tumor	universal normal control
	PRO344	breast tumor	universal normal control
	PRO272	lung tumor	universal normal control
15	PRO301	colon tumor	universal normal control
	PRO301	lung tumor	universal normal control
	PRO301	breast tumor	universal normal control
	PRO331	colon tumor	universal normal control
	PRO331	lung tumor	universal normal control
20	PRO331	breast tumor	universal normal control
	PRO332	colon tumor	universal normal control
	PRO332	lung tumor	universal normal control
	PRO332	breast tumor	universal normal control
	PRO353	colon tumor	universal normal control
25	PRO353	lung tumor	universal normal control
	PRO353	breast tumor	universal normal control
	PRO310	colon tumor	universal normal control
	PRO310	lung tumor	universal normal control
	PRO310	breast tumor	universal normal control
30	PRO310	rectal tumor	universal normal control
	PRO337	colon tumor	universal normal control
	PRO337	lung tumor	universal normal control
	PRO337	breast tumor	universal normal control
	PRO346	lung tumor	universal normal control
35	PRO350	lung tumor	universal normal control
	PRO350	breast tumor	universal normal control
	PRO526	colon tumor	universal normal control
	PRO526	lung tumor	universal normal control
	PRO526	breast tumor	universal normal control
40	PRO381	colon tumor	universal normal control
	PRO381	lung tumor	universal normal control
	PRO381	breast tumor	universal normal control
	PRO381	prostate tumor	universal normal control
	PRO846	colon tumor	universal normal control
45	PRO846	lung tumor	universal normal control
	PRO363	colon tumor	universal normal control
	PRO363	lung tumor	universal normal control
	PRO365	lung tumor	universal normal control
	PRO365	breast tumor	universal normal control
50	PRO1310	breast tumor	universal normal control
	PRO731	colon tumor	universal normal control
	PRO731	lung tumor	universal normal control
	PRO731	breast tumor	universal normal control
	PRO322	colon tumor	universal normal control
55	PRO322	lung tumor	universal normal control

Table 8 (cont')

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO322	breast tumor	universal normal control
PRO322	rectal tumor	universal normal control
PRO322	liver tumor	universal normal control
5 PRO536	lung tumor	universal normal control
PRO536	breast tumor	universal normal control
PRO536	liver tumor	universal normal control
PRO719	colon tumor	universal normal control
PRO719	lung tumor	universal normal control
10 PRO719	breast tumor	universal normal control
PRO619	colon tumor	universal normal control
PRO619	lung tumor	universal normal control
PRO619	breast tumor	universal normal control
PRO771	colon tumor	universal normal control
15 PRO771	lung tumor	universal normal control
PRO771	breast tumor	universal normal control
PRO1083	colon tumor	universal normal control
PRO1083	lung tumor	universal normal control
PRO1083	breast tumor	universal normal control
20 PRO1083	prostate tumor	universal normal control
PRO862	colon tumor	universal normal control
PRO862	lung tumor	universal normal control
PRO862	breast tumor	universal normal control
PRO733	colon tumor	universal normal control
25 PRO733	lung tumor	universal normal control
PRO733	breast tumor	universal normal control
PRO733	liver tumor	universal normal control
PRO1188	lung tumor	universal normal control
PRO1188	breast tumor	universal normal control
30 PRO1188	rectal tumor	universal normal control
PRO770	lung tumor	universal normal control
PRO770	breast tumor	universal normal control
PRO1080	colon tumor	universal normal control
PRO1080	lung tumor	universal normal control
35 PRO1080	breast tumor	universal normal control
PRO1017	colon tumor	universal normal control
PRO1017	lung tumor	universal normal control
PRO1017	breast tumor	universal normal control
40 PRO1016	colon tumor	universal normal control
PRO1016	lung tumor	universal normal control
PRO1016	breast tumor	universal normal control
PRO1016	rectal tumor	universal normal control
PRO792	lung tumor	universal normal control
45 PRO938	colon tumor	universal normal control
PRO938	lung tumor	universal normal control
PRO938	breast tumor	universal normal control
PRO1012	colon tumor	universal normal control
PRO1012	lung tumor	universal normal control
50 PRO1012	rectal tumor	universal normal control
PRO1012	liver tumor	universal normal control
PRO1008	lung tumor	universal normal control
PRO1075	colon tumor	universal normal control
PRO1075	lung tumor	universal normal control
PRO1007	colon tumor	universal normal control
55 PRO1007	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1007	breast tumor	universal normal control
	PRO1007	rectal tumor	universal normal control
	PRO1056	colon tumor	universal normal control
5	PRO1056	lung tumor	universal normal control
	PRO1056	breast tumor	universal normal control
	PRO791	colon tumor	universal normal control
	PRO791	lung tumor	universal normal control
	PRO791	breast tumor	universal normal control
10	PRO791	rectal tumor	universal normal control
	PRO1111	colon tumor	universal normal control
	PRO1111	lung tumor	universal normal control
	PRO1111	breast tumor	universal normal control
	PRO812	lung tumor	universal normal control
15	PRO812	breast tumor	universal normal control
	PRO812	rectal tumor	universal normal control
	PRO1066	lung tumor	universal normal control
	PRO1185	colon tumor	universal normal control
	PRO1185	lung tumor	universal normal control
20	PRO1185	breast tumor	universal normal control
	PRO1031	lung tumor	universal normal control
	PRO1360	lung tumor	universal normal control
	PRO1360	breast tumor	universal normal control
	PRO1309	lung tumor	universal normal control
25	PRO1309	breast tumor	universal normal control
	PRO1107	lung tumor	universal normal control
	PRO1107	breast tumor	universal normal control
	PRO836	colon tumor	universal normal control
	PRO836	lung tumor	universal normal control
30	PRO1132	lung tumor	universal normal control
	PRO1132	breast tumor	universal normal control
	PRO1131	colon tumor	universal normal control
	PRO1131	lung tumor	universal normal control
	PRO1131	breast tumor	universal normal control
35	PRO1131	liver tumor	universal normal control
	PRO1130	colon tumor	universal normal control
	PRO1130	lung tumor	universal normal control
	PRO1130	breast tumor	universal normal control
	PRO844	colon tumor	universal normal control
40	PRO844	lung tumor	universal normal control
	PRO844	breast tumor	universal normal control
	PRO844	rectal tumor	universal normal control
	PRO1154	colon tumor	universal normal control
	PRO1154	lung tumor	universal normal control
45	PRO1154	rectal tumor	universal normal control
	PRO1154	liver tumor	universal normal control
	PRO1181	lung tumor	universal normal control
	PRO1181	breast tumor	universal normal control
	PRO1126	colon tumor	universal normal control
50	PRO1126	lung tumor	universal normal control
	PRO1126	breast tumor	universal normal control
	PRO1126	adrenal tumor	universal normal control
	PRO1186	colon tumor	universal normal control
	PRO1186	lung tumor	universal normal control
55	PRO1186	breast tumor	universal normal control

Table 8 (cont')

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO1186	liver tumor	universal normal control
PRO1198	colon tumor	universal normal control
PRO1198	lung tumor	universal normal control
5 PRO1159	lung tumor	universal normal control
PRO1159	breast tumor	universal normal control
PRO1159	liver tumor	universal normal control
10 PRO1265	colon tumor	universal normal control
PRO1265	breast tumor	universal normal control
PRO1250	colon tumor	universal normal control
PRO1250	lung tumor	universal normal control
PRO1250	breast tumor	universal normal control
PRO1475	colon tumor	universal normal control
15 PRO1475	breast tumor	universal normal control
PRO1312	colon tumor	universal normal control
PRO1312	lung tumor	universal normal control
PRO1312	breast tumor	universal normal control
PRO1308	colon tumor	universal normal control
20 PRO1308	lung tumor	universal normal control
PRO1308	liver tumor	universal normal control
PRO1326	colon tumor	universal normal control
PRO1325	lung tumor	universal normal control
PRO1326	breast tumor	universal normal control
PRO1192	colon tumor	universal normal control
25 PRO1192	lung tumor	universal normal control
PRO1192	breast tumor	universal normal control
PRO1246	colon tumor	universal normal control
PRO1246	lung tumor	universal normal control
30 PRO1246	breast tumor	universal normal control
PRO1246	prostate tumor	universal normal control
PRO1356	colon tumor	universal normal control
PRO1356	lung tumor	universal normal control
PRO1356	breast tumor	universal normal control
35 PRO1275	lung tumor	universal normal control
PRO1275	breast tumor	universal normal control
PRO1274	lung tumor	universal normal control
PRO1358	colon tumor	universal normal control
PRO1358	lung tumor	universal normal control
40 PRO1358	prostate tumor	universal normal control
PRO1286	colon tumor	universal normal control
PRO1286	lung tumor	universal normal control
PRO1286	prostate tumor	universal normal control
PRO1286	rectal tumor	universal normal control
45 PRO1294	colon tumor	universal normal control
PRO1294	lung tumor	universal normal control
PRO1294	breast tumor	universal normal control
PRO1294	rectal tumor	universal normal control
PRO1273	lung tumor	universal normal control
50 PRO1273	rectal tumor	universal normal control
PRO1279	colon tumor	universal normal control
PRO1279	lung tumor	universal normal control
PRO1195	lung tumor	universal normal control
PRO1195	breast tumor	universal normal control
55 PRO1271	lung tumor	universal normal control
PRO1271	breast tumor	universal normal control

Table 8 (cont')

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO1271	liver tumor	universal normal control
PRO1338	colon tumor	universal normal control
5 PRO1338	lung tumor	universal normal control
PRO1338	breast tumor	universal normal control
PRO1343	colon tumor	universal normal control
PRO1343	lung tumor	universal normal control
PRO1343	breast tumor	universal normal control
10 PRO1343	rectal tumor	universal normal control
PRO1434	lung tumor	universal normal control
PRO1418	lung tumor	universal normal control
PRO1418	liver tumor	universal normal control
PRO1387	colon tumor	universal normal control
15 PRO1387	lung tumor	universal normal control
PRO1387	prostate tumor	universal normal control
PRO1387	rectal tumor	universal normal control
PRO1384	colon tumor	universal normal control
PRO1384	lung tumor	universal normal control
20 PRO1565	colon tumor	universal normal control
PRO1565	lung tumor	universal normal control
PRO1565	prostate tumor	universal normal control
PRO1474	colon tumor	universal normal control
PRO1474	lung tumor	universal normal control
25 PRO1474	breast tumor	universal normal control
PRO1474	rectal tumor	universal normal control
PRO1917	colon tumor	universal normal control
PRO1917	lung tumor	universal normal control
PRO1917	breast tumor	universal normal control
PRO1787	colon tumor	universal normal control
30 PRO1787	lung tumor	universal normal control
PRO1787	breast tumor	universal normal control
PRO1556	lung tumor	universal normal control
PRO1556	breast tumor	universal normal control
35 PRO1561	colon tumor	universal normal control
PRO1561	lung tumor	universal normal control
PRO1561	rectal tumor	universal normal control
PRO1693	colon tumor	universal normal control
PRO1693	lung tumor	universal normal control
40 PRO1693	breast tumor	universal normal control
PRO1868	lung tumor	universal normal control
PRO1868	breast tumor	universal normal control
PRO1890	colon tumor	universal normal control
PRO1890	lung tumor	universal normal control
45 PRO1890	breast tumor	universal normal control
PRO1890	prostate tumor	universal normal control
PRO1887	colon tumor	universal normal control
PRO1887	breast tumor	universal normal control
PRO4353	lung tumor	universal normal control
50 PRO4353	breast tumor	universal normal control
PRO4353	colon tumor	universal normal control
PRO1801	lung tumor	universal normal control
PRO1801	breast tumor	universal normal control
PRO4357	colon tumor	universal normal control
PRO4357	lung tumor	universal normal control
PRO4302	breast tumor	universal normal control
55 PRO4302	colon tumor	universal normal control
PRO4302	lung tumor	universal normal control

Table 8 (cont')

<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
PRO4302	breast tumor	universal normal control
PRO4302	prostate tumor	universal normal control
PRO5990	colon tumor	universal normal control
5 PRO5990	lung tumor	universal normal control
PRO5990	breast tumor	universal normal control

EXAMPLE 31: Identification of Receptor/Ligand Interactions

In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor or ligand molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise 10 cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a 15 biological or immunological activity of a cell expressing the receptor or ligand, and various other indications 20 which will be readily apparent to the ordinarily skilled artisan.

The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound 25 immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible 30 receptor binding. The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding 35 a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is "broken down") to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine "His" tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have

been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel of potential receptors.

5 Using these assays, the following receptor/ligand interactions have been herein identified:

- (1) PRO1801 binds to PRO1114 and PRO4978.
- (2) PRO100 binds to PRO1114.

10 The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

PCT

P3330R1

Original (for SUBMISSION) - printed on 01.12.2000 02:57:35 PM

0-1	Form - PCT/RO/134 (EASY) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis)	
0-1-1	Prepared using	<b>PCT-EASY Version 2.91 (updated 10.10.2000)</b>
0-2	International Application No.	
0-3	Applicant's or agent's file reference	<b>P3330R1</b>
1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	page	<b>98</b>
1-2	line	<b>34</b>
1-3	Identification of Deposit Name of depositary institution	<b>American Type Culture Collection</b>
1-3-1	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
1-3-3	Date of deposit	<b>14 April 1998 (14.04.1998)</b>
1-3-4	Accession Number	<b>ATCC 209771</b>
1-4	Additional Indications	<b>NONE</b>
1-5	Designated States for Which Indications are Made	<b>all designated States</b>
1-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
2	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
2-1	page	<b>98</b>
2-2	line	<b>35</b>
2-3	Identification of Deposit Name of depositary institution	<b>American Type Culture Collection</b>
2-3-1	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
2-3-3	Date of deposit	<b>09 February 1999 (09.02.1999)</b>
2-3-4	Accession Number	<b>ATCC 203654</b>
2-4	Additional Indications	<b>NONE</b>
2-5	Designated States for Which Indications are Made	<b>all designated States</b>
2-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
3	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
3-1	page	<b>98</b>
3-2	line	<b>36</b>

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3-3	<b>Identification of Deposit</b>	
3-3-1	Name of depositary institution	
3-3-2	Address of depositary institution	
3-3-3	Date of deposit	
3-3-4	Accession Number	
3-4	<b>Additional Indications</b>	
3-5	<b>Designated States for Which Indications are Made</b>	
3-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	
4	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
4-1	page	98
4-2	line	37
4-3	<b>Identification of Deposit</b>	
4-3-1	Name of depositary institution	
4-3-2	Address of depositary institution	
4-3-3	Date of deposit	
4-3-4	Accession Number	
4-4	<b>Additional Indications</b>	
4-5	<b>Designated States for Which Indications are Made</b>	
4-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	
5	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
5-1	page	98
5-2	line	38
5-3	<b>Identification of Deposit</b>	
5-3-1	Name of depositary institution	
5-3-2	Address of depositary institution	
5-3-3	Date of deposit	
5-3-4	Accession Number	
5-4	<b>Additional Indications</b>	
5-5	<b>Designated States for Which Indications are Made</b>	
5-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	

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<b>6</b> The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
6-1 page	98	
6-2 line	39	
6-3 Identification of Deposit		
6-3-1 Name of depositary institution	American Type Culture Collection	
6-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
6-3-3 Date of deposit	10 December 1997 (10.12.1997)	
6-3-4 Accession Number	ATCC 209525	
6-4 Additional Indications	NONE	
6-5 Designated States for Which Indications are Made	all designated States	
6-6 Separate Furnishing of Indications	NONE	
These indications will be submitted to the International Bureau later		
<b>7</b> The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
7-1 page	99	
7-2 line	2	
7-3 Identification of Deposit		
7-3-1 Name of depositary institution	American Type Culture Collection	
7-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
7-3-3 Date of deposit	12 January 1999 (12.01.1999)	
7-3-4 Accession Number	ATCC 203577	
7-4 Additional Indications	NONE	
7-5 Designated States for Which Indications are Made	all designated States	
7-6 Separate Furnishing of Indications	NONE	
These indications will be submitted to the International Bureau later		
<b>8</b> The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
8-1 page	99	
8-2 line	3	
8-3 Identification of Deposit		
8-3-1 Name of depositary institution	American Type Culture Collection	
8-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
8-3-3 Date of deposit	27 July 1999 (27.07.1999)	
8-3-4 Accession Number	ATCC PTA-430	
8-4 Additional Indications	NONE	
8-5 Designated States for Which Indications are Made	all designated States	

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8-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
9	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
9-1	page	99
9-2	line	4
9-3	Identification of Deposit	
9-3-1	Name of depositary institution	American Type Culture Collection
9-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
9-3-3	Date of deposit	08 June 1999 (08.06.1999)
9-3-4	Accession Number	ATCC PTA-203
9-4	Additional Indications	NONE
9-5	Designated States for Which Indications are Made	all designated States
9-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
10	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
10-1	page	99
10-2	line	5
10-3	Identification of Deposit	
10-3-1	Name of depositary institution	American Type Culture Collection
10-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
10-3-3	Date of deposit	01 July 1998 (01.07.1998)
10-3-4	Accession Number	ATCC 203040
10-4	Additional Indications	NONE
10-5	Designated States for Which Indications are Made	all designated States
10-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
11	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
11-1	page	99
11-2	line	6
11-3	Identification of Deposit	
11-3-1	Name of depositary institution	American Type Culture Collection
11-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
11-3-3	Date of deposit	31 August 1999 (31.08.1999)
11-3-4	Accession Number	ATCC PTA-611

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11-4	Additional Indications	<b>NONE</b>
11-5	Designated States for Which Indications are Made	<b>all designated States</b>
11-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
12	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
12-1	page	99
12-2	line	7
12-3	Identification of Deposit	
12-3-1	Name of depositary institution	American Type Culture Collection
12-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
12-3-3	Date of deposit	21 January 1998 (21.01.1998)
12-3-4	Accession Number	ATCC 209593
12-4	Additional Indications	<b>NONE</b>
12-5	Designated States for Which Indications are Made	<b>all designated States</b>
12-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
13	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
13-1	page	99
13-2	line	8
13-3	Identification of Deposit	
13-3-1	Name of depositary institution	American Type Culture Collection
13-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
13-3-3	Date of deposit	09 February 1999 (09.02.1999)
13-3-4	Accession Number	ATCC 203649
13-4	Additional Indications	<b>NONE</b>
13-5	Designated States for Which Indications are Made	<b>all designated States</b>
13-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
14	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
14-1	page	99
14-2	line	9

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14-3	<b>Identification of Deposit</b>		
14-3-1	Name of depositary institution		American Type Culture Collection
14-3-2	Address of depositary institution		10801 University Blvd., Manassas, Virginia 20110-2209United States of America
14-3-3	Date of deposit	12 January 1999 (12.01.1999)	
14-3-4	Accession Number	ATCC 203574	
14-4	<b>Additional Indications</b>		NONE
14-5	<b>Designated States for Which Indications are Made</b>		all designated States
14-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later		NONE
15	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
15-1	page	99	
15-2	line	10	
15-3	<b>Identification of Deposit</b>		
15-3-1	Name of depositary institution		American Type Culture Collection
15-3-2	Address of depositary institution		10801 University Blvd., Manassas, Virginia 20110-2209United States of America
15-3-3	Date of deposit	25 May 1999 (25.05.1999)	
15-3-4	Accession Number	ATCC PTA-129	
15-4	<b>Additional Indications</b>		NONE
15-5	<b>Designated States for Which Indications are Made</b>		all designated States
15-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later		NONE
16	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
16-1	page	99	
16-2	line	11	
16-3	<b>Identification of Deposit</b>		
16-3-1	Name of depositary institution		American Type Culture Collection
16-3-2	Address of depositary institution		10801 University Blvd., Manassas, Virginia 20110-2209United States of America
16-3-3	Date of deposit	27 May 1998 (27.05.1998)	
16-3-4	Accession Number	ATCC 209905	
16-4	<b>Additional Indications</b>		NONE
16-5	<b>Designated States for Which Indications are Made</b>		all designated States
16-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later		NONE

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<b>17</b> The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
17-1 page	99	
17-2 line	12	
<b>17-3 Identification of Deposit</b>		
17-3-1 Name of depositary institution	American Type Culture Collection	
17-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
<b>17-3-3 Date of deposit</b>	12 January 1999 (12.01.1999)	
17-3-4 Accession Number	ATCC 203585	
<b>17-4 Additional Indications</b>	NONE	
<b>17-5 Designated States for Which Indications are Made</b>	all designated States	
<b>17-6 Separate Furnishing of Indications</b>	NONE	
These indications will be submitted to the International Bureau later		
<b>18</b> The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
18-1 page	99	
18-2 line	13	
<b>18-3 Identification of Deposit</b>		
18-3-1 Name of depositary institution	American Type Culture Collection	
18-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
<b>18-3-3 Date of deposit</b>	09 February 1999 (09.02.1999)	
18-3-4 Accession Number	ATCC 203665	
<b>18-4 Additional Indications</b>	NONE	
<b>18-5 Designated States for Which Indications are Made</b>	all designated States	
<b>18-6 Separate Furnishing of Indications</b>	NONE	
These indications will be submitted to the International Bureau later		
<b>19</b> The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
19-1 page	99	
19-2 line	14	
<b>19-3 Identification of Deposit</b>		
19-3-1 Name of depositary institution	American Type Culture Collection	
19-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
<b>19-3-3 Date of deposit</b>	27 July 1999 (27.07.1999)	
19-3-4 Accession Number	ATCC PTA-427	
<b>19-4 Additional Indications</b>	NONE	
<b>19-5 Designated States for Which Indications are Made</b>	all designated States	

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19-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
20	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
20-1	page	99
20-2	line	15
20-3	Identification of Deposit	
20-3-1	Name of depositary institution	American Type Culture Collection
20-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
20-3-3	Date of deposit	31 August 1999 (31.08.1999)
20-3-4	Accession Number	ATCC PTA-615
20-4	Additional Indications	NONE
20-5	Designated States for Which Indications are Made	all designated States
20-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
21	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
21-1	page	99
21-2	line	16
21-3	Identification of Deposit	
21-3-1	Name of depositary institution	American Type Culture Collection
21-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
21-3-3	Date of deposit	12 January 1999 (12.01.1999)
21-3-4	Accession Number	ATCC 203582
21-4	Additional Indications	NONE
21-5	Designated States for Which Indications are Made	all designated States
21-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
22	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
22-1	page	99
22-2	line	17
22-3	Identification of Deposit	
22-3-1	Name of depositary institution	American Type Culture Collection
22-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
22-3-3	Date of deposit	09 March 1999 (09.03.1999)
22-3-4	Accession Number	ATCC 203838

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22-4	Additional Indications	NONE
22-5	Designated States for Which Indications are Made	all designated States
22-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
23	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
23-1	page	99
23-2	line	18
23-3	Identification of Deposit	
23-3-1	Name of depositary institution	American Type Culture Collection
23-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
23-3-3	Date of deposit	27 July 1999 (27.07.1999)
23-3-4	Accession Number	ATCC PTA-428
23-4	Additional Indications	NONE
23-5	Designated States for Which Indications are Made	all designated States
23-6	Separate Furnishing of Indications.  These indications will be submitted to the International Bureau later	NONE
24	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
24-1	page	99
24-2	line	19
24-3	Identification of Deposit	
24-3-1	Name of depositary institution	American Type Culture Collection
24-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
24-3-3	Date of deposit	09 March 1999 (09.03.1999)
24-3-4	Accession Number	ATCC 203836
24-4	Additional Indications	NONE
24-5	Designated States for Which Indications are Made	all designated States
24-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
25	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
25-1	page	99
25-2	line	20

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25-3	<b>Identification of Deposit</b>	
25-3-1	Name of depositary institution	
25-3-2	Address of depositary institution	
25-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America 08 June 1999 (08.06.1999)
25-3-4	Accession Number	ATCC PTA-205
25-4	<b>Additional Indications</b>	
25-5	<b>Designated States for Which Indications are Made</b>	
25-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	
26	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
26-1	page	99
26-2	line	21
26-3	<b>Identification of Deposit</b>	
26-3-1	Name of depositary institution	
26-3-2	Address of depositary institution	
26-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America 27 July 1999 (27.07.1999)
26-3-4	Accession Number	ATCC PTA-431
26-4	<b>Additional Indications</b>	
26-5	<b>Designated States for Which Indications are Made</b>	
26-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	
27	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
27-1	page	99
27-2	line	22
27-3	<b>Identification of Deposit</b>	
27-3-1	Name of depositary institution	
27-3-2	Address of depositary institution	
27-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America 09 February 1999 (09.02.1999)
27-3-4	Accession Number	ATCC 203659
27-4	<b>Additional Indications</b>	
27-5	<b>Designated States for Which Indications are Made</b>	
27-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	

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28	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
28-1	page	99
28-2	line	23
28-3	Identification of Deposit Name of depositary institution Address of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
28-3-3	Date of deposit	12 January 1999 (12.01.1999)
28-3-4	Accession Number	ATCC 203584
28-4	Additional Indications	NONE
28-5	Designated States for Which Indications are Made	all designated States
28-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
29	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
29-1	page	99
29-2	line	24
29-3	Identification of Deposit Name of depositary institution Address of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
29-3-3	Date of deposit	25 May 1999 (25.05.1999)
29-3-4	Accession Number	ATCC PTA-126
29-4	Additional Indications	NONE
29-5	Designated States for Which Indications are Made	all designated States
29-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
30	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
30-1	page	99
30-2	line	25
30-3	Identification of Deposit Name of depositary institution Address of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
30-3-3	Date of deposit	25 May 1999 (25.05.1999)
30-3-4	Accession Number	ATCC PTA-128
30-4	Additional Indications	NONE
30-5	Designated States for Which Indications are Made	all designated States

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30-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
31	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
31-1	page	99
31-2	line	26
31-3	Identification of Deposit	
31-3-1	Name of depositary institution	American Type Culture Collection
31-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
31-3-3	Date of deposit	09 February 1999 (09.02.1999)
31-3-4	Accession Number	ATCC 203664
31-4	Additional Indications	NONE
31-5	Designated States for Which Indications are Made	all designated States
31-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
32	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
32-1	page	99
32-2	line	27
32-3	Identification of Deposit	
32-3-1	Name of depositary institution	American Type Culture Collection
32-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
32-3-3	Date of deposit	12 January 1999 (12.01.1999)
32-3-4	Accession Number	ATCC 203578
32-4	Additional Indications	NONE
32-5	Designated States for Which Indications are Made	all designated States
32-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
33	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
33-1	page	99
33-2	line	28
33-3	Identification of Deposit	
33-3-1	Name of depositary institution	American Type Culture Collection
33-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
33-3-3	Date of deposit	22 December 1998 (22.12.1998)
33-3-4	Accession Number	ATCC 203554

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33-4	Additional Indications	NONE
33-5	Designated States for Which Indications are Made	all designated States
33-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
34	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
34-1	page	99
34-2	line	29
34-3	Identification of Deposit	
34-3-1	Name of depositary institution	American Type Culture Collection
34-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
34-3-3	Date of deposit	16 March 1999 (16.03.1999)
34-3-4	Accession Number	ATCC 203850
34-4	Additional Indications	NONE
34-5	Designated States for Which Indications are Made	all designated States
34-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
35	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
35-1	page	99
35-2	line	30
35-3	Identification of Deposit	
35-3-1	Name of depositary institution	American Type Culture Collection
35-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
35-3-3	Date of deposit	11 May 1999 (11.05.1999)
35-3-4	Accession Number	ATCC PTA-45
35-4	Additional Indications	NONE
35-5	Designated States for Which Indications are Made	all designated States
35-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
36	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
36-1	page	99
36-2	line	31

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36-3	<b>Identification of Deposit</b>	
36-3-1	Name of depository institution	<b>American Type Culture Collection</b>
36-3-2	Address of depository institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
36-3-3	Date of deposit	<b>22 December 1998 (22.12.1998)</b>
36-3-4	Accession Number	<b>ATCC 203545</b>
36-4	<b>Additional Indications</b>	<b>NONE</b>
36-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
36-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	<b>NONE</b>
37	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
37-1	page	<b>99</b>
37-2	line	<b>32</b>
37-3	<b>Identification of Deposit</b>	
37-3-1	Name of depository institution	<b>American Type Culture Collection</b>
37-3-2	Address of depository institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
37-3-3	Date of deposit	<b>22 December 1998 (22.12.1998)</b>
37-3-4	Accession Number	<b>ATCC 203544</b>
37-4	<b>Additional Indications</b>	<b>NONE</b>
37-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
37-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	<b>NONE</b>
38	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
38-1	page	<b>99</b>
38-2	line	<b>33</b>
38-3	<b>Identification of Deposit</b>	
38-3-1	Name of depository institution	<b>American Type Culture Collection</b>
38-3-2	Address of depository institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
38-3-3	Date of deposit	<b>15 June 1999 (15.06.1999)</b>
38-3-4	Accession Number	<b>ATCC PTA-234</b>
38-4	<b>Additional Indications</b>	<b>NONE</b>
38-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
38-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	<b>NONE</b>

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39	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
39-1	page	99
39-2	line	34
39-3	Identification of Deposit	
39-3-1	Name of depositary institution	American Type Culture Collection
39-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
39-3-3	Date of deposit	16 March 1999 (16.03.1999)
39-3-4	Accession Number	ATCC 203848
39-4	Additional Indications	NONE
39-5	Designated States for Which Indications are Made	all designated States
39-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
40	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
40-1	page	99
40-2	line	35
40-3	Identification of Deposit	
40-3-1	Name of depositary institution	American Type Culture Collection
40-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
40-3-3	Date of deposit	22 December 1998 (22.12.1998)
40-3-4	Accession Number	ATCC 203555
40-4	Additional Indications	NONE
40-5	Designated States for Which Indications are Made	all designated States
40-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
41	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
41-1	page	99
41-2	line	36
41-3	Identification of Deposit	
41-3-1	Name of depositary institution	American Type Culture Collection
41-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
41-3-3	Date of deposit	20 April 1999 (20.04.1999)
41-3-4	Accession Number	ATCC 203949
41-4	Additional Indications	NONE
41-5	Designated States for Which Indications are Made	all designated States

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41-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
42	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
42-1	page	99
42-2	line	37
42-3	Identification of Deposit	
42-3-1	Name of depositary institution	American Type Culture Collection
42-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
42-3-3	Date of deposit	15 December 1998 (15.12.1998)
42-3-4	Accession Number	ATCC 203539
42-4	Additional Indications	NONE
42-5	Designated States for Which Indications are Made	all designated States
42-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
43	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
43-1	page	99
43-2	line	38
43-3	Identification of Deposit	
43-3-1	Name of depositary institution	American Type Culture Collection
43-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
43-3-3	Date of deposit	23 March 1999 (23.03.1999)
43-3-4	Accession Number	ATCC 203871
43-4	Additional Indications	NONE
43-5	Designated States for Which Indications are Made	all designated States
43-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
44	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
44-1	page	99
44-2	line	39
44-3	Identification of Deposit	
44-3-1	Name of depositary institution	American Type Culture Collection
44-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
44-3-3	Date of deposit	23 March 1999 (23.03.1999)
44-3-4	Accession Number	ATCC 203862

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44-4	Additional Indications	NONE
44-5	Designated States for Which Indications are Made	all designated States
44-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
45	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
45-1	page	99
45-2	line	40
45-3	Identification of Deposit Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
45-3-2	Address of depositary institution	
45-3-3	Date of deposit	10 August 1999 (10.08.1999)
45-3-4	Accession Number	ATCC PTA-510
45-4	Additional Indications	NONE
45-5	Designated States for Which Indications are Made	all designated States
45-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
46	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
46-1	page	99
46-2	line	41
46-3	Identification of Deposit Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
46-3-2	Address of depositary institution	
46-3-3	Date of deposit	20 January 1999 (20.01.1999)
46-3-4	Accession Number	ATCC 203603
46-4	Additional Indications	NONE
46-5	Designated States for Which Indications are Made	all designated States
46-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
47	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
47-1	page	99
47-2	line	42

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47-3	<b>Identification of Deposit</b>	
47-3-1	Name of depositary institution	
47-3-2	Address of depositary institution	
47-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
47-3-4	Accession Number	02 March 1999 (02.03.1999) ATCC 203813
47-4	<b>Additional Indications</b>	
47-5	<b>Designated States for Which Indications are Made</b>	
47-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	
48	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
48-1	page	99
48-2	line	43
48-3	<b>Identification of Deposit</b>	
48-3-1	Name of depositary institution	
48-3-2	Address of depositary institution	
48-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
48-3-4	Accession Number	02 March 1999 (02.03.1999) ATCC 203812
48-4	<b>Additional Indications</b>	
48-5	<b>Designated States for Which Indications are Made</b>	
48-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	
49	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
49-1	page	99
49-2	line	44
49-3	<b>Identification of Deposit</b>	
49-3-1	Name of depositary institution	
49-3-2	Address of depositary institution	
49-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
49-3-4	Accession Number	29 October 1998 (29.10.1998) ATCC 203391
49-4	<b>Additional Indications</b>	
49-5	<b>Designated States for Which Indications are Made</b>	
49-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	

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<b>50</b>	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
50-1 page		99
50-2 line		45
<b>50-3</b>	<b>Identification of Deposit</b>	
50-3-1	Name of depositary institution	American Type Culture Collection
50-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
<b>50-3-3</b>	Date of deposit	27 April 1999 (27.04.1999)
50-3-4	Accession Number	ATCC 203965
<b>50-4</b>	<b>Additional Indications</b>	NONE
<b>50-5</b>	<b>Designated States for Which Indications are Made</b>	all designated States
<b>50-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
<b>51</b>	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
51-1 page		99
51-2 line		46
<b>51-3</b>	<b>Identification of Deposit</b>	
51-3-1	Name of depositary institution	American Type Culture Collection
51-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
51-3-3	Date of deposit	02 March 1999 (02.03.1999)
51-3-4	Accession Number	ATCC 203816
<b>51-4</b>	<b>Additional Indications</b>	NONE
<b>51-5</b>	<b>Designated States for Which Indications are Made</b>	all designated States
<b>51-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
<b>52</b>	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
52-1 page		99
52-2 line		47
<b>52-3</b>	<b>Identification of Deposit</b>	
52-3-1	Name of depositary institution	American Type Culture Collection
52-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
52-3-3	Date of deposit	02 March 1999 (02.03.1999)
52-3-4	Accession Number	ATCC 203814
<b>52-4</b>	<b>Additional Indications</b>	NONE
<b>52-5</b>	<b>Designated States for Which Indications are Made</b>	all designated States

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52-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
53	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
53-1	page	99
53-2	line	48
53-3	<b>Identification of Deposit</b>	
53-3-1	Name of depositary institution	American Type Culture Collection
53-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
53-3-3	Date of deposit	02 March 1999 (02.03.1999)
53-3-4	Accession Number	ATCC 203810
53-4	<b>Additional Indications</b>	<b>NONE</b>
53-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
53-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
54	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
54-1	page	99
54-2	line	49
54-3	<b>Identification of Deposit</b>	
54-3-1	Name of depositary institution	American Type Culture Collection
54-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
54-3-3	Date of deposit	04 May 1999 (04.05.1999)
54-3-4	Accession Number	ATCC PTA-22
54-4	<b>Additional Indications</b>	<b>NONE</b>
54-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
54-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
55	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
55-1	page	99
55-2	line	50
55-3	<b>Identification of Deposit</b>	
55-3-1	Name of depositary institution	American Type Culture Collection
55-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
55-3-3	Date of deposit	12 January 1999 (12.01.1999)
55-3-4	Accession Number	ATCC 203580

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55-4	Additional Indications	NONE
55-5	Designated States for Which Indications are Made	all designated States
55-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
56	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
56-1	page	99
56-2	line	51
56-3	Identification of Deposit	
56-3-1	Name of depositary institution	American Type Culture Collection
56-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
56-3-3	Date of deposit	30 March 1999 (30.03.1999)
56-3-4	Accession Number	ATCC 203889
56-4	Additional Indications	NONE
56-5	Designated States for Which Indications are Made	all designated States
56-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
57	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
57-1	page	99
57-2	line	52
57-3	Identification of Deposit	
57-3-1	Name of depositary institution	American Type Culture Collection
57-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
57-3-3	Date of deposit	27 April 1999 (27.04.1999)
57-3-4	Accession Number	ATCC 203964
57-4	Additional Indications	NONE
57-5	Designated States for Which Indications are Made	all designated States
57-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
58	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
58-1	page	99
58-2	line	53

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58-3	<b>Identification of Deposit</b>	
58-3-1	Name of depositary institution	
58-3-2	Address of depositary institution	
58-3-3	Date of deposit	
58-3-4	Accession Number	
58-4	<b>Additional Indications</b>	
58-5	<b>Designated States for Which Indications are Made</b>	
58-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	
59	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
59-1	page	99
59-2	line	54
59-3	<b>Identification of Deposit</b>	
59-3-1	Name of depositary institution	
59-3-2	Address of depositary institution	
59-3-3	Date of deposit	
59-3-4	Accession Number	
59-4	<b>Additional Indications</b>	
59-5	<b>Designated States for Which Indications are Made</b>	
59-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	
60	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
60-1	page	99
60-2	line	55
60-3	<b>Identification of Deposit</b>	
60-3-1	Name of depositary institution	
60-3-2	Address of depositary institution	
60-3-3	Date of deposit	
60-3-4	Accession Number	
60-4	<b>Additional Indications</b>	
60-5	<b>Designated States for Which Indications are Made</b>	
60-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	

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<b>61</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
61-1	page	100
61-2	line	2
<b>61-3</b>	<b>Identification of Deposit</b>	
61-3-1	Name of depositary institution	American Type Culture Collection
61-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
<b>61-3-3</b>	<b>Date of deposit</b>	27 April 1999 (27.04.1999)
61-3-4	Accession Number	ATCC 203968
<b>61-4</b>	<b>Additional Indications</b>	NONE
<b>61-5</b>	<b>Designated States for Which Indications are Made</b>	all designated States
<b>61-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
<b>62</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
62-1	page	100
62-2	line	3
<b>62-3</b>	<b>Identification of Deposit</b>	
62-3-1	Name of depositary institution	American Type Culture Collection
62-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
<b>62-3-3</b>	<b>Date of deposit</b>	30 March 1999 (30.03.1999)
62-3-4	Accession Number	ATCC 203894
<b>62-4</b>	<b>Additional Indications</b>	NONE
<b>62-5</b>	<b>Designated States for Which Indications are Made</b>	all designated States
<b>62-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
<b>63</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
63-1	page	100
63-2	line	4
<b>63-3</b>	<b>Identification of Deposit</b>	
63-3-1	Name of depositary institution	American Type Culture Collection
63-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
<b>63-3-3</b>	<b>Date of deposit</b>	30 March 1999 (30.03.1999)
63-3-4	Accession Number	ATCC 203893
<b>63-4</b>	<b>Additional Indications</b>	NONE
<b>63-5</b>	<b>Designated States for Which Indications are Made</b>	all designated States

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<b>63-6</b>	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
<b>64</b>	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
64-1	page	100
64-2	line	5
<b>64-3</b>	<b>Identification of Deposit</b>	
64-3-1	Name of depositary institution	American Type Culture Collection
64-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
64-3-3	Date of deposit	02 March 1999 (02.03.1999)
64-3-4	Accession Number	ATCC 203811
<b>64-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>64-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>64-6</b>	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
<b>65</b>	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
65-1	page	100
65-2	line	6
<b>65-3</b>	<b>Identification of Deposit</b>	
65-3-1	Name of depositary institution	American Type Culture Collection
65-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
65-3-3	Date of deposit	23 March 1999 (23.03.1999)
65-3-4	Accession Number	ATCC 203867
<b>65-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>65-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>65-6</b>	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
<b>66</b>	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
66-1	page	100
66-2	line	7
<b>66-3</b>	<b>Identification of Deposit</b>	
66-3-1	Name of depositary institution	American Type Culture Collection
66-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
66-3-3	Date of deposit	27 April 1999 (27.04.1999)
66-3-4	Accession Number	ATCC 203963

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66-4	Additional Indications	NONE
66-5	Designated States for Which Indications are Made	all designated States
66-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
67	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
67-1	page	100
67-2	line	8
67-3	Identification of Deposit	
67-3-1	Name of depositary institution	American Type Culture Collection
67-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
67-3-3	Date of deposit	02 March 1999 (02.03.1999)
67-3-4	Accession Number	ATCC 203815
67-4	Additional Indications	NONE
67-5	Designated States for Which Indications are Made	all designated States
67-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
68	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
68-1	page	100
68-2	line	9
68-3	Identification of Deposit	
68-3-1	Name of depositary institution	American Type Culture Collection
68-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
68-3-3	Date of deposit	30 March 1999 (30.03.1999)
68-3-4	Accession Number	ATCC 203890
68-4	Additional Indications	NONE
68-5	Designated States for Which Indications are Made	all designated States
68-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
69	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
69-1	page	100
69-2	line	10

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69-3	<b>Identification of Deposit</b>	
69-3-1	Name of depositary institution	
69-3-2	Address of depositary institution	
69-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America <b>25 May 1999 (25.05.1999)</b>
69-3-4	Accession Number	<b>ATCC PTA-130</b>
69-4	<b>Additional Indications</b>	
69-5	<b>Designated States for Which Indications are Made</b>	
69-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	
70	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
70-1	page	<b>100</b>
70-2	line	<b>11</b>
70-3	<b>Identification of Deposit</b>	
70-3-1	Name of depositary institution	
70-3-2	Address of depositary institution	
70-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America <b>27 April 1999 (27.04.1999)</b>
70-3-4	Accession Number	<b>ATCC 203970</b>
70-4	<b>Additional Indications</b>	
70-5	<b>Designated States for Which Indications are Made</b>	
70-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	
71	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
71-1	page	<b>100</b>
71-2	line	<b>12</b>
71-3	<b>Identification of Deposit</b>	
71-3-1	Name of depositary institution	
71-3-2	Address of depositary institution	
71-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America <b>16 March 1999 (16.03.1999)</b>
71-3-4	Accession Number	<b>ATCC 203845</b>
71-4	<b>Additional Indications</b>	
71-5	<b>Designated States for Which Indications are Made</b>	
71-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	

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72	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on: page line	100 13
72-3	Identification of Deposit Name of depositary institution Address of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
72-3-3	Date of deposit	23 March 1999 (23.03.1999)
72-3-4	Accession Number	ATCC 203861
72-4	Additional Indications	NONE
72-5	Designated States for Which Indications are Made	all designated States
72-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
73	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on: page line	100 14
73-3	Identification of Deposit Name of depositary institution Address of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
73-3-3	Date of deposit	16 March 1999 (16.03.1999)
73-3-4	Accession Number	ATCC 203844
73-4	Additional Indications	NONE
73-5	Designated States for Which Indications are Made	all designated States
73-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
74	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on: page line	100 15
74-3	Identification of Deposit Name of depositary institution Address of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
74-3-3	Date of deposit	10 August 1999 (10.08.1999)
74-3-4	Accession Number	ATCC PTA-513
74-4	Additional Indications	NONE
74-5	Designated States for Which Indications are Made	all designated States

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74-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
75	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
75-1	page	100
75-2	line	16
75-3	Identification of Deposit	
75-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
75-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
75-3-3	Date of deposit	<b>09 February 1999 (09.02.1999)</b>
75-3-4	Accession Number	<b>ATCC 203663</b>
75-4	Additional Indications	<b>NONE</b>
75-5	Designated States for Which Indications are Made	<b>all designated States</b>
75-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
76	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
76-1	page	100
76-2	line	17
76-3	Identification of Deposit	
76-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
76-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
76-3-3	Date of deposit	<b>16 March 1999 (16.03.1999)</b>
76-3-4	Accession Number	<b>ATCC 203851</b>
76-4	Additional Indications	<b>NONE</b>
76-5	Designated States for Which Indications are Made	<b>all designated States</b>
76-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
77	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
77-1	page	100
77-2	line	18
77-3	Identification of Deposit	
77-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
77-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
77-3-3	Date of deposit	<b>20 April 1999 (20.04.1999)</b>
77-3-4	Accession Number	<b>ATCC 203950</b>

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77-4	Additional Indications	<b>NONE</b>
77-5	Designated States for Which Indications are Made	<b>all designated States</b>
77-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
78	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
78-1	page	100
78-2	line	19
78-3	Identification of Deposit	
78-3-1	Name of depositary institution	American Type Culture Collection
78-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
78-3-3	Date of deposit	30 March 1999 (30.03.1999)
78-3-4	Accession Number	ATCC 203895
78-4	Additional Indications	<b>NONE</b>
78-5	Designated States for Which Indications are Made	<b>all designated States</b>
78-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
79	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
79-1	page	100
79-2	line	20
79-3	Identification of Deposit	
79-3-1	Name of depositary institution	American Type Culture Collection
79-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
79-3-3	Date of deposit	25 May 1999 (25.05.1999)
79-3-4	Accession Number	ATCC PTA-134
79-4	Additional Indications	<b>NONE</b>
79-5	Designated States for Which Indications are Made	<b>all designated States</b>
79-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
80	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
80-1	page	100
80-2	line	21

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80-3	Identification of Deposit	
80-3-1	Name of depositary institution	American Type Culture Collection
80-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
80-3-3	Date of deposit	16 March 1999 (16.03.1999)
80-3-4	Accession Number	ATCC 203852
80-4	Additional Indications	NONE
80-5	Designated States for Which Indications are Made	all designated States
80-6	Separate Furnishing of Indications	NONE
These indications will be submitted to the International Bureau later		
81	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
81-1	page	100
81-2	line	22
81-3	Identification of Deposit	
81-3-1	Name of depositary institution	American Type Culture Collection
81-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
81-3-3	Date of deposit	22 June 1999 (22.06.1999)
81-3-4	Accession Number	ATCC PTA-258
81-4	Additional Indications	NONE
81-5	Designated States for Which Indications are Made	all designated States
81-6	Separate Furnishing of Indications	NONE
These indications will be submitted to the International Bureau later		
82	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
82-1	page	100
82-2	line	23
82-3	Identification of Deposit	
82-3-1	Name of depositary institution	American Type Culture Collection
82-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
82-3-3	Date of deposit	22 June 1999 (22.06.1999)
82-3-4	Accession Number	ATCC PTA-259
82-4	Additional Indications	NONE
82-5	Designated States for Which Indications are Made	all designated States
82-6	Separate Furnishing of Indications	NONE
These indications will be submitted to the International Bureau later		

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83	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
83-1	page	100
83-2	line	24
83-3	Identification of Deposit	
83-3-1	Name of depositary institution	American Type Culture Collection
83-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
83-3-3	Date of deposit	23 March 1999 (23.03.1999)
83-3-4	Accession Number	ATCC 203866
83-4	Additional Indications	NONE
83-5	Designated States for Which Indications are Made	all designated States
83-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	NONE
84	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
84-1	page	100
84-2	line	25
84-3	Identification of Deposit	
84-3-1	Name of depositary institution	American Type Culture Collection
84-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
84-3-3	Date of deposit	16 March 1999 (16.03.1999)
84-3-4	Accession Number	ATCC 203853
84-4	Additional Indications	NONE
84-5	Designated States for Which Indications are Made	all designated States
84-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	NONE
85	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
85-1	page	100
85-2	line	26
85-3	Identification of Deposit	
85-3-1	Name of depositary institution	American Type Culture Collection
85-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
85-3-3	Date of deposit	30 March 1999 (30.03.1999)
85-3-4	Accession Number	ATCC 203892
85-4	Additional Indications	NONE
85-5	Designated States for Which Indications are Made	all designated States

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85-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
86	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
86-1	page	100
86-2	line	27
86-3	Identification of Deposit	
86-3-1	Name of depositary institution	American Type Culture Collection
86-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
86-3-3	Date of deposit	16 March 1999 (16.03.1999)
86-3-4	Accession Number	ATCC 203847
86-4	Additional Indications	NONE
86-5	Designated States for Which Indications are Made	all designated States
86-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
87	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
87-1	page	100
87-2	line	28
87-3	Identification of Deposit	
87-3-1	Name of depositary institution	American Type Culture Collection
87-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
87-3-3	Date of deposit	04 May 1999 (04.05.1999)
87-3-4	Accession Number	ATCC PTA-21
87-4	Additional Indications	NONE
87-5	Designated States for Which Indications are Made	all designated States
87-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
88	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
88-1	page	100
88-2	line	29
88-3	Identification of Deposit	
88-3-1	Name of depositary institution	American Type Culture Collection
88-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
88-3-3	Date of deposit	25 May 1999 (25.05.1999)
88-3-4	Accession Number	ATCC PTA-121

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88-4	Additional Indications	NONE
88-5	Designated States for Which Indications are Made	<b>all designated States</b>
88-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
89	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
89-1	page	100
89-2	line	30
89-3	Identification of Deposit	
89-3-1	Name of depositary institution	American Type Culture Collection
89-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
89-3-3	Date of deposit	20 April 1999 (20.04.1999)
89-3-4	Accession Number	ATCC 203951
89-4	Additional Indications	NONE
89-5	Designated States for Which Indications are Made	<b>all designated States</b>
89-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
90	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
90-1	page	100
90-2	line	31
90-3	Identification of Deposit	
90-3-1	Name of depositary institution	American Type Culture Collection
90-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
90-3-3	Date of deposit	23 March 1999 (23.03.1999)
90-3-4	Accession Number	ATCC 203869
90-4	Additional Indications	NONE
90-5	Designated States for Which Indications are Made	<b>all designated States</b>
90-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
91	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
91-1	page	100
91-2	line	32

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91-3	<b>Identification of Deposit</b>	
91-3-1	Name of depositary institution	American Type Culture Collection
91-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
91-3-3	Date of deposit	15 June 1999 (15.06.1999)
91-3-4	Accession Number	ATCC PTA-232
91-4	<b>Additional Indications</b>	NONE
91-5	<b>Designated States for Which Indications are Made</b>	all designated States
91-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
92	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
92-1	page	100
92-2	line	33
92-3	<b>Identification of Deposit</b>	
92-3-1	Name of depositary institution	American Type Culture Collection
92-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
92-3-3	Date of deposit	20 July 1999 (20.07.1999)
92-3-4	Accession Number	ATCC PTA-385
92-4	<b>Additional Indications</b>	NONE
92-5	<b>Designated States for Which Indications are Made</b>	all designated States
92-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
93	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
93-1	page	100
93-2	line	34
93-3	<b>Identification of Deposit</b>	
93-3-1	Name of depositary institution	American Type Culture Collection
93-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
93-3-3	Date of deposit	23 March 1999 (23.03.1999)
93-3-4	Accession Number	ATCC 203864
93-4	<b>Additional Indications</b>	NONE
93-5	<b>Designated States for Which Indications are Made</b>	all designated States
93-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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94	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
94-1	page	100
94-2	line	35
94-3	Identification of Deposit	
94-3-1	Name of depositary institution	
94-3-2	Address of depositary institution	
94-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
94-3-4	Accession Number	22 June 1999 (22.06.1999) ATCC PTA-262
94-4	Additional Indications	
94-5	Designated States for Which Indications are Made	
94-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	
95	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
95-1	page	100
95-2	line	36
95-3	Identification of Deposit	
95-3-1	Name of depositary institution	
95-3-2	Address of depositary institution	
95-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
95-3-4	Accession Number	20 July 1999 (20.07.1999) ATCC PTA-381
95-4	Additional Indications	
95-5	Designated States for Which Indications are Made	
95-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	
96	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
96-1	page	100
96-2	line	37
96-3	Identification of Deposit	
96-3-1	Name of depositary institution	
96-3-2	Address of depositary institution	
96-3-3	Date of deposit	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
96-3-4	Accession Number	04 May 1999 (04.05.1999) ATCC PTA-15
96-4	Additional Indications	
96-5	Designated States for Which Indications are Made	

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96-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
97	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
97-1	page	<b>100</b>
97-2	line	<b>38</b>
97-3	Identification of Deposit	
97-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
97-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209 United States of America</b>
97-3-3	Date of deposit	<b>15 June 1999 (15.06.1999)</b>
97-3-4	Accession Number	<b>ATCC PTA-239</b>
97-4	Additional Indications	<b>NONE</b>
97-5	Designated States for Which Indications are Made	<b>all designated States</b>
97-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
98	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
98-1	page	<b>100</b>
98-2	line	<b>39</b>
98-3	Identification of Deposit	
98-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
98-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209 United States of America</b>
98-3-3	Date of deposit	<b>20 July 1999 (20.07.1999)</b>
98-3-4	Accession Number	<b>ATCC PTA-384</b>
98-4	Additional Indications	<b>NONE</b>
98-5	Designated States for Which Indications are Made	<b>all designated States</b>
98-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
99	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
99-1	page	<b>100</b>
99-2	line	<b>40</b>
99-3	Identification of Deposit	
99-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
99-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209 United States of America</b>
99-3-3	Date of deposit	<b>03 August 1999 (03.08.1999)</b>
99-3-4	Accession Number	<b>ATCC PTA-475</b>

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99-4	Additional Indications	NONE
99-5	Designated States for Which Indications are Made	all designated States
99-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
100	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
100-1	page	100
100-2	line	41
100-3	Identification of Deposit	
100-3-1	Name of depositary institution	American Type Culture Collection
100-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
100-3-3	Date of deposit	16 March 1999 (16.03.1999)
100-3-4	Accession Number	ATCC 203854
100-4	Additional Indications	NONE
100-5	Designated States for Which Indications are Made	all designated States
100-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
101	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
101-1	page	100
101-2	line	42
101-3	Identification of Deposit	
101-3-1	Name of depositary institution	American Type Culture Collection
101-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
101-3-3	Date of deposit	20 July 1999 (20.07.1999)
101-3-4	Accession Number	ATCC PTA-378
101-4	Additional Indications	NONE
101-5	Designated States for Which Indications are Made	all designated States
101-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
102	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
102-1	page	100
102-2	line	43

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102-3	Identification of Deposit	
102-3-1	Name of depositary institution	American Type Culture Collection
102-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
102-3-3	Date of deposit	22 June 1999 (22.06.1999)
102-3-4	Accession Number	ATCC PTA-257
102-4	Additional Indications	NONE
102-5	Designated States for Which Indications are Made	all designated States
102-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
103	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
103-1	page	100
103-2	line	44
103-3	Identification of Deposit	
103-3-1	Name of depositary institution	American Type Culture Collection
103-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
103-3-3	Date of deposit	15 June 1999 (15.06.1999)
103-3-4	Accession Number	ATCC PTA-231
103-4	Additional Indications	NONE
103-5	Designated States for Which Indications are Made	all designated States
103-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
104	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
104-1	page	100
104-2	line	45
104-3	Identification of Deposit	
104-3-1	Name of depositary institution	American Type Culture Collection
104-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
104-3-3	Date of deposit	20 July 1999 (20.07.1999)
104-3-4	Accession Number	ATCC PTA-388
104-4	Additional Indications	NONE
104-5	Designated States for Which Indications are Made	all designated States
104-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

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105	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
105-1	page	100
105-2	line	46
105-3	Identification of Deposit	
105-3-1	Name of depositary institution	American Type Culture Collection
105-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
105-3-3	Date of deposit	31 August 1999 (31.08.1999)
105-3-4	Accession Number	ATCC PTA-620
105-4	Additional Indications	NONE
105-5	Designated States for Which Indications are Made	all designated States
105-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
106	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
106-1	page	100
106-2	line	47
106-3	Identification of Deposit	
106-3-1	Name of depositary institution	American Type Culture Collection
106-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
106-3-3	Date of deposit	25 May 1999 (25.05.1999)
106-3-4	Accession Number	ATCC PTA-118
106-4	Additional Indications	NONE
106-5	Designated States for Which Indications are Made	all designated States
106-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
107	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
107-1	page	100
107-2	line	48
107-3	Identification of Deposit	
107-3-1	Name of depositary institution	American Type Culture Collection
107-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
107-3-3	Date of deposit	03 August 1999 (03.08.1999)
107-3-4	Accession Number	ATCC PTA-477
107-4	Additional Indications	NONE
107-5	Designated States for Which Indications are Made	all designated States

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107-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
108	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
108-1	page	100
108-2	line	49
108-3	Identification of Deposit	
108-3-1	Name of depositary institution	American Type Culture Collection
108-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
108-3-3	Date of deposit	03 August 1999 (03.08.1999)
108-3-4	Accession Number	ATCC PTA-488
108-4	Additional Indications	NONE
108-5	Designated States for Which Indications are Made	all designated States
108-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
109	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
109-1	page	100
109-2	line	50
109-3	Identification of Deposit	
109-3-1	Name of depositary institution	American Type Culture Collection
109-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
109-3-3	Date of deposit	16 March 1999 (16.03.1999)
109-3-4	Accession Number	ATCC 203849
109-4	Additional Indications	NONE
109-5	Designated States for Which Indications are Made	all designated States
109-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
110	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
110-1	page	100
110-2	line	51
110-3	Identification of Deposit	
110-3-1	Name of depositary institution	American Type Culture Collection
110-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
110-3-3	Date of deposit	09 March 1999 (09.03.1999)
110-3-4	Accession Number	ATCC 203837

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110-4	Additional Indications	NONE
110-5	Designated States for Which Indications are Made	<b>all designated States</b>
110-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
111	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
111-1	page	100
111-2	line	52
111-3	Identification of Deposit	
111-3-1	Name of depositary institution	American Type Culture Collection
111-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
111-3-3	Date of deposit	20 July 1999 (20.07.1999)
111-3-4	Accession Number	ATCC PTA-380
111-4	Additional Indications	NONE
111-5	Designated States for Which Indications are Made	<b>all designated States</b>
111-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
112	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
112-1	page	100
112-2	line	53
112-3	Identification of Deposit	
112-3-1	Name of depositary institution	American Type Culture Collection
112-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
112-3-3	Date of deposit	11 May 1999 (11.05.1999)
112-3-4	Accession Number	ATCC PTA-44
112-4	Additional Indications	NONE
112-5	Designated States for Which Indications are Made	<b>all designated States</b>
112-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
113	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
113-1	page	100
113-2	line	54

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113-3	<b>Identification of Deposit</b>	
113-3-1	Name of depositary institution	American Type Culture Collection
113-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
113-3-3	Date of deposit	11 May 1999 (11.05.1999)
113-3-4	Accession Number	ATCC PTA-42
113-4	<b>Additional Indications</b>	NONE
113-5	<b>Designated States for Which Indications are Made</b>	all designated States
113-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
114	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
114-1	page	100
114-2	line	55
114-3	<b>Identification of Deposit</b>	
114-3-1	Name of depositary institution	American Type Culture Collection
114-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
114-3-3	Date of deposit	25 May 1999 (25.05.1999)
114-3-4	Accession Number	ATCC PTA-123
114-4	<b>Additional Indications</b>	NONE
114-5	<b>Designated States for Which Indications are Made</b>	all designated States
114-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
115	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
115-1	page	101
115-2	line	2
115-3	<b>Identification of Deposit</b>	
115-3-1	Name of depositary institution	American Type Culture Collection
115-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
115-3-3	Date of deposit	03 August 1999 (03.08.1999)
115-3-4	Accession Number	ATCC PTA-482
115-4	<b>Additional Indications</b>	NONE
115-5	<b>Designated States for Which Indications are Made</b>	all designated States
115-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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116	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
116-1	page	101
116-2	line	3
116-3	Identification of Deposit	
116-3-1	Name of depositary institution	American Type Culture Collection
116-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
116-3-3	Date of deposit	03 August 1999 (03.08.1999)
116-3-4	Accession Number	ATCC PTA-483
116-4	Additional Indications	NONE
116-5	Designated States for Which Indications are Made	all designated States
116-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
117	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
117-1	page	101
117-2	line	4
117-3	Identification of Deposit	
117-3-1	Name of depositary institution	American Type Culture Collection
117-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
117-3-3	Date of deposit	03 August 1999 (03.08.1999)
117-3-4	Accession Number	ATCC PTA-485
117-4	Additional Indications	NONE
117-5	Designated States for Which Indications are Made	all designated States
117-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
118	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
118-1	page	101
118-2	line	5
118-3	Identification of Deposit	
118-3-1	Name of depositary institution	American Type Culture Collection
118-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
118-3-3	Date of deposit	03 August 1999 (03.08.1999)
118-3-4	Accession Number	ATCC PTA-480
118-4	Additional Indications	NONE
118-5	Designated States for Which Indications are Made	all designated States

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118-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
119	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
119-1	page	101
119-2	line	6
119-3	Identification of Deposit	
119-3-1	Name of depositary institution	American Type Culture Collection
119-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
119-3-3	Date of deposit	03 August 1999 (03.08.1999)
119-3-4	Accession Number	ATCC PTA-476
119-4	Additional Indications	<b>NONE</b>
119-5	Designated States for Which Indications are Made	<b>all designated States</b>
119-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
120	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
120-1	page	101
120-2	line	7
120-3	Identification of Deposit	
120-3-1	Name of depositary institution	American Type Culture Collection
120-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
120-3-3	Date of deposit	03 August 1999 (03.08.1999)
120-3-4	Accession Number	ATCC PTA-472
120-4	Additional Indications	<b>NONE</b>
120-5	Designated States for Which Indications are Made	<b>all designated States</b>
120-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
121	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
121-1	page	101
121-2	line	8
121-3	Identification of Deposit	
121-3-1	Name of depositary institution	American Type Culture Collection
121-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
121-3-3	Date of deposit	03 August 1999 (03.08.1999)
121-3-4	Accession Number	ATCC PTA-487

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121-4	Additional Indications	<b>NONE</b>
121-5	Designated States for Which Indications are Made	<b>all designated States</b>
121-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
122	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
122-1	page	101
122-2	line	9
122-3	Identification of Deposit	
122-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
122-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
122-3-3	Date of deposit	<b>03 August 1999 (03.08.1999)</b>
122-3-4	Accession Number	<b>ATCC PTA-484</b>
122-4	Additional Indications	<b>NONE</b>
122-5	Designated States for Which Indications are Made	<b>all designated States</b>
122-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
123	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
123-1	page	101
123-2	line	10
123-3	Identification of Deposit	
123-3-1	Name of depositary institution	<b>American Type Culture Collection</b>
123-3-2	Address of depositary institution	<b>10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
123-3-3	Date of deposit	<b>17 August 1999 (17.08.1999)</b>
123-3-4	Accession Number	<b>ATCC PTA-546</b>
123-4	Additional Indications	<b>NONE</b>
123-5	Designated States for Which Indications are Made	<b>all designated States</b>
123-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
124	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
124-1	page	101
124-2	line	11

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124-3	<b>Identification of Deposit</b>	
124-3-1	Name of depositary institution	American Type Culture Collection
124-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
124-3-3	Date of deposit	10 August 1999 (10.08.1999)
124-3-4	Accession Number	ATCC PTA-515
124-4	<b>Additional Indications</b>	NONE
124-5	<b>Designated States for Which Indications are Made</b>	all designated States
124-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
125	<b>The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
125-1	page	101
125-2	line	12
125-3	<b>Identification of Deposit</b>	
125-3-1	Name of depositary institution	American Type Culture Collection
125-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
125-3-3	Date of deposit	19 October 1999 (19.10.1999)
125-3-4	Accession Number	ATCC PTA-861
125-4	<b>Additional Indications</b>	NONE
125-5	<b>Designated States for Which Indications are Made</b>	all designated States
125-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
126	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
126-1	page	101
126-2	line	13
126-3	<b>Identification of Deposit</b>	
126-3-1	Name of depositary institution	American Type Culture Collection
126-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
126-3-3	Date of deposit	10 August 1999 (10.08.1999)
126-3-4	Accession Number	ATCC PTA-518
126-4	<b>Additional Indications</b>	NONE
126-5	<b>Designated States for Which Indications are Made</b>	all designated States
126-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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127	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
127-1	page	101
127-2	line	14
127-3	Identification of Deposit	
127-3-1	Name of depositary institution	American Type Culture Collection
127-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
127-3-3	Date of deposit	10 August 1999 (10.08.1999)
127-3-4	Accession Number	ATCC PTA-512
127-4	Additional Indications	NONE
127-5	Designated States for Which Indications are Made	all designated States
127-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
128	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
128-1	page	101
128-2	line	15
128-3	Identification of Deposit	
128-3-1	Name of depositary institution	American Type Culture Collection
128-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
128-3-3	Date of deposit	03 August 1999 (03.08.1999)
128-3-4	Accession Number	ATCC PTA-489
128-4	Additional Indications	NONE
128-5	Designated States for Which Indications are Made	all designated States
128-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
129	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
129-1	page	101
129-2	line	16
129-3	Identification of Deposit	
129-3-1	Name of depositary institution	American Type Culture Collection
129-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
129-3-3	Date of deposit	31 August 1999 (31.08.1999)
129-3-4	Accession Number	ATCC PTA-614
129-4	Additional Indications	NONE
129-5	Designated States for Which Indications are Made	all designated States

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129-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
130	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
130-1	page	101
130-2	line	17
130-3	Identification of Deposit	
130-3-1	Name of depositary institution	American Type Culture Collection
130-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
130-3-3	Date of deposit	16 November 1999 (16.11.1999)
130-3-4	Accession Number	ATCC PTA-957
130-4	Additional Indications	NONE
130-5	Designated States for Which Indications are Made	all designated States
130-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
131	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
131-1	page	101
131-2	line	18
131-3	Identification of Deposit	
131-3-1	Name of depositary institution	American Type Culture Collection
131-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
131-3-3	Date of deposit	05 October 1999 (05.10.1999)
131-3-4	Accession Number	ATCC PTA-819
131-4	Additional Indications	NONE
131-5	Designated States for Which Indications are Made	all designated States
131-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
132	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
132-1	page	101
132-2	line	19
132-3	Identification of Deposit	
132-3-1	Name of depositary institution	American Type Culture Collection
132-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
132-3-3	Date of deposit	18 September 1997 (18.09.1997)
132-3-4	Accession Number	ATCC 209280

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132-4	Additional Indications	<b>NONE</b>
132-5	Designated States for Which Indications are Made	<b>all designated States</b>
132-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
133	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
133-1	page	101
133-2	line	20
133-3	Identification of Deposit Name of depositary institution Address of depositary institution	<b>American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
133-3-3	Date of deposit	<b>14 April 1998 (14.04.1998)</b>
133-3-4	Accession Number	<b>ATCC 209772</b>
133-4	Additional Indications	<b>NONE</b>
133-5	Designated States for Which Indications are Made	<b>all designated States</b>
133-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
134	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
134-1	page	101
134-2	line	21
134-3	Identification of Deposit Name of depositary institution Address of depositary institution	<b>American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
134-3-3	Date of deposit	<b>16 October 1997 (16.10.1997)</b>
134-3-4	Accession Number	<b>ATCC 209375</b>
134-4	Additional Indications	<b>NONE</b>
134-5	Designated States for Which Indications are Made	<b>all designated States</b>
134-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
135	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
135-1	page	101
135-2	line	22

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135-3	<b>Identification of Deposit</b>	
135-3-1	Name of depositary institution	American Type Culture Collection
135-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
135-3-3	Date of deposit	23 September 1997 (23.09.1997)
135-3-4	Accession Number	ATCC 209296
135-4	<b>Additional Indications</b>	NONE
135-5	<b>Designated States for Which Indications are Made</b>	all designated States
135-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
136	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
136-1	page	101
136-2	line	23
136-3	<b>Identification of Deposit</b>	
136-3-1	Name of depositary institution	American Type Culture Collection
136-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
136-3-3	Date of deposit	18 September 1997 (18.09.1997)
136-3-4	Accession Number	ATCC 209279
136-4	<b>Additional Indications</b>	NONE
136-5	<b>Designated States for Which Indications are Made</b>	all designated States
136-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
137	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
137-1	page	101
137-2	line	24
137-3	<b>Identification of Deposit</b>	
137-3-1	Name of depositary institution	American Type Culture Collection
137-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
137-3-3	Date of deposit	05 March 1998 (05.03.1998)
137-3-4	Accession Number	ATCC 209653
137-4	<b>Additional Indications</b>	NONE
137-5	<b>Designated States for Which Indications are Made</b>	all designated States
137-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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138	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
138-1	page	101
138-2	line	25
138-3	Identification of Deposit	
138-3-1	Name of depositary institution	American Type Culture Collection
138-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
138-3-3	Date of deposit	16 October 1997 (16.10.1997)
138-3-4	Accession Number	ATCC 209385
138-4	Additional Indications	NONE
138-5	Designated States for Which Indications are Made	all designated States
138-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	NONE
139	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
139-1	page	101
139-2	line	26
139-3	Identification of Deposit	
139-3-1	Name of depositary institution	American Type Culture Collection
139-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
139-3-3	Date of deposit	16 September 1997 (16.09.1997)
139-3-4	Accession Number	ATCC 209261
139-4	Additional Indications	NONE
139-5	Designated States for Which Indications are Made	all designated States
139-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	NONE
140	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
140-1	page	101
140-2	line	27
140-3	Identification of Deposit	
140-3-1	Name of depositary institution	American Type Culture Collection
140-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
140-3-3	Date of deposit	16 October 1997 (16.10.1997)
140-3-4	Accession Number	ATCC 209384
140-4	Additional Indications	NONE
140-5	Designated States for Which Indications are Made	all designated States

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140-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
141	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
141-1	page	101
141-2	line	28
141-3	Identification of Deposit	
141-3-1	Name of depositary institution	American Type Culture Collection
141-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
141-3-3	Date of deposit	16 September 1997 (16.09.1997)
141-3-4	Accession Number	ATCC 209258
141-4	Additional Indications	NONE
141-5	Designated States for Which Indications are Made	all designated States
141-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
142	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
142-1	page	101
142-2	line	29
142-3	Identification of Deposit	
142-3-1	Name of depositary institution	American Type Culture Collection
142-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
142-3-3	Date of deposit	16 September 1997 (16.09.1997)
142-3-4	Accession Number	ATCC 209257
142-4	Additional Indications	NONE
142-5	Designated States for Which Indications are Made	all designated States
142-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
143	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
143-1	page	101
143-2	line	30
143-3	Identification of Deposit	
143-3-1	Name of depositary institution	American Type Culture Collection
143-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
143-3-3	Date of deposit	30 May 1997 (30.05.1997)
143-3-4	Accession Number	ATCC 209087

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143-4	Additional Indications	NONE
143-5	Designated States for Which Indications are Made	all designated States
143-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
144	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
144-1	page	101
144-2	line	31
144-3	Identification of Deposit	
144-3-1	Name of depositary institution	American Type Culture Collection
144-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
144-3-3	Date of deposit	16 October 1997 (16.10.1997)
144-3-4	Accession Number	ATCC 209381
144-4	Additional Indications	NONE
144-5	Designated States for Which Indications are Made	all designated States
144-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
145	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
145-1	page	101
145-2	line	32
145-3	Identification of Deposit	
145-3-1	Name of depositary institution	American Type Culture Collection
145-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
145-3-3	Date of deposit	16 September 1997 (16.09.1997)
145-3-4	Accession Number	ATCC 209262
145-4	Additional Indications	NONE
145-5	Designated States for Which Indications are Made	all designated States
145-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
146	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
146-1	page	101
146-2	line	33

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146-3	<b>Identification of Deposit</b>	
146-3-1	Name of depositary institution	American Type Culture Collection
146-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
146-3-3	Date of deposit	28 October 1997 (28.10.1997)
146-3-4	Accession Number	ATCC 209420
146-4	<b>Additional Indications</b>	NONE
146-5	<b>Designated States for Which Indications are Made</b>	all designated States
146-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
147	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
147-1	page	101
147-2	line	34
147-3	<b>Identification of Deposit</b>	
147-3-1	Name of depositary institution	American Type Culture Collection
147-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
147-3-3	Date of deposit	16 September 1997 (16.09.1997)
147-3-4	Accession Number	ATCC 209256
147-4	<b>Additional Indications</b>	NONE
147-5	<b>Designated States for Which Indications are Made</b>	all designated States
147-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
148	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
148-1	page	101
148-2	line	35
148-3	<b>Identification of Deposit</b>	
148-3-1	Name of depositary institution	American Type Culture Collection
148-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
148-3-3	Date of deposit	16 September 1997 (16.09.1997)
148-3-4	Accession Number	ATCC 209251
148-4	<b>Additional Indications</b>	NONE
148-5	<b>Designated States for Which Indications are Made</b>	all designated States
148-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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149	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
149-1	page	101
149-2	line	36
149-3	Identification of Deposit	
149-3-1	Name of depositary institution	American Type Culture Collection
149-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
149-3-3	Date of deposit	16 September 1997 (16.09.1997)
149-3-4	Accession Number	ATCC 209263
149-4	Additional Indications	NONE
149-5	Designated States for Which Indications are Made	all designated States
149-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
150	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
150-1	page	101
150-2	line	37
150-3	Identification of Deposit	
150-3-1	Name of depositary institution	American Type Culture Collection
150-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
150-3-3	Date of deposit	16 September 1997 (16.09.1997)
150-3-4	Accession Number	ATCC 209264
150-4	Additional Indications	NONE
150-5	Designated States for Which Indications are Made	all designated States
150-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
151	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
151-1	page	101
151-2	line	38
151-3	Identification of Deposit	
151-3-1	Name of depositary institution	American Type Culture Collection
151-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
151-3-3	Date of deposit	16 October 1997 (16.10.1997)
151-3-4	Accession Number	ATCC 209376
151-4	Additional Indications	NONE
151-5	Designated States for Which Indications are Made	all designated States

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151-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
152	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
152-1	page	101
152-2	line	39
152-3	Identification of Deposit	
152-3-1	Name of depositary institution	American Type Culture Collection
152-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
152-3-3	Date of deposit	17 October 1997 (17.10.1997)
152-3-4	Accession Number	ATCC 209391
152-4	Additional Indications	NONE
152-5	Designated States for Which Indications are Made	all designated States
152-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
153	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
153-1	page	101
153-2	line	40
153-3	Identification of Deposit	
153-3-1	Name of depositary institution	American Type Culture Collection
153-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
153-3-3	Date of deposit	28 October 1997 (28.10.1997)
153-3-4	Accession Number	ATCC 209417
153-4	Additional Indications	NONE
153-5	Designated States for Which Indications are Made	all designated States
153-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
154	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
154-1	page	101
154-2	line	41
154-3	Identification of Deposit	
154-3-1	Name of depositary institution	American Type Culture Collection
154-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
154-3-3	Date of deposit	16 September 1997 (16.09.1997)
154-3-4	Accession Number	ATCC 209253

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154-4	Additional Indications	<b>NONE</b>
154-5	Designated States for Which Indications are Made	<b>all designated States</b>
154-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
155	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
155-1	page	101
155-2	line	42
155-3	Identification of Deposit	
155-3-1	Name of depositary institution	American Type Culture Collection
155-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
155-3-3	Date of deposit	12 May 1998 (12.05.1998)
155-3-4	Accession Number	ATCC 209855
155-4	Additional Indications	<b>NONE</b>
155-5	Designated States for Which Indications are Made	<b>all designated States</b>
155-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
156	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
156-1	page	101
156-2	line	43
156-3	Identification of Deposit	
156-3-1	Name of depositary institution	American Type Culture Collection
156-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
156-3-3	Date of deposit	10 December 1997 (10.12.1997)
156-3-4	Accession Number	ATCC 209526
156-4	Additional Indications	<b>NONE</b>
156-5	Designated States for Which Indications are Made	<b>all designated States</b>
156-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
157	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
157-1	page	101
157-2	line	44

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157-3	Identification of Deposit	
157-3-1	Name of depositary institution	American Type Culture Collection
157-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
157-3-3	Date of deposit	16 September 1997 (16.09.1997)
157-3-4	Accession Number	ATCC 209252
157-4	Additional Indications	NONE
157-5	Designated States for Which Indications are Made	all designated States
157-6	Separate Furnishing of Indications	NONE
These indications will be submitted to the International Bureau later		
158	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
158-1	page	101
158-2	line	45
158-3	Identification of Deposit	
158-3-1	Name of depositary institution	American Type Culture Collection
158-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
158-3-3	Date of deposit	16 October 1997 (16.10.1997)
158-3-4	Accession Number	ATCC 209374
158-4	Additional Indications	NONE
158-5	Designated States for Which Indications are Made	all designated States
158-6	Separate Furnishing of Indications	NONE
These indications will be submitted to the International Bureau later		
159	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
159-1	page	101
159-2	line	46
159-3	Identification of Deposit	
159-3-1	Name of depositary institution	American Type Culture Collection
159-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
159-3-3	Date of deposit	10 December 1997 (10.12.1997)
159-3-4	Accession Number	ATCC 209528
159-4	Additional Indications	NONE
159-5	Designated States for Which Indications are Made	all designated States
159-6	Separate Furnishing of Indications	NONE
These indications will be submitted to the International Bureau later		

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160	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
160-1	page	101
160-2	line	47
160-3	Identification of Deposit	
160-3-1	Name of depositary institution	American Type Culture Collection
160-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
160-3-3	Date of deposit	16 September 1997 (16.09.1997)
160-3-4	Accession Number	ATCC 209265
160-4	Additional Indications	NONE
160-5	Designated States for Which Indications are Made	all designated States
160-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
161	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
161-1	page	101
161-2	line	48
161-3	Identification of Deposit	
161-3-1	Name of depositary institution	American Type Culture Collection
161-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
161-3-3	Date of deposit	17 October 1997 (17.10.1997)
161-3-4	Accession Number	ATCC 209396 .
161-4	Additional Indications	NONE
161-5	Designated States for Which Indications are Made	all designated States
161-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
162	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
162-1	page	101
162-2	line	49
162-3	Identification of Deposit	
162-3-1	Name of depositary institution	American Type Culture Collection
162-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
162-3-3	Date of deposit	18 August 1997 (18.08.1997)
162-3-4	Accession Number	ATCC 209201
162-4	Additional Indications	NONE
162-5	Designated States for Which Indications are Made	all designated States

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162-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
163	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
163-1	page	101
163-2	line	50
163-3	Identification of Deposit	
163-3-1	Name of depositary institution	American Type Culture Collection
163-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
163-3-3	Date of deposit	28 October 1997 (28.10.1997)
163-3-4	Accession Number	ATCC 209416
163-4	Additional Indications	NONE
163-5	Designated States for Which Indications are Made	all designated States
163-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
164	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
164-1	page	101
164-2	line	51
164-3	Identification of Deposit	
164-3-1	Name of depositary institution	American Type Culture Collection
164-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
164-3-3	Date of deposit	17 October 1997 (17.10.1997)
164-3-4	Accession Number	ATCC 209403
164-4	Additional Indications	NONE
164-5	Designated States for Which Indications are Made	all designated States
164-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
165	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
165-1	page	101
165-2	line	52
165-3	Identification of Deposit	
165-3-1	Name of depositary institution	American Type Culture Collection
165-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
165-3-3	Date of deposit	28 October 1997 (28.10.1997)
165-3-4	Accession Number	ATCC 209419

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165-4	Additional Indications	NONE
165-5	Designated States for Which Indications are Made	all designated States
165-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
166	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
166-1	page	101
166-2	line	53
166-3	Identification of Deposit	
166-3-1	Name of depositary institution	American Type Culture Collection
166-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
166-3-3	Date of deposit	17 October 1997 (17.10.1997)
166-3-4	Accession Number	ATCC 209402
166-4	Additional Indications	NONE
166-5	Designated States for Which Indications are Made	all designated States
166-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
167	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
167-1	page	101
167-2	line	54
167-3	Identification of Deposit	
167-3-1	Name of depositary institution	American Type Culture Collection
167-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
167-3-3	Date of deposit	16 October 1997 (16.10.1997)
167-3-4	Accession Number	ATCC 209378
167-4	Additional Indications	NONE
167-5	Designated States for Which Indications are Made	all designated States
167-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
168	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
168-1	page	101
168-2	line	55

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168-3	Identification of Deposit	
168-3-1	Name of depositary institution	American Type Culture Collection
168-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
168-3-3	Date of deposit	21 November 1997 (21.11.1997)
168-3-4	Accession Number	ATCC 209489
168-4	Additional Indications	NONE
168-5	Designated States for Which Indications are Made	all designated States
168-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
169	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
169-1	page	102
169-2	line	2
169-3	Identification of Deposit	
169-3-1	Name of depositary institution	American Type Culture Collection
169-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
169-3-3	Date of deposit	17 October 1997 (17.10.1997)
169-3-4	Accession Number	ATCC 209401
169-4	Additional Indications	NONE
169-5	Designated States for Which Indications are Made	all designated States
169-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
170	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
170-1	page	102
170-2	line	3
170-3	Identification of Deposit	
170-3-1	Name of depositary institution	American Type Culture Collection
170-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
170-3-3	Date of deposit	17 October 1997 (17.10.1997)
170-3-4	Accession Number	ATCC 209397
170-4	Additional Indications	NONE
170-5	Designated States for Which Indications are Made	all designated States
170-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

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171	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
.171-1 171-2	page line	102 4
171-3	Identification of Deposit	
171-3-1	Name of depositary institution	American Type Culture Collection
171-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
171-3-3	Date of deposit	17 October 1997 (17.10.1997)
171-3-4	Accession Number	ATCC 209389
171-4	Additional Indications	NONE
171-5	Designated States for Which Indications are Made	all designated States
171-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
172	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
172-1 172-2	page line	102 5
172-3	Identification of Deposit	
172-3-1	Name of depositary institution	American Type Culture Collection
172-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
172-3-3	Date of deposit	07 November 1997 (07.11.1997)
172-3-4	Accession Number	ATCC 209438
172-4	Additional Indications	NONE
172-5	Designated States for Which Indications are Made	all designated States
172-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
173	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
173-1 173-2	page line	102 6
173-3	Identification of Deposit	
173-3-1	Name of depositary institution	American Type Culture Collection
173-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
173-3-3	Date of deposit	21 November 1997 (21.11.1997)
173-3-4	Accession Number	ATCC 209492
173-4	Additional Indications	NONE
173-5	Designated States for Which Indications are Made	all designated States

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173-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
174	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
174-1	page	102
174-2	line	7
174-3	<b>Identification of Deposit</b>	
174-3-1	Name of depositary institution	American Type Culture Collection
174-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
174-3-3	Date of deposit	17 October 1997 (17.10.1997)
174-3-4	Accession Number	ATCC 209388
174-4	<b>Additional Indications</b>	<b>NONE</b>
174-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
174-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
175	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
175-1	page	102
175-2	line	8
175-3	<b>Identification of Deposit</b>	
175-3-1	Name of depositary institution	American Type Culture Collection
175-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
175-3-3	Date of deposit	07 November 1997 (07.11.1997)
175-3-4	Accession Number	ATCC 209432
175-4	<b>Additional Indications</b>	<b>NONE</b>
175-5	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
175-6	<b>Separate Furnishing of Indications</b> These indications will be submitted to the International Bureau later	<b>NONE</b>
176	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
176-1	page	102
176-2	line	9
176-3	<b>Identification of Deposit</b>	
176-3-1	Name of depositary institution	American Type Culture Collection
176-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
176-3-3	Date of deposit	07 November 1997 (07.11.1997)
176-3-4	Accession Number	ATCC 209439

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176-4	Additional Indications	<b>NONE</b>
176-5	Designated States for Which Indications are Made	<b>all designated States</b>
176-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
177	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
177-1	page	102
177-2	line	10
177-3	Identification of Deposit	
177-3-1	Name of depositary institution	American Type Culture Collection
177-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
177-3-3	Date of deposit	07 November 1997 (07.11.1997)
177-3-4	Accession Number	ATCC 209433
177-4	Additional Indications	<b>NONE</b>
177-5	Designated States for Which Indications are Made	<b>all designated States</b>
177-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
178	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
178-1	page	102
178-2	line	11
178-3	Identification of Deposit	
178-3-1	Name of depositary institution	American Type Culture Collection
178-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
178-3-3	Date of deposit	05 February 1998 (05.02.1998)
178-3-4	Accession Number	ATCC 209618
178-4	Additional Indications	<b>NONE</b>
178-5	Designated States for Which Indications are Made	<b>all designated States</b>
178-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
179	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
179-1	page	102
179-2	line	12

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179-3	<b>Identification of Deposit</b>	
179-3-1	Name of depositary institution	American Type Culture Collection
179-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
179-3-3	Date of deposit	21 November 1997 (21.11.1997)
179-3-4	Accession Number	ATCC 209484
179-4	<b>Additional Indications</b>	NONE
179-5	<b>Designated States for Which Indications are Made</b>	all designated States
179-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
180	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
180-1	page	102
180-2	line	13
180-3	<b>Identification of Deposit</b>	
180-3-1	Name of depositary institution	American Type Culture Collection
180-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
180-3-3	Date of deposit	21 November 1997 (21.11.1997)
180-3-4	Accession Number	ATCC 209487
180-4	<b>Additional Indications</b>	NONE
180-5	<b>Designated States for Which Indications are Made</b>	all designated States
180-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
181	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
181-1	page	102
181-2	line	14
181-3	<b>Identification of Deposit</b>	
181-3-1	Name of depositary institution	American Type Culture Collection
181-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
181-3-3	Date of deposit	07 November 1997 (07.11.1997)
181-3-4	Accession Number	ATCC 209434
181-4	<b>Additional Indications</b>	NONE
181-5	<b>Designated States for Which Indications are Made</b>	all designated States
181-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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182 The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
182-1 page	102	
182-2 line	15	
182-3 Identification of Deposit		
182-3-1 Name of depositary institution	American Type Culture Collection	
182-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
182-3-3 Date of deposit	26 March 1998 (26.03.1998)	
182-3-4 Accession Number	ATCC 209704	
182-4 Additional Indications	NONE	
182-5 Designated States for Which Indications are Made	all designated States	
182-6 Separate Furnishing of Indications	NONE	
These indications will be submitted to the International Bureau later		
183 The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
183-1 page	102	
183-2 line	16	
183-3 Identification of Deposit		
183-3-1 Name of depositary institution	American Type Culture Collection	
183-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
183-3-3 Date of deposit	28 April 1998 (28.04.1998)	
183-3-4 Accession Number	ATCC 209808	
183-4 Additional Indications	NONE	
183-5 Designated States for Which Indications are Made	all designated States	
183-6 Separate Furnishing of Indications	NONE	
These indications will be submitted to the International Bureau later		
184 The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:		
184-1 page	102	
184-2 line	17	
184-3 Identification of Deposit		
184-3-1 Name of depositary institution	American Type Culture Collection	
184-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
184-3-3 Date of deposit	06 May 1998 (06.05.1998)	
184-3-4 Accession Number	ATCC 209847	
184-4 Additional Indications	NONE	
184-5 Designated States for Which Indications are Made	all designated States	

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184-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
185	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:  185-1 page 185-2 line	  102 18
185-3	Identification of Deposit	
185-3-1	Name of depositary institution	American Type Culture Collection
185-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
185-3-3	Date of deposit	05 February 1998 (05.02.1998)
185-3-4	Accession Number	ATCC 209616
185-4	Additional Indications	NONE
185-5	Designated States for Which Indications are Made	all designated States
185-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
186	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:  186-1 page 186-2 line	  102 19
186-3	Identification of Deposit	
186-3-1	Name of depositary institution	American Type Culture Collection
186-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
186-3-3	Date of deposit	05 February 1998 (05.02.1998)
186-3-4	Accession Number	ATCC 209619
186-4	Additional Indications	NONE
186-5	Designated States for Which Indications are Made	all designated States
186-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
187	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:  187-1 page 187-2 line	  102 20
187-3	Identification of Deposit	
187-3-1	Name of depositary institution	American Type Culture Collection
187-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
187-3-3	Date of deposit	11 August 1998 (11.08.1998)
187-3-4	Accession Number	ATCC 203109

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187-4	Additional Indications	<b>NONE</b>
187-5	Designated States for Which Indications are Made	<b>all designated States</b>
187-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
188	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
188-1	page	102
188-2	line	21
188-3	Identification of Deposit	
188-3-1	Name of depositary institution	American Type Culture Collection
188-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
188-3-3	Date of deposit	31 March 1998 (31.03.1998)
188-3-4	Accession Number	ATCC 209715
188-4	Additional Indications	<b>NONE</b>
188-5	Designated States for Which Indications are Made	<b>all designated States</b>
188-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
189	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
189-1	page	102
189-2	line	22
189-3	Identification of Deposit	
189-3-1	Name of depositary institution	American Type Culture Collection
189-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
189-3-3	Date of deposit	11 March 1998 (11.03.1998)
189-3-4	Accession Number	ATCC 209669
189-4	Additional Indications	<b>NONE</b>
189-5	Designated States for Which Indications are Made	<b>all designated States</b>
189-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
190	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
190-1	page	102
190-2	line	23

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190-3	<b>Identification of Deposit</b>	
190-3-1	Name of depositary institution	American Type Culture Collection
190-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
190-3-3	Date of deposit	23 June 1998 (23.06.1998)
190-3-4	Accession Number	ATCC 203002
190-4	<b>Additional Indications</b>	NONE
190-5	<b>Designated States for Which Indications are Made</b>	all designated States
190-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
191	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
191-1	page	102
191-2	line	24
191-3	<b>Identification of Deposit</b>	
191-3-1	Name of depositary institution	American Type Culture Collection
191-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
191-3-3	Date of deposit	26 March 1998 (26.03.1998)
191-3-4	Accession Number	ATCC 209705
191-4	<b>Additional Indications</b>	NONE
191-5	<b>Designated States for Which Indications are Made</b>	all designated States
191-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
192	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
192-1	page	102
192-2	line	25
192-3	<b>Identification of Deposit</b>	
192-3-1	Name of depositary institution	American Type Culture Collection
192-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
192-3-3	Date of deposit	16 June 1998 (16.06.1998)
192-3-4	Accession Number	ATCC 209981
192-4	<b>Additional Indications</b>	NONE
192-5	<b>Designated States for Which Indications are Made</b>	all designated States
192-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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193	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
193-1	page	102
193-2	line	26
193-3	Identification of Deposit	
193-3-1	Name of depositary institution	American Type Culture Collection
193-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
193-3-3	Date of deposit	07 April 1998 (07.04.1998)
193-3-4	Accession Number	ATCC 209749
193-4	Additional Indications	NONE
193-5	Designated States for Which Indications are Made	all designated States
193-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
194	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
194-1	page	102
194-2	line	27
194-3	Identification of Deposit	
194-3-1	Name of depositary institution	American Type Culture Collection
194-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
194-3-3	Date of deposit	12 May 1998 (12.05.1998)
194-3-4	Accession Number	ATCC 209859
194-4	Additional Indications	NONE
194-5	Designated States for Which Indications are Made	all designated States
194-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
195	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
195-1	page	102
195-2	line	28
195-3	Identification of Deposit	
195-3-1	Name of depositary institution	American Type Culture Collection
195-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
195-3-3	Date of deposit	06 May 1998 (06.05.1998)
195-3-4	Accession Number	ATCC 209845
195-4	Additional Indications	NONE
195-5	Designated States for Which Indications are Made	all designated States

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195-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
196	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
196-1	page	102
196-2	line	29
196-3	Identification of Deposit	
196-3-1	Name of depositary institution	American Type Culture Collection
196-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
196-3-3	Date of deposit	07 April 1998 (07.04.1998)
196-3-4	Accession Number	ATCC 209748
196-4	Additional Indications	NONE
196-5	Designated States for Which Indications are Made	all designated States
196-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
197	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
197-1	page	102
197-2	line	30
197-3	Identification of Deposit	
197-3-1	Name of depositary institution	American Type Culture Collection
197-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
197-3-3	Date of deposit	11 August 1998 (11.08.1998)
197-3-4	Accession Number	ATCC 203107
197-4	Additional Indications	NONE
197-5	Designated States for Which Indications are Made	all designated States
197-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
198	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
198-1	page	102
198-2	line	31
198-3	Identification of Deposit	
198-3-1	Name of depositary institution	American Type Culture Collection
198-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
198-3-3	Date of deposit	23 April 1998 (23.04.1998)
198-3-4	Accession Number	ATCC 209801

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198-4	Additional Indications	NONE
198-5	Designated States for Which Indications are Made	all designated States
198-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
199	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
199-1	page	102
199-2	line	32
199-3	Identification of Deposit Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
199-3-2	Address of depositary institution	
199-3-3	Date of deposit	09 June 1998 (09.06.1998)
199-3-4	Accession Number	ATCC 209948
199-4	Additional Indications	NONE
199-5	Designated States for Which Indications are Made	all designated States
199-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
200	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
200-1	page	102
200-2	line	33
200-3	Identification of Deposit Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
200-3-2	Address of depositary institution	
200-3-3	Date of deposit	20 May 1998 (20.05.1998)
200-3-4	Accession Number	ATCC 209883
200-4	Additional Indications	NONE
200-5	Designated States for Which Indications are Made	all designated States
200-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
201	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
201-1	page	102
201-2	line	34

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201-3	<b>Identification of Deposit</b>	
201-3-1	Name of depositary institution	American Type Culture Collection
201-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
201-3-3	Date of deposit	01 July 1998 (01.07.1998)
201-3-4	Accession Number	ATCC 203049
201-4	<b>Additional Indications</b>	NONE
201-5	<b>Designated States for Which Indications are Made</b>	all designated States
201-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
202	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
202-1	page	102
202-2	line	35
202-3	<b>Identification of Deposit</b>	
202-3-1	Name of depositary institution	American Type Culture Collection
202-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
202-3-3	Date of deposit	06 May 1998 (06.05.1998)
202-3-4	Accession Number	ATCC 209846
202-4	<b>Additional Indications</b>	NONE
202-5	<b>Designated States for Which Indications are Made</b>	all designated States
202-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
203	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
203-1	page	102
203-2	line	36
203-3	<b>Identification of Deposit</b>	
203-3-1	Name of depositary institution	American Type Culture Collection
203-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
203-3-3	Date of deposit	12 May 1998 (12.05.1998)
203-3-4	Accession Number	ATCC 209857
203-4	<b>Additional Indications</b>	NONE
203-5	<b>Designated States for Which Indications are Made</b>	all designated States
203-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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204	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
204-1	page	102
204-2	line	37
204-3	Identification of Deposit	
204-3-1	Name of depositary institution	American Type Culture Collection
204-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
204-3-3	Date of deposit	14 May 1998 (14.05.1998)
204-3-4	Accession Number	ATCC 209864
204-4	Additional Indications	NONE
204-5	Designated States for Which Indications are Made	all designated States
204-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	
205	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
205-1	page	102
205-2	line	38
205-3	Identification of Deposit	
205-3-1	Name of depositary institution	American Type Culture Collection
205-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
205-3-3	Date of deposit	20 May 1998 (20.05.1998)
205-3-4	Accession Number	ATCC 209880
205-4	Additional Indications	NONE
205-5	Designated States for Which Indications are Made	all designated States
205-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	
206	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
206-1	page	102
206-2	line	39
206-3	Identification of Deposit	
206-3-1	Name of depositary institution	American Type Culture Collection
206-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
206-3-3	Date of deposit	14 May 1998 (14.05.1998)
206-3-4	Accession Number	ATCC 209869
206-4	Additional Indications	NONE
206-5	Designated States for Which Indications are Made	all designated States

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206-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
207	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
207-1	page	102
207-2	line	40
207-3	Identification of Deposit	
207-3-1	Name of depositary institution	American Type Culture Collection
207-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
207-3-3	Date of deposit	09 June 1998 (09.06.1998)
207-3-4	Accession Number	ATCC 209950
207-4	Additional Indications	NONE
207-5	Designated States for Which Indications are Made	all designated States
207-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
208	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
208-1	page	102
208-2	line	41
208-3	Identification of Deposit	
208-3-1	Name of depositary institution	American Type Culture Collection
208-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
208-3-3	Date of deposit	23 June 1998 (23.06.1998)
208-3-4	Accession Number	ATCC 203008
208-4	Additional Indications	NONE
208-5	Designated States for Which Indications are Made	all designated States
208-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
209	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
209-1	page	102
209-2	line	42
209-3	Identification of Deposit	
209-3-1	Name of depositary institution	American Type Culture Collection
209-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
209-3-3	Date of deposit	23 June 1998 (23.06.1998)
209-3-4	Accession Number	ATCC 203014

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209-4	Additional Indications	<b>NONE</b>
209-5	Designated States for Which Indications are Made	<b>all designated States</b>
209-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
210	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
210-1	page	102
210-2	line	43
210-3	Identification of Deposit	
210-3-1	Name of depositary institution	American Type Culture Collection
210-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
210-3-3	Date of deposit	11 August 1998 (11.08.1998)
210-3-4	Accession Number	ATCC 203110
210-4	Additional Indications	<b>NONE</b>
210-5	Designated States for Which Indications are Made	<b>all designated States</b>
210-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
211	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
211-1	page	102
211-2	line	44
211-3	Identification of Deposit	
211-3-1	Name of depositary institution	American Type Culture Collection
211-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
211-3-3	Date of deposit	23 June 1998 (23.06.1998)
211-3-4	Accession Number	ATCC 203009
211-4	Additional Indications	<b>NONE</b>
211-5	Designated States for Which Indications are Made	<b>all designated States</b>
211-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
212	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
212-1	page	102
212-2	line	45

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212-3	Identification of Deposit	
212-3-1	Name of depositary institution	American Type Culture Collection
212-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
212-3-3	Date of deposit	09 June 1998 (09.06.1998)
212-3-4	Accession Number	ATCC 209961
212-4	Additional Indications	NONE
212-5	Designated States for Which Indications are Made	all designated States
212-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
213	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
213-1	page	102
213-2	line	46
213-3	Identification of Deposit	
213-3-1	Name of depositary institution	American Type Culture Collection
213-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
213-3-3	Date of deposit	09 June 1998 (09.06.1998)
213-3-4	Accession Number	ATCC 209962
213-4	Additional Indications	NONE
213-5	Designated States for Which Indications are Made	all designated States
213-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
214	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
214-1	page	102
214-2	line	47
214-3	Identification of Deposit	
214-3-1	Name of depositary institution	American Type Culture Collection
214-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
214-3-3	Date of deposit	14 May 1998 (14.05.1998)
214-3-4	Accession Number	ATCC 209866
214-4	Additional Indications	NONE
214-5	Designated States for Which Indications are Made	all designated States
214-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

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215	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
215-1	page	102
215-2	line	48
215-3	Identification of Deposit	
215-3-1	Name of depositary institution	
215-3-2	Address of depositary institution	
	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
215-3-3	Date of deposit	
215-3-4	Accession Number	
	25 August 1998 (25.08.1998) ATCC 203157	
215-4	Additional Indications	
	NONE	
215-5	Designated States for Which Indications are Made	
	all designated States	
215-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	
216	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
216-1	page	102
216-2	line	49
216-3	Identification of Deposit	
216-3-1	Name of depositary institution	
216-3-2	Address of depositary institution	
	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
216-3-3	Date of deposit	
216-3-4	Accession Number	
	11 August 1998 (11.08.1998) ATCC 203106	
216-4	Additional Indications	
	NONE	
216-5	Designated States for Which Indications are Made	
	all designated States	
216-6	Separate Furnishing of Indications	
	These indications will be submitted to the International Bureau later	
217	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
217-1	page	102
217-2	line	50
217-3	Identification of Deposit	
217-3-1	Name of depositary institution	
217-3-2	Address of depositary institution	
	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
217-3-3	Date of deposit	
217-3-4	Accession Number	
	09 June 1998 (09.06.1998) ATCC 209945	
217-4	Additional Indications	
	NONE	
217-5	Designated States for Which Indications are Made	
	all designated States	

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217-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
218	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
218-1	page	102
218-2	line	51
218-3	Identification of Deposit	
218-3-1	Name of depositary institution	American Type Culture Collection
218-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
218-3-3	Date of deposit	16 June 1998 (16.06.1998)
218-3-4	Accession Number	ATCC 209989
218-4	Additional Indications	NONE
218-5	Designated States for Which Indications are Made	all designated States
218-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
219	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
219-1	page	102
219-2	line	52
219-3	Identification of Deposit	
219-3-1	Name of depositary institution	American Type Culture Collection
219-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
219-3-3	Date of deposit	11 August 1998 (11.08.1998)
219-3-4	Accession Number	ATCC 203108
219-4	Additional Indications	NONE
219-5	Designated States for Which Indications are Made	all designated States
219-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
220	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
220-1	page	102
220-2	line	53
220-3	Identification of Deposit	
220-3-1	Name of depositary institution	American Type Culture Collection
220-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
220-3-3	Date of deposit	11 August 1998 (11.08.1998)
220-3-4	Accession Number	ATCC 203111

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220-4	Additional Indications	<b>NONE</b>
220-5	Designated States for Which Indications are Made	<b>all designated States</b>
220-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
221	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
221-1	page	102
221-2	line	54
221-3	Identification of Deposit	
221-3-1	Name of depositary institution	American Type Culture Collection
221-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
221-3-3	Date of deposit	20 October 1998 (20.10.1998)
221-3-4	Accession Number	ATCC 203359
221-4	Additional Indications	<b>NONE</b>
221-5	Designated States for Which Indications are Made	<b>all designated States</b>
221-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
222	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
222-1	page	102
222-2	line	55
222-3	Identification of Deposit	
222-3-1	Name of depositary institution	American Type Culture Collection
222-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
222-3-3	Date of deposit	16 June 1998 (16.06.1998)
222-3-4	Accession Number	ATCC 209988
222-4	Additional Indications	<b>NONE</b>
222-5	Designated States for Which Indications are Made	<b>all designated States</b>
222-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
223	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
223-1	page	103
223-2	line	2

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223-3	<b>Identification of Deposit</b>	
223-3-1	Name of depositary institution	American Type Culture Collection
223-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
223-3-3	Date of deposit	16 June 1998 (16.06.1998)
223-3-4	Accession Number	ATCC 209978
223-4	<b>Additional Indications</b>	NONE
223-5	<b>Designated States for Which Indications are Made</b>	all designated States
223-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
224	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
224-1	page	103
224-2	line	3
224-3	<b>Identification of Deposit</b>	
224-3-1	Name of depositary institution	American Type Culture Collection
224-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
224-3-3	Date of deposit	04 August 1998 (04.08.1998)
224-3-4	Accession Number	ATCC 203098
224-4	<b>Additional Indications</b>	NONE
224-5	<b>Designated States for Which Indications are Made</b>	all designated States
224-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE
225	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
225-1	page	103
225-2	line	4
225-3	<b>Identification of Deposit</b>	
225-3-1	Name of depositary institution	American Type Culture Collection
225-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
225-3-3	Date of deposit	16 June 1998 (16.06.1998)
225-3-4	Accession Number	ATCC 209980
225-4	<b>Additional Indications</b>	NONE
225-5	<b>Designated States for Which Indications are Made</b>	all designated States
225-6	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	NONE

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226	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
226-1	page	103
226-2	line	5
226-3	Identification of Deposit	
226-3-1	Name of depositary institution	American Type Culture Collection
226-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
226-3-3	Date of deposit	04 August 1998 (04.08.1998)
226-3-4	Accession Number	ATCC 203091
226-4	Additional Indications	NONE
226-5	Designated States for Which Indications are Made	all designated States
226-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
227	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
227-1	page	103
227-2	line	6
227-3	Identification of Deposit	
227-3-1	Name of depositary institution	American Type Culture Collection
227-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
227-3-3	Date of deposit	04 August 1998 (04.08.1998)
227-3-4	Accession Number	ATCC 203090
227-4	Additional Indications	NONE
227-5	Designated States for Which Indications are Made	all designated States
227-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
228	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
228-1	page	103
228-2	line	7
228-3	Identification of Deposit	
228-3-1	Name of depositary institution	American Type Culture Collection
228-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
228-3-3	Date of deposit	04 August 1998 (04.08.1998)
228-3-4	Accession Number	ATCC 203092
228-4	Additional Indications	NONE
228-5	Designated States for Which Indications are Made	all designated States

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228-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
229	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
229-1	page	103
229-2	line	8
229-3	Identification of Deposit	
229-3-1	Name of depositary institution	American Type Culture Collection
229-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
229-3-3	Date of deposit	10 November 1998 (10.11.1998)
229-3-4	Accession Number	ATCC 203452
229-4	Additional Indications	NONE
229-5	Designated States for Which Indications are Made	all designated States
229-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
230	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
230-1	page	103
230-2	line	9
230-3	Identification of Deposit	
230-3-1	Name of depositary institution	American Type Culture Collection
230-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
230-3-3	Date of deposit	01 September 1998 (01.09.1998)
230-3-4	Accession Number	ATCC 203173
230-4	Additional Indications	NONE
230-5	Designated States for Which Indications are Made	all designated States
230-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
231	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
231-1	page	103
231-2	line	10
231-3	Identification of Deposit	
231-3-1	Name of depositary institution	American Type Culture Collection
231-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
231-3-3	Date of deposit	17 November 1998 (17.11.1998)
231-3-4	Accession Number	ATCC 203464

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231-4	Additional Indications	NONE
231-5	Designated States for Which Indications are Made	all designated States
231-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
232	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
232-1	page	103
232-2	line	11
232-3	Identification of Deposit	
232-3-1	Name of depositary institution	American Type Culture Collection
232-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
232-3-3	Date of deposit	18 August 1998 (18.08.1998)
232-3-4	Accession Number	ATCC 203132
232-4	Additional Indications	NONE
232-5	Designated States for Which Indications are Made	all designated States
232-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
233	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
233-1	page	103
233-2	line	12
233-3	Identification of Deposit	
233-3-1	Name of depositary institution	American Type Culture Collection
233-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
233-3-3	Date of deposit	09 September 1998 (09.09.1998)
233-3-4	Accession Number	ATCC 203254
233-4	Additional Indications	NONE
233-5	Designated States for Which Indications are Made	all designated States
233-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
234	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
234-1	page	103
234-2	line	13

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234-3	Identification of Deposit	
234-3-1	Name of depositary institution	American Type Culture Collection
234-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
234-3-3	Date of deposit	20 October 1998 (20.10.1998)
234-3-4	Accession Number	ATCC 203358
234-4	Additional Indications	NONE
234-5	Designated States for Which Indications are Made	all designated States
234-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
235	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
235-1	page	103
235-2	line	14
235-3	Identification of Deposit	
235-3-1	Name of depositary institution	American Type Culture Collection
235-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
235-3-3	Date of deposit	04 August 1998 (04.08.1998)
235-3-4	Accession Number	ATCC 203093
235-4	Additional Indications	NONE
235-5	Designated States for Which Indications are Made	all designated States
235-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
236	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
236-1	page	103
236-2	line	15
236-3	Identification of Deposit	
236-3-1	Name of depositary institution	American Type Culture Collection
236-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
236-3-3	Date of deposit	03 November 1998 (03.11.1998)
236-3-4	Accession Number	ATCC 203457
236-4	Additional Indications	NONE
236-5	Designated States for Which Indications are Made	all designated States
236-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

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237		The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
237-1	page	103	
237-2	line	16	
237-3	Identification of Deposit		
237-3-1	Name of depositary institution	American Type Culture Collection	
237-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
237-3-3	Date of deposit	09 September 1998 (09.09.1998)	
237-3-4	Accession Number	ATCC 203241	
237-4	Additional Indications	NONE	
237-5	Designated States for Which Indications are Made	all designated States	
237-6	Separate Furnishing of Indications	NONE	
These indications will be submitted to the International Bureau later			
238		The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
238-1	page	103	
238-2	line	17	
238-3	Identification of Deposit		
238-3-1	Name of depositary institution	American Type Culture Collection	
238-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
238-3-3	Date of deposit	09 September 1998 (09.09.1998)	
238-3-4	Accession Number	ATCC 203249	
238-4	Additional Indications	NONE	
238-5	Designated States for Which Indications are Made	all designated States	
238-6	Separate Furnishing of Indications	NONE	
These indications will be submitted to the International Bureau later			
239		The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
239-1	page	103	
239-2	line	18	
239-3	Identification of Deposit		
239-3-1	Name of depositary institution	American Type Culture Collection	
239-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
239-3-3	Date of deposit	09 September 1998 (09.09.1998)	
239-3-4	Accession Number	ATCC 203250	
239-4	Additional Indications	NONE	
239-5	Designated States for Which Indications are Made	all designated States	

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239-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
240	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
240-1	page	103
240-2	line	19
240-3	Identification of Deposit	
240-3-1	Name of depositary institution	American Type Culture Collection
240-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
240-3-3	Date of deposit	18 August 1998 (18.08.1998)
240-3-4	Accession Number	ATCC 203131
240-4	Additional Indications	NONE
240-5	Designated States for Which Indications are Made	all designated States
240-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
241	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
241-1	page	103
241-2	line	20
241-3	Identification of Deposit	
241-3-1	Name of depositary institution	American Type Culture Collection
241-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
241-3-3	Date of deposit	15 September 1998 (15.09.1998)
241-3-4	Accession Number	ATCC 203223
241-4	Additional Indications	NONE
241-5	Designated States for Which Indications are Made	all designated States
241-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
242	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
242-1	page	103
242-2	line	21
242-3	Identification of Deposit	
242-3-1	Name of depositary institution	American Type Culture Collection
242-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
242-3-3	Date of deposit	15 September 1998 (15.09.1998)
242-3-4	Accession Number	ATCC 203233

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242-4	Additional Indications	<b>NONE</b>
242-5	Designated States for Which Indications are Made	<b>all designated States</b>
242-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
243	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:  page line	103 22
243-3	Identification of Deposit Name of depositary institution Address of depositary institution	<b>American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
243-3-3	Date of deposit	<b>09 September 1998 (09.09.1998)</b>
243-3-4	Accession Number	<b>ATCC 203252</b>
243-4	Additional Indications	<b>NONE</b>
243-5	Designated States for Which Indications are Made	<b>all designated States</b>
243-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
244	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:  page line	103 23
244-3	Identification of Deposit Name of depositary institution Address of depositary institution	<b>American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America</b>
244-3-3	Date of deposit	<b>17 November 1998 (17.11.1998)</b>
244-3-4	Accession Number	<b>ATCC 203476</b>
244-4	Additional Indications	<b>NONE</b>
244-5	Designated States for Which Indications are Made	<b>all designated States</b>
244-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	<b>NONE</b>
245	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:  page line	103 24

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245-3	Identification of Deposit	
245-3-1	Name of depositary institution	American Type Culture Collection
245-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
245-3-3	Date of deposit	04 August 1998 (04.08.1998)
245-3-4	Accession Number	ATCC 203094
245-4	Additional Indications	NONE
245-5	Designated States for Which Indications are Made	all designated States
245-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
246	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
246-1	page	103
246-2	line	25
246-3	Identification of Deposit	
246-3-1	Name of depositary institution	American Type Culture Collection.
246-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
246-3-3	Date of deposit	15 September 1998 (15.09.1998)
246-3-4	Accession Number	ATCC 203235
246-4	Additional Indications	NONE
246-5	Designated States for Which Indications are Made	all designated States
246-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
247	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
247-1	page	103
247-2	line	26
247-3	Identification of Deposit	
247-3-1	Name of depositary institution	American Type Culture Collection
247-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
247-3-3	Date of deposit	22 September 1998 (22.09.1998)
247-3-4	Accession Number	ATCC 203267
247-4	Additional Indications	NONE
247-5	Designated States for Which Indications are Made	all designated States
247-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

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248	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
248-1	page	103
248-2	line	27
248-3	Identification of Deposit	
248-3-1	Name of depositary institution	American Type Culture Collection
248-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
248-3-3	Date of deposit	22 September 1998 (22.09.1998)
248-3-4	Accession Number	ATCC 203282
248-4	Additional Indications	NONE
248-5	Designated States for Which Indications are Made	all designated States
248-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
249	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
249-1	page	103
249-2	line	28
249-3	Identification of Deposit	
249-3-1	Name of depositary institution	American Type Culture Collection
249-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
249-3-3	Date of deposit	09 February 1999 (09.02.1999)
249-3-4	Accession Number	ATCC 203657
249-4	Additional Indications	NONE
249-5	Designated States for Which Indications are Made	all designated States
249-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
250	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
250-1	page	103
250-2	line	29
250-3	Identification of Deposit	
250-3-1	Name of depositary institution	American Type Culture Collection
250-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
250-3-3	Date of deposit	22 September 1998 (22.09.1998)
250-3-4	Accession Number	ATCC 203276
250-4	Additional Indications	NONE
250-5	Designated States for Which Indications are Made	all designated States

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250-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
251	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
251-1	page	103
251-2	line	30
251-3	Identification of Deposit	
251-3-1	Name of depositary institution	American Type Culture Collection
251-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
251-3-3	Date of deposit	25 August 1998 (25.08.1998)
251-3-4	Accession Number	ATCC 203160
251-4	Additional Indications	<b>NONE</b>
251-5	Designated States for Which Indications are Made	<b>all designated States</b>
251-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
252	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
252-1	page	103
252-2	line	31
252-3	Identification of Deposit	
252-3-1	Name of depositary institution	American Type Culture Collection
252-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
252-3-3	Date of deposit	18 August 1998 (18.08.1998)
252-3-4	Accession Number	ATCC 203135
252-4	Additional Indications	<b>NONE</b>
252-5	Designated States for Which Indications are Made	<b>all designated States</b>
252-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	<b>NONE</b>
253	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
253-1	page	103
253-2	line	32
253-3	Identification of Deposit	
253-3-1	Name of depositary institution	American Type Culture Collection
253-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
253-3-3	Date of deposit	03 November 1998 (03.11.1998)
253-3-4	Accession Number	ATCC 203459

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253-4	Additional Indications	NONE
253-5	Designated States for Which Indications are Made	all designated States
253-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
254	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
254-1	page	103
254-2	line	33
254-3	Identification of Deposit Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
254-3-2	Address of depositary institution	
254-3-3	Date of deposit	22 September 1998 (22.09.1998)
254-3-4	Accession Number	ATCC 203270
254-4	Additional Indications	NONE
254-5	Designated States for Which Indications are Made	all designated States
254-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
255	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
255-1	page	103
255-2	line	34
255-3	Identification of Deposit Name of depositary institution	American Type Culture Collection 10801 University Blvd., Manassas, Virginia 20110-2209United States of America
255-3-2	Address of depositary institution	
255-3-3	Date of deposit	12 January 1999 (12.01.1999)
255-3-4	Accession Number	ATCC 203573
255-4	Additional Indications	NONE
255-5	Designated States for Which Indications are Made	all designated States
255-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
256	The Indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
256-1	page	103
256-2	line	35

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256-3	Identification of Deposit	
256-3-1	Name of depositary institution	American Type Culture Collection
256-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
256-3-3	Date of deposit	17 November 1998 (17.11.1998)
256-3-4	Accession Number	ATCC 203477
256-4	Additional Indications	NONE
256-5	Designated States for Which Indications are Made	all designated States
256-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
257	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
257-1	page	103
257-2	line	36
257-3	Identification of Deposit	
257-3-1	Name of depositary institution	American Type Culture Collection
257-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
257-3-3	Date of deposit	06 October 1998 (06.10.1998)
257-3-4	Accession Number	ATCC 203315
257-4	Additional Indications	NONE
257-5	Designated States for Which Indications are Made	all designated States
257-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
258	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
258-1	page	103
258-2	line	37
258-3	Identification of Deposit	
258-3-1	Name of depositary institution	American Type Culture Collection
258-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
258-3-3	Date of deposit	06 October 1998 (06.10.1998)
258-3-4	Accession Number	ATCC 203313
258-4	Additional Indications	NONE
258-5	Designated States for Which Indications are Made	all designated States
258-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

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259	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
259-1 page	103	
259-2 line	38	
259-3 Identification of Deposit		
259-3-1 Name of depositary institution	American Type Culture Collection	
259-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
259-3-3 Date of deposit	27 October 1998 (27.10.1998)	
259-3-4 Accession Number	ATCC 203407	
259-4 Additional Indications	NONE	
259-5 Designated States for Which Indications are Made	all designated States	
259-6 Separate Furnishing of Indications	NONE	
	These indications will be submitted to the International Bureau later	
260	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
260-1 page	103	
260-2 line	39	
260-3 Identification of Deposit		
260-3-1 Name of depositary institution	American Type Culture Collection	
260-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
260-3-3 Date of deposit	22 December 1998 (22.12.1998)	
260-3-4 Accession Number	ATCC 203553	
260-4 Additional Indications	NONE	
260-5 Designated States for Which Indications are Made	all designated States	
260-6 Separate Furnishing of Indications	NONE	
	These indications will be submitted to the International Bureau later	
261	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
261-1 page	103	
261-2 line	40	
261-3 Identification of Deposit		
261-3-1 Name of depositary institution	American Type Culture Collection	
261-3-2 Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America	
261-3-3 Date of deposit	22 December 1998 (22.12.1998)	
261-3-4 Accession Number	ATCC 203549	
261-4 Additional Indications	NONE	
261-5 Designated States for Which Indications are Made	all designated States	

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261-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
262	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
262-1	page	103
262-2	line	41
262-3	Identification of Deposit	
262-3-1	Name of depositary institution	American Type Culture Collection
262-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
262-3-3	Date of deposit	22 December 1998 (22.12.1998)
262-3-4	Accession Number	ATCC 203550
262-4	Additional Indications	NONE
262-5	Designated States for Which Indications are Made	all designated States
262-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
263	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
263-1	page	103
263-2	line	42
263-3	Identification of Deposit	
263-3-1	Name of depositary institution	American Type Culture Collection
263-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
263-3-3	Date of deposit	08 June 1999 (08.06.1999)
263-3-4	Accession Number	ATCC PTA-204
263-4	Additional Indications	NONE
263-5	Designated States for Which Indications are Made	all designated States
263-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE
264	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
264-1	page	103
264-2	line	43
264-3	Identification of Deposit	
264-3-1	Name of depositary institution	American Type Culture Collection
264-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
264-3-3	Date of deposit	29 October 1998 (29.10.1998)
264-3-4	Accession Number	ATCC 203391

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<b>264-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>264-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>264-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	<b>NONE</b>
<b>265</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
265-1	page	103
265-2	line	44
<b>265-3</b>	<b>Identification of Deposit</b>	
265-3-1	Name of depositary institution	American Type Culture Collection
265-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
265-3-3	Date of deposit	23 March 1999 (23.03.1999)
265-3-4	Accession Number	ATCC 203863
<b>265-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>265-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>265-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	<b>NONE</b>
<b>266</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
266-1	page	103
266-2	line	45
<b>266-3</b>	<b>Identification of Deposit</b>	
266-3-1	Name of depositary institution	American Type Culture Collection
266-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
266-3-3	Date of deposit	09 March 1999 (09.03.1999)
266-3-4	Accession Number	ATCC 203834
<b>266-4</b>	<b>Additional Indications</b>	<b>NONE</b>
<b>266-5</b>	<b>Designated States for Which Indications are Made</b>	<b>all designated States</b>
<b>266-6</b>	<b>Separate Furnishing of Indications</b>  These indications will be submitted to the International Bureau later	<b>NONE</b>
<b>267</b>	<b>The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:</b>	
267-1	page	103
267-2	line	46

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Original (for SUBMISSION) - printed on 01.12.2000 02:57:35 PM

267-3	Identification of Deposit	
267-3-1	Name of depositary institution	American Type Culture Collection
267-3-2	Address of depositary institution	10801 University Blvd., Manassas, Virginia 20110-2209United States of America
267-3-3	Date of deposit	20 July 1999 (20.07.1999)
267-3-4	Accession Number	ATCC PTA-382
267-4	Additional Indications	NONE
267-5	Designated States for Which Indications are Made	all designated States
267-6	Separate Furnishing of Indications  These indications will be submitted to the International Bureau later	NONE

**FOR RECEIVING OFFICE USE ONLY**

0-4	This form was received with the international application: (yes or no)	
0-4-1	Authorized officer	

**FOR INTERNATIONAL BUREAU USE ONLY**

0-5	This form was received by the international Bureau on:	
0-5-1	Authorized officer	

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16),  
5 Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54),  
10 Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92),  
15 Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID



NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) and Figure 550 (SEQ ID NO:550).

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2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:1390), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID

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- 10       3.     Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:1390), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ

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Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figure 525 (SEQ ID NO:525), Figure 527 (SEQ  
10 ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533),  
Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ  
ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547) and  
Figure 549 (SEQ ID NO:549).

15 4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding  
sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.

20 6. The vector of Claim 5 operably linked to control sequences recognized by a host cell  
transformed with the vector.

7. A host cell comprising the vector of Claim 5.

25 8. The host cell of Claim 7, wherein said cell is a CHO cell.

9. The host cell of Claim 7, wherein said cell is an *E. coli*.

10. The host cell of Claim 7, wherein said cell is a yeast cell.

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11. A process for producing a PRO polypeptides comprising culturing the host cell of Claim 7  
under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the  
cell culture.

35

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid  
sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2),  
Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10),

Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48),  
5 Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86),  
10 Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure

284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) and

Figure 550 (SEQ ID NO:550).

13. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

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14. A chimeric molecule comprising a polypeptide according to Claim 12 fused to a heterologous amino acid sequence.

10 15. The chimeric molecule of Claim 14, wherein said heterologous amino acid sequence is an epitope tag sequence.

16. The chimeric molecule of Claim 14, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

15 17. An antibody which specifically binds to a polypeptide according to Claim 12.

18. The antibody of Claim 17, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

20 19. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ

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30 ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340),  
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35 Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ  
ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382),  
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ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410),  
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ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424),  
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ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438),  
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ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452),  
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ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480),  
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ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508),  
Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ  
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Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ  
20 ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536),  
Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ  
ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550),  
lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2  
25 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ  
ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18  
(SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure  
26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32),  
Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID  
30 NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ  
ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56  
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64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70),  
Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID  
35 NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ  
ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94  
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Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114),  
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Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240),  
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Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380),  
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ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478),  
15 Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ  
ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492),  
Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ  
ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506),  
20 Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ  
ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520),  
Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ  
ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534),  
Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ  
ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or  
25 Figure 550 (SEQ ID NO:550), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2  
(SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ  
ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18  
30 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure  
26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32),  
Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID  
NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ  
ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56  
35 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure  
64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70),  
Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID

NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114),  
5 Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ  
10 ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184),  
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20 ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254),  
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ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352),  
Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ  
ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366),  
Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ  
ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380),  
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Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ  
ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408),  
Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ  
10 ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422),  
Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ  
ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436),  
Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ  
ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450),  
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ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464),  
Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ  
ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478),  
Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ  
20 ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492),  
Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ  
ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506),  
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ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520),  
25 Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ  
ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534),  
Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ  
ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or  
Figure 550 (SEQ ID NO:550), lacking its associated signal peptide.

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20. An isolated polypeptide having at least 80% amino acid sequence identity to:
- (a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ  
ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ  
ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20  
35 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure  
28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34),  
Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID

NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116),  
5 Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ  
10 ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186),  
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25 ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256),  
30 Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ  
35 ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312),

Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326),  
5 Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340),  
Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354),  
10 Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368),  
Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382),  
15 Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396),  
Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410),  
Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424),  
20 Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438),  
Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452),  
25 Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466),  
Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480),  
Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494),  
30 Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508),  
Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522),  
35 Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536),  
Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550),  
lacking its associated signal peptide;  
35 (b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ

ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ  
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Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ  
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15 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID  
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30 NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure  
35 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID

NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 5 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 10 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 20 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 35

270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure

536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548) or Figure 550 (SEQ ID NO:550), lacking its associated signal peptide.

5 21. A method of detecting a PRO1801 polypeptide in a sample suspected of containing a PRO1801 polypeptide, said method comprising contacting said sample with a PRO1114 or PRO4978 polypeptide and determining the formation of a PRO1801/PRO1114 or PRO1801/PRO4978 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1801 polypeptide in said sample.

10 22. The method according to Claim 21, wherein said sample comprises cells suspected of expressing said PRO1801 polypeptide.

23. The method according to Claim 21, wherein said PRO1114 or PRO4978 polypeptide is labeled with a detectable label.

15 24. The method according to Claim 21, wherein said PRO1114 or PRO4978 polypeptide is attached to a solid support.

20 25. A method of detecting a PRO1114 or PRO4978 polypeptide in a sample suspected of containing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said sample with a PRO1801 polypeptide and determining the formation of a PRO1801/PRO1114 or PRO1801/PRO4978 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1114 or PRO4978 polypeptide in said sample.

25 26. The method according to Claim 25, wherein said sample comprises cells suspected of expressing said PRO1114 or PRO4978 polypeptide.

27. The method according to Claim 25, wherein said PRO1801 polypeptide is labeled with a detectable label.

30 28. The method according to Claim 25, wherein said PRO1801 polypeptide is attached to a solid support.

35 29. A method of linking a bioactive molecule to a cell expressing a PRO1801 polypeptide, said method comprising contacting said cell with a PRO1114 or PRO4978 polypeptide that is bound to said bioactive molecule and allowing said PRO1801 and said PRO1114 or PRO4978 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

30. The method according to Claim 29, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

31. The method according to Claim 29, wherein said bioactive molecule causes the death of said cell.

5

32. A method of linking a bioactive molecule to a cell expressing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said cell with a PRO1801 polypeptide that is bound to said bioactive molecule and allowing said PRO1801 and said PRO1114 or PRO4978 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

10

33. The method according to Claim 32, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

15

34. The method according to Claim 32, wherein said bioactive molecule causes the death of said cell.

20

35. A method of modulating at least one biological activity of a cell expressing a PRO1801 polypeptide, said method comprising contacting said cell with a PRO1114 or PRO4978 polypeptide or an anti-PRO1801 polypeptide antibody, whereby said PRO1114 or PRO4978 polypeptide or anti-PRO1801 polypeptide antibody binds to said PRO1801 polypeptide, thereby modulating at least one biological activity of said cell.

36. The method according to Claim 35, wherein said cell is killed.

25

37. A method of modulating at least one biological activity of a cell expressing a PRO1114 or PRO4978 polypeptide, said method comprising contacting said cell with a PRO1801 polypeptide or an anti-PRO1114 or anti-PRO4978 polypeptide antibody, whereby said PRO1801 polypeptide or anti-PRO1114 or anti-PRO4978 polypeptide antibody binds to said PRO1114 or PRO4978 polypeptide, thereby modulating at least one biological activity of said cell.

30

38. The method according to Claim 37, wherein said cell is killed.

35

39. A method of detecting a PRO1114 polypeptide in a sample suspected of containing a PRO1114 polypeptide, said method comprising contacting said sample with a PRO100 polypeptide and determining the formation of a PRO100/PRO1114 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1114 polypeptide in said sample.

40. The method according to Claim 39, wherein said sample comprises cells suspected of expressing said PRO1114 polypeptide.

41. The method according to Claim 39, wherein said PRO100 polypeptide is labeled with a detectable label.

5

42. The method according to Claim 39, wherein said PRO100 polypeptide is attached to a solid support.

10 43. A method of detecting a PRO100 polypeptide in a sample suspected of containing a PRO100 polypeptide, said method comprising contacting said sample with a PRO1114 polypeptide and determining the formation of a PRO100/PRO1114 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO100 polypeptide in said sample.

15 44. The method according to Claim 43, wherein said sample comprises cells suspected of expressing said PRO100 polypeptide.

45. The method according to Claim 43, wherein said PRO1114 polypeptide is labeled with a detectable label.

20 46. The method according to Claim 43, wherein said PRO1114 polypeptide is attached to a solid support.

25 47. A method of linking a bioactive molecule to a cell expressing a PRO100 polypeptide, said method comprising contacting said cell with a PRO1114 polypeptide that is bound to said bioactive molecule and allowing said PRO100 and said PRO1114 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

48. The method according to Claim 47, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

30

49. The method according to Claim 47, wherein said bioactive molecule causes the death of said cell.

35 50. A method of linking a bioactive molecule to a cell expressing a PRO1114 polypeptide, said method comprising contacting said cell with a PRO100 polypeptide that is bound to said bioactive molecule and allowing said PRO100 and said PRO1114 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

51. The method according to Claim 50, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

52. The method according to Claim 50, wherein said bioactive molecule causes the death of said cell.

5

53. A method of modulating at least one biological activity of a cell expressing a PRO100 polypeptide, said method comprising contacting said cell with a PRO1114 polypeptide or an anti-PRO100 polypeptide antibody, whereby said PRO1114 polypeptide or anti-PRO100 polypeptide antibody binds to said PRO100 polypeptide, thereby modulating at least one biological activity of said cell.

10

54. The method according to Claim 53, wherein said cell is killed.

55. A method of modulating at least one biological activity of a cell expressing a PRO1114 polypeptide, said method comprising contacting said cell with a PRO100 polypeptide or an anti-PRO1114 polypeptide antibody, whereby said PRO100 polypeptide or anti-PRO1114 polypeptide antibody binds to said PRO1114 polypeptide, thereby modulating at least one biological activity of said cell.

15

56. The method according to Claim 55, wherein said cell is killed.

20

57. A method for stimulating the release of TNF- $\alpha$  from human blood, said method comprising contacting said blood with a PRO195, PRO202, PRO215, PRO221, PRO217, PRO222, PRO198, PRO245, PRO172, PRO265, PRO266, PRO344, PRO337, PRO322, PRO1286, PRO1279, PRO1338 or PRO1343 polypeptide, wherein the release of TNF- $\alpha$  from said blood is stimulated.

25

58. A method for modulating the uptake of glucose or FFA by skeletal muscle cells, said method comprising contacting said cells with a PRO182, PRO366, PRO198, PRO172 or PRO719 polypeptide, wherein the uptake of glucose or FFA by said cells is modulated.

30

59. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO182, PRO366, PRO198, PRO1868, PRO202, PRO224, PRO172, PRO301 or PRO1312 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

35

60. A method for modulating the uptake of glucose or FFA by adipocyte cells, said method comprising contacting said cells with a PRO202, PRO211, PRO344 or PRO1338 polypeptide, wherein the uptake of glucose or FFA by said cells is modulated.

61. A method for stimulating the proliferation of or gene expression in pericyte cells, said method comprising contacting said cells with a PRO366 polypeptide, wherein the proliferation of or gene expression in said cells is stimulated.

5 62. A method for stimulating the release of proteoglycans from cartilage, said method comprising contacting said cartilage with a PRO216 polypeptide, wherein the release of proteoglycans from said cartilage is stimulated.

10 63. A method for stimulating the proliferation of inner ear utricular supporting cells, said method comprising contacting said cells with a PRO172 polypeptide, wherein the proliferation of said cells is stimulated.

15 64. A method for stimulating the proliferation of T-lymphocyte cells, said method comprising contacting said cells with a PRO344 polypeptide, wherein the proliferation of said cells is stimulated.

15 65. A method for stimulating the release of a cytokine from PBMC cells, said method comprising contacting said cells with a PRO526 or PRO1343 polypeptide, wherein the release of a cytokine from said cells is stimulated.

20 66. A method for inhibiting the binding of A-peptide to factor VIIA, said method comprising contacting a composition comprising said A-peptide and said factor VIIA with a PRO182 polypeptide, wherein the binding of said A-peptide to said factor VIIA is inhibited.

67. A method for inhibiting the differentiation of adipocyte cells, said method comprising contacting said cells with a PRO185 or PRO198 polypeptide, wherein the differentiation of said cells is inhibited.

25 68. A method for stimulating the proliferation of endothelial cells, said method comprising contacting said cells with a PRO222 polypeptide, wherein the proliferation of said cells is inhibited.

30 69. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

35 70. The method of Claim 69, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

71. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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**FIGURE 1**

GTTACTCGGTGGTGGCGGAGTCTACCGAAGCCCTTCGCTTCACTTTCTGGCTGTAGAGC  
GCTTTCCCCCTGGCGGGTGAGAGTGCAGAGACGAAGGTGCGAGTGAGCACTATGTTCGCGGA  
CACTCTCCTCATCGTTTATCTCTGTGTGCACGGCTCTGCTCGCAGAGGGCATAACCTGGGT  
CCTGGTTTACAGGACAGACAAGTACAAGAGACTGAAGGCAGAAGTGGAAAAACAGAGTAAAAAA  
ATTGGAAAAGAAGAAGGAAACAATAACAGAGTCAGCTGGTCGACAACAGAAAAGAAAATAGA  
GAGACAGAAGAGAAA**ACT**GAAGAATAACAACAGAGATCTATCAATGGTTCGAATGAAATCCAT  
GTTTGCTATTGGCTTTGTTACTGCCCTAATGGGAATGTTCAATTCCATATTGATGGTAG  
AGTGGTGGCAAAGCTTCCCTTACCCCTCTTACATCCAAGGACTGTCTCATCGAAATCT  
GCTGGGAGATGACACCACAGACTGTTCCCTCATTTCCTGTATATTCTCTGTACTATGTCGAT  
TCGACAGAACATTCTAGAAGATTCTGGCCTTGCCCCTCACGAGCCGCCACCAAGCAGGCAGG  
TGGATTCTGGCCCACCACCTCTGGGAAGTCTCTTGAACTCAAGAACTCTTATTT  
CTATCATTCTTCTAGACACACACACATCAGACTGGCAACTGTTTGTAGCAAGAGCCATAGG  
TAGCCTTA**ACT**ACTGGCCTCTTAGTTGAATTATTCTAAGCCTTGGGTATGATTA  
GAGTGAAAATGGCAGCCAGCAA**ACT**TGATAGTGTCTGGCCTAGATGATTTTATCAAATA  
AGTGGATTGATTAGTTAAGTTCAAGGTAATGTTATGTAATGAAAAACAAATAGCATTCTCTT  
GTTTCATTACATAAGTATTTCTGTGGGACCGACTCTCAAGGCACTGTGTATGCCCTGCAAG  
TTGGCTGTCTATGAGCATTAGAGATTAGAAGAAAATTAGTTGTTAACCTTGTA**ACT**  
GTTTGTGTTGTTGTTGTTCAAGCCAATACATGACATAAGATCAATAAGAGGCCA  
AATTTTAGCTGTTATGTAACAGGAGAGATCTGTTCAAGGACTAAAATAAGGTTAAGGTACAAAAAA  
AAAA

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**FIGURE 2**

MSTMFADTLLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGR  
QQKKKIERQEEKLKNNNRDLSTMVRMKSMAIGFCFTALMGMFNSIFDGRVVAKLPFTPLSYIQ  
GLSHRNLLGDDTTDCSFIFLYILCTMSIRQNIQKILGLAPSRAATKQAGGFLGPPPSGKFS

**Important features:****Signal peptide:**

amino acids 1-22

**N-myristoylation sites..**

amino acids 103-109, 163-169

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 53-57

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**FIGURE 3**

AGCCGGGGCGGGTTGAAGACGCGTCGTTGGGTTTGGAGGCCGTAAACAGCCGTTGAGT  
TTGGCTGCGGTGGAGAACGTTGTCAGGGGCCGCAAGAAGGAGGCCGCTGTTACG**AT**  
**G**GTGTCCATGAGTTCAAGCGAACCGCAGTGACCGGTCTACAGCACCCGGTGCCTGGCTG  
TTGCCATGTCCGCACCAGGACGATCATCCTGGGACCTGGTACATGGTAGTAAACCTATTGAT  
GGCAATTTGCTGACTGTGGAAGTGACTCATCCAAACTCCATGCCAGCTGTCAACATTAGTA  
TGAAGTCATCGTAATTACTATTGCTGAGAGAATGGCTGATAATGCCGTGTTCTTTGC  
CGTCTCTGTTCTATGTTATAATCAGTTCAATGCTGGTTATGGAGCAATTCTTATCAAGT  
GGGTTGGCTGATTCCATTCTCTGTTACCGACTTTGACTTCGTCCTCAGTTGCCTGGTTGC  
TATTAGTTCTCACCTATTGCCAAGAACATCAAAGAATATCTGGATCAACTACCTGATTTC  
CTACAAAGATGACCTCCTGGCCTTGGACTCCAGCTGCCCTGTTCAATTGTTCTGTGTTCTT  
TGCCTTATTCATCATTAAAGGCTATCTAATTAACTGTGTTGGAACGTCTATAAACAT  
CAACAACCGAAACGTGCCGGAGATTGCTGTGACCTGCCTTGAAAGCACCTC**T**ACG  
TTTGCCAACCTATGAAATGGCGTGAAAATGCCGAAAAAGAACACCACCTCCTTACCTAC  
CTGCCTGAAAGAAATTCTGCCTTGACAATAAACCTATACCAGCTTTGTTGTTATGTTA  
CAGAATGCTGCAATTAGGGCTCTCAAACCTGTTGATATAAAATATGTTGCTTTGTTA  
AGCATTTATTTCAAACACTAAGGAGCTTTGACATCTGTTAAACGTCTTTGTTTTG  
TTAAGTCTTTACATTAAAGTTTGAAGACAACTAGGTTAAGCAAGAGCAAAGTGCCA  
TTGTTGCCTTAATTGGGGGTGGGAAGGGAAAGAGGGTACTGCCACATAGTTCTTT  
AACTGCACTTCTTATATAATCGTTGCATTTGTTACTGCTACCCGTAGTACTTCAGGA  
AGACTGACTAAATATTGGGGTGAGTAAGTAGTTGGGTATAAGATCTGAACCTTCATCTGC  
AGAGGCAAGAAAATATTGACATTGACTGTGACTGTGGAAGATGATGGTTGCATGTTCTA  
GTTGTTGATATGTTCCATTTGTTGATAAGATGATTAAATAATCTCTTAAATACTAAAAAA  
AAAAAAA

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**FIGURE 4**

MVSMASFKNRSDRFYSTRCCGCCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQ  
YEVIGNYYSSERMAVDNACVLFAVSVLMDIISMLVYGAISYQVGWLIPFFCYRLFDFVLSCLV  
AISSILTYLPRIKEYLDQLPDFPYKDDLLALDSSCLLFIVLVFFALFIIIFKAYLINCWNNCYKY  
INNRNVPEIAVYPAFESTSSVRFANL

**Important features of the protein:**

**Transmembrane domain (Possible type II transmembrane protein):**

amino acids 30-49, 81-100, 111-131, 158-175

**N-glycosylation site.**

amino acids 9-13

**Tyrosine kinase phosphorylation sites.**

amino acids 8-16, 193-202

**N-myristoylation site.**

amino acids 68-74

5/550

**FIGURE 5**

CCCGCTGGCCCGTCAGTGCTCTCCCCGCGTTGCCCTCTCCAGTCCCCCAGTGCCTGCCCT  
ACGCACCCCGATGGCGGAGCTGCGGCTAGCGCGCCCCCGGCCAACCGCGCCCCGGCCC  
TGGCCCGACTGCCCTGGCTTCGCTCTTCCCCGGACTGCACGCCATCTACGG  
AGAGTGCCGCCCTTACCTGACCAGCGAACCCGCTCCAGGTTACCGCTATCGTAAGTA  
CTGGTTGGGTGGCCAGACCCCTGGACTATGTTAGCATGTACAGGAATGTGGGGAGCCCTC  
TGCTAACATCCCCGAGCACTGGCACTACATCAGCTTGGCCCTGAGTGATCTATGGTGACAA  
CAGAGTCATGAGTTACAGGAACAGATGGACCTAGTGGTTGGCTTGAGTTGACCTTCG  
TCTGAAGAGAGAAACTGGGAGTCTGCCCCACCAACATGGCCCGAGAGTTAATGCAGGGCTT  
GGCACGATACGTGTCCAGTCAGAGAACACCTCTGCAGTGGGACCATGTGTCCTGGCACAG  
CCCTTGGATAACAGTGAGTCAGAACATTAGCACATGCTGCTGACAGAGGACCCACAGATGCA  
GCCCGTGCAGACACCCTTGGGTAGTTACCTCCTCCAGATCGTGGTGTCTGCACTGAAGA  
GCTACACTCAGCCCAGCAGTGGAACGGCAGGGCATCCTGGAGCTGCTGCGGACAGTCCTAT  
TGCTGGCGCCCTGGCTGATAACTGACATGCGGAGGGAGAGACCATAATTGAGATCGATCC  
ACACCTGCAAGAGAGAGTTGACAAAGGCATCGAGACAGATGGCTCAAACCTGAGTGGTGTCA  
TGCCAAGTGTGCTGGATGACCTGAGCCGGCCCCCGAGGGATGACGGAGCACGCCAGCAT  
CTGCATCGGCACACAGCCCCGGGACTCTGGCAAAGACACAGAGCAGATCCGGAGACCC  
GAGGAGAGGACTCGAGATCAACAGCAAACCTGCTCCACCAATCAACCCCTAGCGGCAGAA  
TGGCCTGCCACGACGGGCCCCGAGCCGCAAAGACAGCAGCTGGAAAGTGACAGCTCACGG  
CATCATTCCCCATGAGCTGATTGACAGCGGGCAGCTTGAGAGCGTACATCTGAAATTCAACCA  
GGAGTCCGGAGCCCTCATTCTCTGCCTAAGGGCAGGCTCTGCATGGACGGCACTTAC  
ATATAAAAGTATCACAGGTGACATGCCATCACGTTGTCCTCACGGAGTGGAAAGGCGCCTT  
TGCCACTGAGGAGCATCCTACGCGGCTCATGGACCTGGTTACAACTTGAAACCTATCCTG  
GAGCTCTGCCCTCCGCTGGAACGTCTTCTGCCCTGAGGAGAGGGTAGTCAGCATCTCCA  
ATTTCAGCAGCTCAAGAACCTTGGCCCCCACAGGACTTCGAGATGTCACATTGCCCTCAG  
TCCCTGAATGCCCTCGGACCCAAACCCCAATTCCCCAAGGCCCTGACCCCTAGCTGCCGG  
GTTCCCACTCCCAGTGCCACAACCCCTCACCTCCCTGGCAGCCCTCAGCGAGCCTGAGGC  
CCAGCACCCGCTGGCTCCCAAGCACATGGTCCCTCCATGGCTGTTGCCAGGGAACCGGG  
GCGCGGTGGAACGAGCTGCTGGCATGTTCAATAAGTTGCTGTGCTGGGAG

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**FIGURE 6**

MAELRPSGAPGPTAPPAPGPTAPPAFASLFPPGLHAIYGECRRLYPDQPNPLQVTAIVKYWL  
GPDPLDYVSMYRNVGSPSANIPEHWHYISFGLSDLYGDNRVHEFTGTDGPSGFGFELTFRLKR  
ETGESAPPTWPAELMQGLARYVFQSENTFCSGDHVSWHSPLDNSESRIQHMLLTEDPQMOPVQ  
TPFGVVTFLQIVGVCTEELHSAQQWNGQGILELLRTVPIAGGPWLITDMRRGETIFEIDPHLQ  
ERVDKGIEDGSNLSGVSAKCAWDDLSRPPEDEDSRSICIGTQPRRLSGKDTEQIRETLRRG  
LEINSKPVLPPINPQRQNLAHDRAPSRKDSLESSTAIIPHELIRTRQLESVHLKFNQESG  
ALIPLCLRGRLLHGRHFTYKSITGDMAITFVSTGVEGAFATEEHPYAAHGPWLQL

**Important features:**

**N-glycosylation site.**

amino acids 265-268

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**FIGURE 7**

CGCGAATGAAGTTGCATTT CCTCTGTTCTTGAGCCCAGCTTCTCGTCTCCACCCAG  
CTTCCCGCATTGGAAGAAGGGACCGTCTTCCTTGCCACCCAAATCCTGGTATC  
GAAAGGGTTGAACGGACCGGAAGTGTGCAGCAGCGACGGTCCCCAGCTAATCGACGCCGAA  
GTAGCAATTACTAGACAAGCATTCCGCCGCCGGCTCGCT**ATGGCGCAATTCCCCAGATTC**  
CTGGCAGCCACCCAACGTTACTTGGAGACCAGCATGGGAATCATTGTGCTGGAGCTGTACTG  
GAAGCATGCTCAAAGACCTGTAAGAACCTTGCTGAGTTGGCTCGTAGGTTACTACAATGG  
CACAAAATTCCACAGAATTATCAAAGACTTCATGATCCAAGGAGGTGACCAACAGGGACAGG  
TCGAGGTGGTGCATCTATCTATGGCAAACAATTGAAGATGAACTTCATCCAGACTTGAAATT  
CACGGGGCTGGAATTCTCGCAATGGCCAATGCGGGGCCAGATAACCAATGGCAGCCAGTTCTT  
TGTGACCCCTGCCCTACCCAGTGGCTTGACGGCAAACACACCATTGGCCGAGTGTCA  
GGGCATAGGAATGGTGAATCGGTGGGAATGGTAGAAACAAACTCCAGGACGCCGTGGA  
CGACGTGAAGATCATTAAGGCATACCCCTCTGGG**TAGACTTGCTACCCCTTGAGCAGCTCTT**  
CTGAGATGGCCCCAGTGAACCAGCTCTAGATGACATAGAATGACATGTAATGCTAAATTCA  
TTTGCTTGCAGTCATGAAGCTTAGGAGGCCCTGGCATCTGGGTGAGTTAGAGATGGAAG  
TACATTTAATAGGATGCTCTTCTCTCCCTAGTGCCTAGGTGCCCCAGCATTGCAC  
AAATGCCCTGTTATCAATAGGTGACTACTTACTACACATGAACCATATACTGCTGCTTGT  
GCATGCTGCTCTGATATACTGCGAACAAATGTAGCAGCCACTGTCATTCTCAGTGGTTTG  
CTAACCAAACCTCTCCTAAGGAGATTATATTCTGGCCTACACAGCAGTCCTGATGGCTGA  
CAGCCACAGAACATCCAAACCAAGTAGTGTCTGTCAGCCCTTAACCTCTGTGACGCCATT  
TCAGTCTTACATTGTTCTCTAGGGATGTATGCATCTCTATATATATTCCCTCTCAA  
AACCAGAACATCAACAGTGCCTGTTCTGACACTCAGACATCCCAGCAAAGCCACATTGAAT  
TTTGCCAAATGAAAAACACATCCAACAATCAAGTTCTAAGAAGGTGTCAAGTGGGAATAA  
TAATAATGTATAATAATCAAGAAATTAGTTATTAAAGGAAGCAGAACGATTGACCATT  
TCCCAGAGAACAGGGAGAAATCTGTAGTGAGCAAAGGACAGACCATGAATCCTCCTTGAGAAGT  
AGTACTCTCAGAAAGGAGAAGCGCCACTCAAGTTCTTAAACCAAGACTTTAGAGAAATTAG  
GTCCAAGATTTATATGTCAGTTGTTATGTATAAAAATACTTCTGGATTTGTGGGA  
GGAGCAGGAGAGGAAGGAAGTTAACCTATGTAATACATAGAAACTCCACAATAAAATGCC  
ATTGATGGTTAAAAAAAAAAAAAA

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**FIGURE 8**

MAAIAPPDSWQPPNVYLETSMGIIVLELYWKHAPKTCKNFAELARRGYYNGTKFHRIIKDFMIQ  
GGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLAPTQWLDGKH  
TIFGRVCQGIGMVNRGMVETNSQDRPVDDVKIIKAYPSG

**Important features:**

**N-glycosylation sites:**

amino acids 49-52, 108-111

**N-myristoylation sites:**

amino acids 64-69, 69-74, 143-148

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature:**

amino acids 48-65

## **FIGURE 9**

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**FIGURE 10**

MWHEARKHERKLRGMMVDYKKRAERRREYYEKIKKDPAQFLQVHGRACKVHLD SAVA LAAESP  
VNMMMPWQGDTNNMIDRFDVRAHLDHIPDYTPPLTTISPEQESDERKCNERYRGLVQNDFAG  
I SEE QCLYQIYIDE LYGGLQR PSEDEKKLAEKKASIGYT YEDSTVAEVEKA AEKPEEEESAA  
EEESNSDEDEVIPDIDVEVDVDELNQE QVADLNKQATTYGMADGDFVRMLRKDK EEA EAI KHA  
KALEEEKAMYSGRRSRRQRFREKRLGRKISPPSYARRDSPTYDPYKRSPSESSSESRSRS  
RSPTPGREEKITFITSGGSDEAAAAAAAASGVITGKPPAPPQPGGPAPGRNASARRSS  
SSSSSSSASRTSSSSRSRGGGYYRSGRHARSRSRSRSRSRSRSRSRSRGRR  
HSGGGSRDGHRYSRSPARRGGYGPRRRSRSRSRSRSRSRSRSRSRSRSRSRSRS  
SRSLSRS  
AKVTQADASGEAETEDAEGAEQAVQGG

**Important features:****N-glycosylation site:**

amino acids 370-373

**Glycosaminoglycan attachment site:**

amino acids 443-446

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**amino acids 159-162, 282-285, 291-294, 374-377, 375-378, 430-433,  
440-443, 466-469**Casein kinase II phosphorylation site:**amino acids 149-152, 166-169, 171-174, 187-190, 193-196, 195-198,  
303-306, 307-310, 335-338, 571-574**N-myristoylation sites:**

amino acids 118-123, 229-234, 350-355, 446-451, 586-591

**Amidation sites:**

amino acids 263-266, 280-283, 438-441

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**FIGURE 11**

GGTAGGCGCGCCCAGACCTGAGACGGTTGGACTGGGCTGCGTCACGCACGGGCTTAAGCG  
CCCGGGGCCCGCCAGTGGCCGGCACAGCCAATCGCAGCGGGAAAGCGGTGGGGCGGG  
AAGGCCGCTGGAAACTTAAATCCGAGGCGGAACCTGCACCAGACCGGGACGTCTGTA  
ATCTCAGAGGCTTGTGAGGGTGCCTGCGCAGCTGCACGGCTGCTGGTTGAAAC**AT**  
**GA**ATCTTCGCTCGCCTGGCTGCCTTTGCTTGGAAATAGCCTCCGCTGTTCAAATTGGA  
CCAAAATTGGATACAAAGTGGTACCAAGTGGAAAGCAACACACAGAAGATTATGGCGCAA  
TGAAGAAGGATGGAGGAGAGCAGTGTGGAAAAGAATATGAAAATGATTGAACATGGA  
GGAATACAGCCAAGGGAAACATGGCTTCACAATGCCATGAATGCTTGGTACATGACCAA  
TGAAGAATTCAAGGCAGATGATGGTTGCTTCGAAACCAGAAATTCAAGGAAGGGGAAAGTGT  
CCGTGAGCCTCTGTTCTGATCTTCCAAATCTGTGGATTGGAGAAAGAAAGGCTACGTGAC  
GCCAGTGAAGAACAGTGTGGTTCTGGCTTTAGTGCACGGTGCCTTG  
AGGACAGATGTTCCGGAAACTGGAAACTTGTCTCACTGAGCGAGCAGAATCTGGTGGACTG  
TTCGCGCCTCAAGGCAATCAGGGCTGCAATGGTGGCTCATGGCTAGGGCCTCCAGTATGT  
CAAGGAGAACGGAGGCCTGGACTCTGAGGAATCCATATGTAGCAGTGGATGAAATCTG  
TAAGTACAGACCTGAGAATTCTGTTGCTAATGACACTGGCTTCACAGTGGTCGACCTGGAAA  
GGAGAACGGCCCTGATGAAAGCAGTCGAACTGTGGGGCCATCTCCGTTGCTATGGATGCAGG  
CCATTCGTCCTCCAGTTCAAATCAGGCATTATTTGAACCAGACTGCAGCAGCAAAAA  
CCTGGATCATGGTGTCTGGTGGCTACGGCTTGAAGGAGCAAATTGAATAACAGCAA  
GTATTGGCTCGTAAAAACAGCTGGGCTCAGAATGGGCTCGAATGGCTATGTAAAATAGC  
CAAAGACAAGAACCAACCAGTGGAAATCGCCACAGCAGCCAGCTACCCAAATGTG**TGAG**GCTGA  
TGGATGGTGGAGGAGGAAGGACTTAAGGACAGCATGTCTGGGAAATTGTGAAACTGAC  
CAAACGCTTATTGTGTAAGATAAACAGTTGAATCATGGAGGATCCAAGTTGAGATTAAATT  
CTGTGACATTTACAAGGGTAAATGTTACCAACTACTTAATTATTGTTACACAGCTTA  
TGATATCAAAGACTCATTGCTTAATTCTAAGACTTTGAATTTCATTTTAAAAAGATGTA  
CAAAACAGTTGAAATAATTAAATTGCTATATA

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**FIGURE 12**

MNLSIVLAAFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRAVWEKNMKMIELHN  
GEYSQGKHGFTMAMNAFGDMTNEEFRQMMGCFRNQKFRKGKFREPLFLDLPKSVDWRKKGYV  
TPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSSEQNLVDCSRPQGNQGCNGGFMARAFQY  
VKENGGLDSEESYPYVAVDEICKYRPENSANDTGFTVVAPGKEKALMKAVATVGPISVAMDA  
GHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEGANSNSKYWLVKNSWGPEWGSNGYVKI  
AKDKNNHCGIATAASYPNV

**Important features:****Signal sequence**

amino acids 1-17

**N-glycosylation sites.**

amino acids 2-6, 221-225, 292-296

**N-myristoylation sites.**amino acids 13-19, 93-99, 136-142, 145-151, 174-180, 177-183,  
180-186, 194-200, 288-294, 324-330**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 132-144

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 275-286

**FIGURE 13**

GGCGGCCGTATGTGATCCGCTTCCCTGCTCCTTAAGCGTCCACAGGCGCGAGCGGCCACA  
ATCACAGCTCCGGGCATTGGGGAACCGAGCCGGCTGCCCGGGGAATCCGTGCCGCC  
TTCCGTCCCCTGGTCCCATCCTCGCCGCGCTCCAGCACCTCTGAAGTTTGCAAGCAGGCCAGAAAG  
GAGGGAGGAAGGGAGGGAGTGTGTGAGAGGGAGGAGCAAAAGCTCACCTAAAACATTATT  
TCAAGGAGAAAGAAAAAGGGGGGGCGCAAAA**ATGGCTGGGCAATTATAGAAAACATGAGCA**  
CCAAGAAGCTGTGCATTGTGGTGGATTCTGCTCGTCTCCAAATCATGCCCTTCTGGTGG  
GAGGCTTGATTGCTCCAGGGCCCACAACGGCAGTGTCTACATGTCGGTGAATGTGTGGATG  
CCCGTAAGAACCATCACAAGACAAAATGGTCGTGCCTGGGACCCAATCATTGTGACAAGA  
TCCGAGACATTGAAGAGGGCAATTCCAAGGGAAATTGAAGCCAATGACATCGTGTGTTCTGTT  
ACATTCCCCTCCCCACATGGAGATGAGTCCTGGTCCAATTCATGCTGTTATCCTGCAGC  
TGGACATTGCCTCAAGCTAAACAACCAAATCAGAGAAAATGCAAGTCTCATGGACGTTT  
CCCTGGCTTACCGTGTGACGCATTGCTGAGTGGACTGAAATGGCCATGAAAGAGTACAC  
GGAAACTCAAATGCACCTTCACATCTCCAAGACTCCAGAGCATGAGGGCGTTACTATGAAT  
GTGATGTCTCTTCTTCATGGAAATTGGGTCTGTGGCCATAAGTTTACCTTTAAACATCC  
GGCTGCCTGTGAATGAGAAGAAAATCAATGTGGAAATTGGGAGATAAAGGATATCCGGT  
TGGTGGGATCCACCAAAATGGAGGCTTCACCAAGGTGTGGTTGCCATGAAGACCTCTTA  
CGCCCAAGCATCTCATCATATGGTGTGGATTGGAGGAGGATCACCATGATGCCCCGACCCC  
CAGTGCCTCTGGAAAAAGTCATCTTGCCTGGATTCCATGACCTTATCAATATCCCAG  
TGGAAATGGTTTCCATCGGGTTGACTGGACCTGGATGCTGCTGTTGGTGAATCCGACAGG  
GCATCTCTATGCATGCTCTGTCCTCTGGATCATCTCTGTGGCAGCACATGATGGATC  
AGCACCGAGCGGAACCACATCGCAGGGTATTGGAAGCAAGTCGGACCCATTGCCGTTGGCTCCT  
TCTGCCCTTCATATTGACATGTGTGAGAGAGGGGTACAACTCACGAATCCCTCTACAGTA  
TCTGGACTACAGACATTGAAACAGAGCTGGCCATGCCCTCATCATCGTGGCTGGAATCGCC  
TCTGCCCTACTTCTGTTCTATGCTTCATGGTATTCAAGGTGTTGGAACATCAGTGGGA  
AGCAGTCCAGCCTGCCAGCTATGAGCAAAGTCCGGCGCTACACTATGAGGGCTAATTGTTA  
GGTCAAGTCCCTCATGCTTATCACCTTGGCCTGCCTGCCATGACTGTCATCTCTTCATCG  
TTAGTCAGGTAACCGAACGGCATTGAAATGGGCGCGCTCACAGTCAAGTGAACAGTGCCT  
TTTCACAGGCATCTATGGGATGTGGAAATCTGTATGTCTTGTCTGATGTTCTGTATGCAC  
CATCCCATAAAACTATGGAGAACGACAGTCCAAATGGCGATCTGGGTGTCATAGTGGGAAG  
AACTCCAGCTCACCACCACTATCACCCATGTGGACGGACCCACTGAGATCTACAAGTTGACCC  
GCAAGGAGGCCAGGAG**TAG**GAGGCTGCAGGCCGGCTGGGACGGTCTCTCCATACCCAGC  
CCCTCTAACTAGAGTGGGAGCATGCCAGAGAGAGCTCAATGTACAATGAATGCCATGGC  
TCTTAGCTGTGGTTCTGGACAGCGGATGGACATTGTCAGTTGCCCTTGACGGTAGC  
TTTGGAGGAAGATTCTGAGCCACTAATGCAATTGTGTATGATAACAAAACCTCTGGTATGA  
CACATTCTGTGATCATTGTTAATTAGTGACATAGTAACATCTGTAGCAGCTGGTAGTAAA  
CCTCATGTGGGGTGGGGTGGGGTGTATTCTGGGGATGGTTGGCGAATGGGAGTG  
GAATATTGACATTTCCTGTTAAATTCTAGGATAGATTAAACATCCTTGCGGTCCA  
GTCCAAGGTAGGCTGGTGTAGTCAGTCTCTCACTCCAATGACCAACTGTTTTCTA  
TTTATATCACCAGGTAGCCTACTGAGTTAATTTAAGTGTCAATAGATAAGTGTCCCTGTT  
TTGTGGCATAATATAACTGAATTCTATGAGAAGATTATTCCACCAAGGGGTATTGAGCTTG  
AAACCAATCTGTGTATCTAATACTAACCAATCTGTTGGATGTGGATTAAACAAAGCTTTAACC  
TAAACTACCCAAAGTAAGATTACTGTATTAAATGGCCTCGGGTCTGAAAAGCTTTTAACC  
TCTTGCTTAAATGCGTTTATTGATAAGATACTTCAAATAGCCTCCAAAAGTGTAGATCC  
AATCACTAAATAACCTGTATGTATGCAAAAAAAAAAAAAAA

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**FIGURE 14**

MAGAIENMSTKKLCIVGGILLVFQIIAFLVGGGLIAPGPTTAVSYMSVKCVDARKNHHKTW  
VPWGPNHCDKIRDIEEAIPREIEANDIVFSVHILPLPHMEMSPWFQFMLFILQLDIAFKLNNQI  
RENAEVSMVDVSLAYRDDAFAEWTMAHERVPRKLKCTFTSPKTPEHEGRYYECDVLPFMEIGS  
VAHKFYLLNIRLPVNEKKINVGIGEIKDIRLVGIHQNGGFTKVWFAMKTFLTPSIFIIMVWY  
WRRITMMMSRPPVLLEKVI FALGISMTRFINIPVEWFSIGFDWTWMLLFGDIRQGIFYAMLLSF  
IIFCGEHMMMDQHERNHIAGYWQVGPPIAVGSFCLFIFDMCERGVQLTNPFYSIWTTDIGELA  
MAFIIVAGICLCLYFLFLCFMFQVFRNISGKQSSLPAMSKVRRLYEGLIFRFKFMLLITLA  
CAAMTVIFFIVSQVTEGHWKWGGVTQVNSAFFTGIYGMWNLYVFALMFYAPSHKNYGEDQS  
NGDLGVHSGEELQLTTITHVDGPTEIYKLTRKEAQE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**amino acids 239-253, 269-284, 302-318, 338-352, 377-399, 434-452,  
471-488**N-glycosylation sites.**

amino acids 8-12, 406-410

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 254-258

**N-myristoylation sites.**amino acids 223-229, 274-280, 305-311, 358-364, 374-380, 386-392,  
509-515

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**FIGURE 15**

GTGAGGGAACAGCTGATCCGTCTGTTGGAGGACAGATATCTCAAGGCCAGG**ATGGA**AGAAT  
CACCACTAACGGGGCACCACATCCCCTGGTGGAGTCACATTCTCAATGTAGCCGGACCTACA  
TCCCCAACACCAAGGTGGAATGTCACTACACCCCTCCCCCAGGCACCATGCCAGTGCCAGTG  
ACTGGATTGGCATCTTCAAGGTGGAGGCTGCCTGTGTTGGGATTACACACATTTGTGTGGT  
CTTCCGTGCCTGAAAGTACAACGTGATGGTCCCCCATTACACACCAGTGTCCAGTTCCAAGCCA  
GCTACCTGCCAACACCAGGAGCTCAGCTTACCAAGTCCGATATGTGAACCGCCAGGGCCAGG  
TGTGTGGCAGAGCCCCCTTCCAGTCCGAGAGCCAAGGCCATGGATGAACGTGGTGAACCC  
TGGAGGAGGCTGATGGGGCTCTGACATCCTGCTGGTGTCCCCAAGGCAACTGTGTTACAGA  
ACCAGCTCGATGAGAGGCCAGCAAGAACGGAATGACCTGATGCAAGCTACAGCTGGAGG  
GACAGGTGACAGAGCTGAGGGAGCGAGTCAGGAGCTCGAGAGGGCTCTGGCAACTGCCAGGC  
AGGAGCACACGGAGCTGATGGAACAGTACAAGGGATTCCCGTCCCAGGGAGATCACAG  
AAGAGAGGGACATCCTGAGCCGGCAACAGGGAGACCATGTGGCACCGCATCCTGGAGCTAGAGG  
ATGACATCCAGACCATCAGTGAGAAAGTGCAGCAAGGAAGTGGAGCTGGACAGGCTTAGAG  
ACACAGTGAAGGCCCTGACTCGGGACAAGAGAAAGCTCCTGGCAACTGAAAGAAGTACAAG  
CAGACAAGGAGCAAAGTGGAGCTGAGCTCCAAAGTGGCACAAACAGGAGAACATCACTAAATT  
TGGACCTGAAGGAGGCGAAGAGCTGGCAAGAGGAGCAGAGTGCTCAGGCTCAGCGACTGAAAG  
ACAAGGTGGCCAGATGAAGGACACCCCTAGGCCAGGCCAGCAGCGGGTGGCCAGCTGGAGC  
CCTTGAAGGAGCAGCTCGAGGGGCCAGGAGCTTGCAAGCCTCAAGCCAGCAGAAAGCCACCC  
TTCTGGGAGGAGTTGGCAGTGCAGCAGCAGCCAGGGACCGCACCATAGCCAACTACACC  
GCAGCCGCTGGAAGTGGCTGAAGTTAACGGCAGGCTGGCTGAGCTCGGTTGCACTTGAAGG  
AAGAAAAATGCCAATGGAGCAAGGAGCGGGCAGGGCTGCTGAGGTGAGGAGAACAGGAAAG  
ACAAGATCCTGAAGCTGAGTGCAAGAGATACTCGATTGGAGAAGGCAGTTCAAGGAGGAGGA  
CCCAAAACCAAGTGTCAAGACTGAGCTGGCCCCGGAGAACGGATTCTAGCCTGGTACAGTTG  
CAGAAAGTAAGCGGGAGCTGACAGAGCTGCCGTAGCCCTGCGTGTCCAGAAGGAAAAGG  
AGCAGTTACAGGAGGAGAACAGGAATTGCTAGAGTACATGAGAAAGCTAGAGGCCGCTGTGG  
AGAAGGTGGCAGATGAGAAGTGAATGAGGATGCCACCACAGAGGATGAGGAGGCCGCTGTGG  
GGCTGAGCTGCCGGCAGCTCTGACAGACTCAGAGGACGAGTCCCCAGAACATGAGGCTCC  
CACCCCTATGCCCTTGTGAGCGTGGAGACCCAGGCTCCTCCTGCTGGCCTCGAGAGGCTT  
CTCCCCCTGTTGTCATCAGCCAGCGCTCCCTACCTCTCTGCTGGCCAGCTGAGG  
ACAGTAGCTCTGACTCGGAGGCTGAAGATGAGAAGTCAGTCTGATGGCAGCTGTGCAGAGT  
GGGGTGAAGGAGGCCAACTTACTGCTTCTGAACTGGCAGTGCCTCTATGACATGCCAGTG  
GCTTACAGTGGGTACCCCTGTCAGAAACCAGCACTGGGGCCCTGCCACCCACATGGAAGG  
AGTGTCTATCTGTAAGGAGCGCTTCTGCTGAGAGTACAAGGATGCCCTGGAGGACCACA  
TGGATGGACACTTTTCAACCCAGGACCCCTCACCTTGAG**GAT**TCTTACTCCCTCG  
TACATGCACAAATACACACTCATGCACACACACTCACACACATGCATACACTTAGTTCA  
TGCCCATTTCTATCACACTGGCTCCATGATATTCTGTTCCCTAAGAACTGCTTCTGTGTGC  
CCTGTTTCTATCCCAAGATTCTCACTTCATCCTCTCCTACCTGGCTTTGTCCCAGGGAG  
GGGTCTGTTCGGAAGCAGTGGCTGAATTATCCCCTGAAAGTGGTTGGAGGAACCGGGAT  
GGAGGAGGCCTCCCTGTGGGAATAGAATCGTCACTCCTAGCCCTGGTTGCTTCTGATACA  
CAGCCACTGCACACACACTCACACTCACACTCCCTGCTGATGCCCAAAGCCAATTCC  
GGGGCACCCTACCCCTCTTATTGGAGTTCCGTTGGTTACCTGAGTTTCTCTGGGTCT  
GCACAGAGGCAGCAGCATGGACATCATGCCCTCTCAGGTCCCTTGGTTCTCAGTTCAATTG  
GTTCTCTTCTGTTCCCCATTGACTTCTGCCCCACCCTAGCCTTTCCATAACCTTAGG  
TATTCAAGTTGGAGGGTTTTGTATTGGAGGATTCTGTATTCTGTATCCTCTCCTCGC  
ATCTCCTCACATGGAAGAAATAATGTATTGTGCTTCTGTGAGGAATGGGGGAACAAGTG  
GTCCCCAGGTATCCCCATTCCAAGGCCCCCTCCCTCTCCAGGTCCCCACAGCAATAAG  
CTTCCCCCTGATATCCATCCCTTGAGTTGAACAAATATTTATATGATATGTAA

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**FIGURE 16**

MEESPLSRAPSRRGVNFNVARTYIPNTKVECHYTLPPTGTMPSASDWIGIFKVEAACVRDYHT  
FVWSSVPESTTDGSPITHSVQFQASYLPKPGALYQFRYVNQRQVGQCGQSPPFQFREPRPMDE  
LVTLEEADGGSDILLVVPKATVLQNQLDESQQERNNDLMLQKLQLEGQVTELRSRVQELERALA  
TARQEHTELMEQYKGISRSHGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD  
RLRDTVKALTREQEKLGGQLKEVQADKEQSEAELOVAQQENHHNLNLDLKEAKSWQEEQSAQAQ  
RLKDKVAQMKTDLGQAQQRVAELEPLKEQLRGAQELAASSQQKATLLGEELASAAGARDTIA  
ELHRSRLEVAVNGRLAELGLHLKEEKCQWSKERAGLLQSVEAEKDYLKLSAEILRLEKAVQ  
EERTQNQVFKTELAREKDSSLVQLSESKERELTELRSALRVLQKEKEQLQEEKQELLEYMRKLE  
ARLEKVADEKWNEADATTEDEEAAVGLSCPAALTDSEDESPEMDRLPPYGLCERGDPGSSPAGP  
REASPLVVISQPAPISP HLSGP AEDSSDSEA EDEKS VLM AAV QSG GEE AN LLL PELGS AFYD  
MASGFTVGTLSSETSTGGPATPTWKECPICKERFPAESDKDALEDHMDGHFFFSTQDPFTFE

**Important features:****Casein kinase II phosphorylation sites:**

amino acids 28-31, 43-46, 68-71, 72-75, 129-132, 156-159, 208-  
211, 239-242, 282-285, 305-308, 376-379, 383-383, 468-471, 520-  
523, 521-524, 537-540, 539-542, 543-546, 593-596, 595-598, 597-  
600, 612-615, 639-642, 652-655, 667-670, 683-686

**N-myristoylation sites:**

amino acids 39-44, 107-112, 204-209, 414-419, 561-566, 613-618

**Cell attachment sequence:**

amino acids 557-559

**Leucine zipper pattern sequence:**

amino acids 163-184, 475-496, 482-503

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**FIGURE 17**

GCAAGTTGGAAATTTAGACTGTCAGTGCACATGGACCTCTGGGAAGACGTCTGGCGAGAGCT  
AGGCCCACTGGCCCTACAGACGGATCTGCTGGCTCACCTGTCCCTGTGGAGGTTCCCTGGG  
**AAGGCAAGATGCCAACAACAGCACTGCTCTGTCAATTGCCAATGTTACCTACATCACCAGG**  
AAATTTCATGGACTCTGCGCCATAGTGGCAACGTGCTGGTCATCTGCGTGGTCAAGCTGA  
ACCCCAGCCTGCAGACCACCACCTCTATTCATTGTCTCTAGCCCTGGCTGACATTGCTG  
TTGGGGTGCCTGGTCATGCCCTTGGCCATTGTTGTCAGCCTGGCATCACAACTCCACTTCTACA  
GCTGCCTTTTATGACTTGCTACTGCTTATCTTACCCACGCCTCCATCATGTCCTTGCCTGG  
CCATCGCTGTGGACCGATACTTGCAGGTCAAGCTTACCGTCAGATTCAAATCCTGGCTCC  
CTGGGTGCATTCTATCATTCCAGTTGAAAGTTGCTTCCTCCAGTCATGTGGCTCTTCATTC  
TACTCTCCTTGGCTCTCATTCAGATGCCATGGTCATGGATGAAAAGGTCAAGAGAAGCTTG  
TGCTGGACACGGCTCTGCCATCTGCAACTACAATGCCACTACAAGAAATCCCCAAATACT  
GGTGCCGAGGCTATTCCGTGACTACTGCAACATCATGCCCTCTCCCTAACAGCACCAATC  
ATGTGCCCTGAGGGACACAGGGAACCCAGCTCATGGTCACTATGTCCTGCCTGACCAAAGAGG  
ACACGGCTGGTACTGGTGTGGCATCCAGCGGACTTGCAGGGATGACATGGATTTACAG  
AGCTGATTGTAACTGACGACAAAGGAACCCCTGCCAATGACTTTGGTCTGGAAAGACCTAT  
CAGGCAACAAAACCAGAAGCTGCAAGGCTCCAAAGTTGTCAGGCTGACCGCTCCAGGA  
CGTCCATTCTCATTTGCATACTGATCACGGTTGGAAATCATCTGTAATCAGTCATT  
TGACCAAAAGGAGGAGAAGTCAAAGGAATAGAAGGGTAGGCAACACTTGAAGCCCTTCGC  
GTGTCCTGACTCCAAGGAAATGGCTCCTACTGAACAGAT**TGACTGAAGATTTTTAATT**  
AGTCATAAAAGTGTGCTACAACAGAATAATCACCAGACAACGGCCACACCTCAGAGACT  
GATTCTGATCTCCAGGAATTCTGAAGGACCCCTATCCTTGACAACAATCATTGCAGCCAG  
GTAGCAACGGCGGTAGTCAGAGGAGCTATGATAGACCACACCAAGCAAGGCTGCCCTCAAAT  
AACATCTCAAGATCTTAGTTCTATGCATTCCATCAGTCAGAAGTGAAGAAGAGGTGGAGAAT  
CTGGATTGGGACCAAGGAAATCACTGTATTTGTTAGCCAATAAATTCTAGCCAGTGTGA  
ATGAAAAAAA

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**FIGURE 18**

MPNNSTALSLANVTYITMEIFIGLCAIVGNVLVICVVKLNPSLQTTFYFIVSLALADIAVGVLVMPLAIVVSLGITIHFYSCLFMTCLLLIFTHASIMSLAIAVDRLRVKLTVRFRIPLPGCILSFQLKVCFLPVMWLFISSLALISDAMVMDEKVKRSEVLDTASAICNYNAHYKNHPKYWCRGYFRDYCNIIAFSPNSTNHVALRTGNQLIVTMSCLTKEDTGWYWCQIQRDFARDDMDEFELIVTDDKGTLANDFWSGKDLSGNKTRSKAPKVVRKADRSRTSILIICILITGLGIISVISHLTKRRRSQRNRRVGNTLKPFSRVLTPKEMAPTEQM

**Important features of the protein:****Transmembrane domains:**

amino acids 16-35, 62-80, 89-101, 134-152, 292-311

**N-glycosylation sites.**

amino acids 3-7, 4-8, 12-16, 204-208, 273-277

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 316-320

**N-myristoylation sites.**

amino acids 122-128, 125-131, 258-264

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 214-225

**G-protein coupled receptors proteins.**

amino acids 29-59, 76-116

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**FIGURE 19**

CTCGGGCGCGCACAGGCAGCTGGTTGCCCTGGATTGAGCTGCGGGTCGGCCGGCCTCTCCAATG  
 GCAAATGTGTGTGGCTGGAGGGAGCGCAGGGCTTGGCAAAGGAGCTGAGTGTGAGTGTGAGACCGGGGGAGTC  
 CTGTGAAAGCAGATAAAAGAAAACATTATAACGTGTATTACGAGGGAGCAGGGGGCTGTGCACT  
 CCCCGCGAACATTGGCTCCCTCCAGCTCGAGAGAGAGAAGAAGAAAGCGGAAAGAGCCAGATTCACTCG  
 TTTCCAGCCAAGTGGACCTGATCGATGCCCTCTGAATTATCACGATATTGATTATTAGCGATGCCCTG  
 GTTTGTGTGTTACGCCACACACAGTCACACAAGGCTCGGCTGCCCTCGTTCCAGCTCTGGCG  
 AATCCCACATCTGTTCAACTCTCCGAGGGCGAGCAGGAGCAGAGTGTGTCGAATCTGGAGTGAAGAGGG  
 ACAGGGAAAAGAAACAAGCCACAGCAGCAACTTGAGACTCCGCACTCCAAAAGAAGCACCAGATCAGAAAA  
 AAAGAAGATGGGCCCCCGAGCCTGCTGCTGCTGCTGAGCTGTGTTCTCCCTGCTGGTGGAGCTC  
 GGCCTTCTGTGCAACCCACCGCCTGAAAGGAGGTTCAAGAGGGACCGAGGAACATCCGCCAACATCATCCT  
 GGTGCTGACGGACGACCAGGATGTGGAGCTGGTTCCATGAGGTGATGAACAGACCCGGCGCATCGAGCA  
 GGGCGGGCGCACTCATCAACGCCCTCGTGAACACCCATGTCGTCGCCCTCACGCTCTCCATCCTCACTGG  
 CAAGTACGTCCACAACCACACCTACACCAACAATGAGAACTGTCCTCGCCCTCTGGCAGGCAAGCAGCA  
 GAGCCGACCTTGGCGTGTACCTCAATAGCACTGGTACCGGACAGCTTCTCGGAAAGTATCTTAATGAATA  
 CAACGGCTCTACGTGCCACCCGGCTGAAAGGAGGTTCAAGAGGGACCGAGCTTCTTATAACTACAC  
 GCTGTGCGAACGGGGTGAAGAGAAGCAGCGGCTCCGACTACTCCAAGGATTACCTCACAGACCTCATCACAA  
 TGACAGCGTAGCTCTTCCGCACTGCAAGAAGATGTACCCGACAGGCCACTCTCATGGTACAGCCATGC  
 AGCCCCCAGGCCCTGAGGATTCAAGCCCAACATATTACGCGCTTCCAAACGCACTCTCACGACATCACGCC  
 GAGCTACAACATACGCCCAACCCGACAACACTGGATCATGCGTACACGGGGCCATGAAGGCCATCCACAT  
 GGAATTCAACACATGCTCCAGCGGAAGCGTTGCAAGACCCCTCATGCGTGGACGACTCCATGGAGACGATT  
 CAACATGCTGGTGAGACGGGAGCTGACAACACGTACATCGTATACACCGCCGACCACGGTTACCATCGG  
 CCAGTTGGCCTGGTGAAGGGAAATCCATCCATATGAGTTTGACATCAGGGTCCGTTCTACGTGAGGGGCC  
 CAACCTGGAAGCCGCTGCTGTAACATGGCCCTCAACATTGACCTGGCCCCACCATCTGGACATTGC  
 AGGCTGGACATACCTGGATATGGACGGGAATCATCTCAAGCTGCTGGACACGGAGCGGCCGGTGAATCG  
 GTTCACTTGAAGAGATGAGGCTGCGGGACTCTCTTGGTGGAGAGAGGCAAGCTGCTACACAAGAG  
 AGACAATGACAAGTGGACGCCAGGAGGAGAACTTCTGCCCAGTACCGCTGTTGAGGACCTGTGTCAGCG  
 TGCTGAGTACCAAGACGGCGTGTGAGCAGCTGGACAGAAGTGGCAGTGTGAGGAGCAGCCACGGGAAGCTGAA  
 GCTGCAATAAGTGAAGGGCCCCATGGCGCTGGCGGAGCAGAGCCCTCTCCAACCTCTGCCCCAAGTACTACGG  
 GCAGGGCAGCGGCTGACCTGAGCAGGGGACTACAAGCTCAGCCTGGCCGACGCCGGAAAAACTCTT  
 CAAGAAGAAGTACAAGGCCAGTATGCGCAGTCGCTCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGGGT  
 GTACCACTGAGGCTGGGTGATGCCGCCAGGGGAAACCTCACCAGCGGACTGGCCAGGGGCCCTGAGGA  
 CCAAGATGACAAGGATGGGGACTTCAGTGGACTGGGACTCCAGTGTGACCTGGACCTGAGGACTCAGCCCAACCCATTAA  
 AGTGACACATCGGTGCTACATCTAGAGAACGACACAGTCCAGTGTGACCTGGACCTGTACAAGTCCCCTGAGG  
 CTGAAAAGACCAAGCTGCACATGACCGAGATTGAAACCTGCAAGAACAAAATTAGAACCTGAGGGAAAGT  
 CCGAGGTACCTGAAGAAAAGGGCCAGAAGAATGTGACTGTCACAAAATCAGCTACCCACCCAGCACAAAGG  
 CGCCTCAAGCACAGGGCTCCAGTCTGCACTCTTCAAGAAGGGCTGCAAGAGAACGAGGAGCAGTGTGTT  
 GCGGGAGCAGAAGCGCAAGAAGAAAACCTCGCAAGCTGCAAGCGCTGCAAGAACACGACACGTGAGCATGCC  
 AGGCCTCACGTGCTTACCCACGACAACCCAGACTGGAGCAGGGCTTCTGGACACTGGGCCCTGTG  
 CTGCACCGGCCAACATAACAGTACTGGCATGAGGACATCAAGAGACTCACAATTCTCTTCTGTGA  
 ATTTGCACTGGCTTCTAGAGTACTTGTATCTCACACAGACCCCTACAGCTGATGAATGCACTGAACACACT  
 GGAGGGATGTCTCAACCAGCTACACGTACAGCTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAA  
 CCCCCGGACTCGAAACATGGACCTGGATGGAGGAAGCTATGAGCAATACAGGAGTTTCACTGCTGAAAGTGGCC  
 AGAAAATGAAGAGACCTCTTCAAAATCACTGGACAATGTGGGAAGGCTGGGAAGGTT**TAAGAAACACAGAGGT**  
 GGACCTCCAAAACATAGAGGACATCACCTGACTGCAAGGCAATGAAAACCATGTTGGTGAATTCCAGCAGACC  
 TGTGCTATTGGCCAGGGCTGAGAAAAGCAAGCAGCAGCACTCTCAGTCACATGACAGATTCTGGAGGATAACCA  
 GCAGGGAGCAGAGATAACCTCAGGAAGTCCATTGGCCCTGCTTGTGTTGATTACCTCACAGCTGCAC  
 AAAATGATTCTTCTGATCAAAAGTCACCACTAACCTCCCCAGAGCTACAAAGGAAAACGGAGAGAGCG  
 AGCGAGAGAGATTCTTGGAAATTCTCCAAAGGGCGAAGTCACTGAAATTAAATCATAGGGGAAAAGCA  
 GTCCCTGTTCTAAATCTTATTCTTGGTTGTCAAAAGAAGGAACTAAGAAGCAGGAGCAGAGGCAACGTGG  
 AGAGGCTGAAAACAGTGCAGAGACGTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTACCTAGCACTAT  
 AAACCTGGTGTGCTGAGAAACTGCCTTCAATTGTATATGTGACTATTACATGTAATCAACATGGAACT  
 TTAGGGGAACCTAATAAGAAATCCAATTTCAGGAGTGGTGTCAATAACGCTCTGCCCCAGTGTAAAA  
 GAAAAA

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**FIGURE 20**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQVMNKTRRIMEQGGAHFINAFTTPMCCPSRSSILTGKYVHHNHTYTNNECSSPSWQAQHESRTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEVGLLKNSRFYNTLCRNGVKEKHGSDDYSKDYLTDLITNDSVSFFRTSKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFVNQASQHITPSNYAPNPDKHWIMRYTGPMPKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNTYIVYTADHGHYHIGQFGLVKGKSMPPYEFDIRPFYVRGPNEAGCLNPHIVLNIDLAPEIYDIPADMDGKSILKLLDTERPVNRFHKKMRWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFKKYKASYVRSRSIRSVAIEVDGRVYHVGLGAAQPRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKD KVWLREQRKKKLRLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNTYWCMRTINETHNFLCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVNLQHVQLMELRSCKGYKQCNPTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**Important features:****Signal peptide:**

amino acids 1-17

**Sulfatases signature 1.**

amino acids 86-99

**Homologous region to sulfatase:**

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

**N-glycosylation sites.**

amino acids 65-69, 112-116, 132-136, 149-153, 171-175, 198-202, 241-245, 561-565, 608-612, 717-721, 754-758, 764-768

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**FIGURE 21**

GGGC CGCG GAGAG CTGCTAGGGCGTTCTGCCTCGGCCTGTTGGCAGGGCCGGCT  
AAGGTGCGCGTGCTCGCTGTTCTAACCTTCTGTTGGCGTTCTGCTGAGAGGCGGGA  
GGCGCTGAGAGTCTGTGCGGAGGTCCGTGGACAGACTGCTTGCTCGTTGCTCTTCG  
GAGGCGCGATCCCCGAAGCGAGCTGAAATACGGCTGCAGGCTACAATTGCAGCCGAC  
GATTATGGAAGACGGAAGCGGGAGAGGTGGCCACCCCTCATGGAGCGCTTGTGCTCGGAT  
GGCTTCGCATTTCCCAATACCCATTAAACCGTATCATCTGAAGAGGATCCACAGAGCT  
GTCTTACATGGTAATCTAGAGAAACTGAAGTACCTTCTGCTCACGTATTATGACGCCAAT  
AAGAGAGACAGGAAGGAAAGGACGCCCTACATTGGCCTGTGCCACTGCCAACCGGAA  
ATGGTACATCTCCTGGTGTCCAGAAGATGTGAGCTAACCTCTGCGACCGTGAAGACAGG  
ACACCTCTGATCAAGGCTGTACAAC TGAGGCAGGAGGCTTGTGCAACTCTCTGCTGCAA  
AATGGCGCAATCCAAATATTACGGATTCTTGGAAGGACTGCTCTGCACTACGCTGTG  
TATAATGAAGATA CATCCATGATAGAAAAACTTCTTCACATGGTACAAATATTGAAGAA  
TGCAGCAAGGTAAGGTCAACCAATGTTATTTCAAACATCTGAAATGAATTATTTA  
ACATTGACACATGTAAGGGCAATTTTCAATTGGAGCTCAAACATTCTGAATGA  
AAATTTGAAATGCCTTAACGTCTAACGATTTACTTTAAATATTGAACTTTAAAG  
AAGCATTATAGGAAACAGCCTTTTCACTGCACCTATGGTAAATAACTATAAAAACAAAT  
GAATTACAATAAAATTATAATTCACTGACAAC TGAAATTGGAAAGGTAATAGTTAAGTGT  
TTTCCACTAAATTACTTTT

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**FIGURE 22**

MERLCSDGFAFPQYPIKPYHLKRIHRAVLHGNLEKLKYLLLTYYDANKRDRKERTALHLACAT  
GQPEMVHLLVSRRCELNLCREDRTPLIKAVQLRQEACATLLLQNGANPNITDFFGRTALHYA  
VYNEDTSMIEKLLSHGTNIEECSKV

**Important features of the protein:**

**N-glycosylation site.**

amino acids 113-117

**N-myristoylation site.**

amino acids 109-115

**Microbodies C-terminal targeting signal.**

amino acids 149-153

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**FIGURE 23**

GAGGCAGAAAGCAGAAAGGAGAAATTCAGGATAACTCCTGAGGGGTGAGCCAAGCCCTG  
CCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAATGATCCATTCCCTGTGGT  
CACTTATTCTAAAGGCCCAACCTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAG  
GGAGCAGTCACGCCCTACTTCTTGCCCTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGT  
TTCCATCCTCCCACGGAAGGAAAGCCCCCTCTGTCGATCCTCCAAAGACGGAAAGCTGCTGGC  
TGCAACCTTGCTGCTGGCACTGCTGTCTGCTGCCTCACGGTGGTCTTCACCAGGTGGC  
CGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGAGAGCTGCAGGGCCACCACGGGAGAAGCT  
GCCAGCAGGAGCAGGAGCCCCAAGGCCGGCTGGAGGAAGCTCCAGCTGTCAACCGCGGGACT  
GAAAATCTTGAACCACCAAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG  
TGCCGTTCAAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTGCACTGATTGCAGACAGTGA  
AACACCAACTATAACAAAAAGGATCTTACACATTGTTCCATGGCTCTCAGCTTAAAGGGG  
AAGTGCCCTAGAAGAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTATATA  
TGGTCAGGTTTATATACTGATAAGACCTACGCCATGGACATCTAATTCAAGAGGAAGAAGGT  
CCATGTCTTGCGGATGAATTGAGTCTGGTGACTTGTGATGTATTCAAATATGCCCTGA  
AACACTACCCAAATAATTCTGCTATTCAAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAAC  
CCAACCTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTG  
TGCATTGAAACTGCTGTGACCTACTTACACCATGCTGTAGCTATTTCCCTTCTCTGT  
ACCTCTAAGAAGAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAA

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**FIGURE 24**

MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKGKLLAATLLLALLSCCLTV  
VSFYQVAALQGDLASLRAELQGHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS  
QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKE  
TGYFFIYGQVLYTDKTYAMGHLIQRKKVHFGDELSVTLFRCIQNMPETLPNNSCYSAGIAK  
LEEGDELQLAIPRENAQISLDGDVTFFGALKLL

**Transmembrane domain:**

amino acids 47-72

**N-glycosylation site.**

amino acids 124-127, 242-245

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36, 173-176

**N-myristoylation site.**

amino acids 96-101

**TNF family proteins.**

amino acids 172-206

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**FIGURE 25**

CTGCTTGGATA CCTCCAGTCCCCAA ACTGTGTTCCAGGAGTTTCTGGCGAAGCTGCCGA  
TGTTT GAGCCTTTCTTCCCAGAGAAGAAGATGGACTGAAAGCTGCCAGTTGGGACTTTTG  
TGATCACGGCGTTGCAGCGTTAAAGGAGGTGATGGGCTTGCCTGGCTTGTCTTCCACC  
CAAGTGAAGAGTTGATGTTCACTGGTTATGCTTAGACAATGTGCAGTTGTGTAATTAAAAA  
TTTGGGTGGGATAGGGCATAGGCTTGTGAAGGGCAGTCGGATCCGGAGGAACCTGTCTT  
GTCCTGGTAGGAGAGACACCCCCAGCTATCCTCGATGCCGTCA GCCATGGCCATCTCACT  
TGCCGCCGAACTCGCACCCGTTCAAGGAGCGTCACTGTCTACCTGGACGAGCCATCAAATC  
GGCGCTCAGTGGCCGCTGACCGAGCGAGAATAATGCCACTTTGATTGCAAAGTGCTA  
TCAAGGAACCACGCTCTCGCTGGTTGATCACAAGACGGCAAGTTTATCTCAAGACACT  
AAAAGTAGTAATGGTACTTTATAAAATGCCAGAGATTGAGTCAGGCTCTGAAGAAAGTCCA  
CCATGTGAAATTCTTCCGGTGACATATCCAGTTGGAGTAGACGTGACAGAGAATACACGG  
AAAGTTACCCATGGGTGTATTGTTCCACAATAAAACTTTCTACAGATGGT**TATGGAAGCC**  
CGGCTCCGCTCAGATGTCACTGCACCATTACCAAGTCCTGTTGACAAAGTTGCTGCTAAC  
ACTCCAAGTATGTA CTCAGGAAC TATTCCAGCTTCTCAGTATCTACAGGAGGCCTACAT  
CGGAAACAATGTTGAACAGAAGTTAGCCACGCTTCAGCGGCTACTAGCCATACCAAGAG  
GCTTCAGATACCAGTTGGCAGGCTTAAAGATGAAGATAGACTCTTACCGTTAGAAGTT  
ATGGGAAACCAATTACAGGCATGCTCCAAAATCAAACAGAAGATAGTTACGAAAGGAACCT  
ATAGCATTACAAGAGGATAAACATAACTATGAGACAACAGCCAAAGAGTCCCTGAGGCGGGTT  
CTTCAGGAGAAATTGAAGTGGTTAGAAACTTCAAGGTTAGCTGAGCGAAGTCTGAGTAATACT  
GAAGATGAATGTACCCATCTGAAAGAAATGAATGAAAGGACTCAGGAAGAATTAAGAGAATTA  
GCCAACAAATATAATGGAGCAGTTAATGAGATTAAAGATTATCTGATAAAATTAAAGGTAGCA  
GAGGGAAAACAAGAGGAAATCCAACAGAAGGGACAGGCTGAGAAAAAAAGAATTACAACATAAA  
ATAGATGAATGGAAGAAAAGAACAGGAGCTCCAGGCAAAATAGAAGCTTGAAGCTGAT  
AATGATTTCACCAATGAAAGGCTAACAGCTTACAAGTACGGTTAGAACATCTCAGGAGAAA  
ACTCTAAAGAATGCAGCAGCTGGCTGATCGTCAGGGCATCTAACAAAGCGGTAGAAGA  
AACAAAGCTTCAAAAGGTTGTTCTGTTCTATGTTTGTGACAGTTCTTGG**TAA**  
TGAAGGTTAGTGTATATTTCAAGGTTAGTATTAACTTACCATCAGTTACTCTTATAGCTC  
ACAAAATAGCAAGCCAGTAACAGTATCAGATAATATAAAATCAGACTCTGTTAAG  
AAGGGTATCGTAACTGGAATGTGTCTTTAAGGGATGTATATTATGGTTTTGAATGTT  
AGTACTTGATATAGGTTCTTAGGTATTAAAGATTGTTGCAATCTCTGTCATTCCCAGCAT  
TAATTCAGCTTGATCTCAAATTAAATCAAACACAATGTAAGTCGTTGTGATACAACCTTA  
AGTGAACATGCTGCACTCTATTGGGGTACAGTACCTTAAACAAATTCTCTATGATGTT  
TAATATTCTTAATTGGCATCTCAGTTGATTAAACAAATTATGACTTTGTGAAAT  
GTAGAATCTCTTATATTGAGTAGTCCAGTAATTGCCAAAGTAGTTATTGTGTTAAT  
TCTGTTACAGTTGAGAGACTTAATTAGTACATTCTATTAAAGTAACGGATTCAATT  
TACATAGGAAATTAGGCAAATAATTGGTGGCATGTGTTATCATAGTAGAACCTTACCA  
GACTATACAGTATAAAATTAAACTAGATTACAGTCAGTCCTTGGCCAATTAAACATTGAG  
TTACAAAAGTTGAGAGACTTAATTAGTACATTCTATTAAAGTAACGGATTCAATT  
TGACTTTTAAACATGTAAGAGGATGGTGTATTCAAATATCTCGTGGTTCCATTGAA  
TTTGTCACGGCAGATGCCATATTGGGGAAAAATGCATAGAATATGCATCATTAATATTG  
TTTGGCAAACAGGCATTGAGTTCAAGACAGTGAACATTAGTACATATGGCAATT  
TTCACCTTATTAAAGTGGAGATGAGAACAGACCTAAAGTAGCTTACCTCACCATCAAATA  
CCTATTCAAGATTAGTGGTTGAATAGCCAGCACTTGAAGTAGGCCTTAGG

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**FIGURE 26**

MEARLRSVDVIHAPLPSPVDKVAANTPSMYSQELFQLSQYLQEALHREQMLEQKLATLQRLLAI  
TQEASDTSWQALIDEDRLLSRLEVMGNQLQACSKNQTEDSLRKELIALQEDKHNYETTAESL  
RRVLOEKIEVVRLSEVERSLSNTEDECTHLKEMNERTQEELRELANKYNGAVNEIKDLSDKL  
KVAEGKQEEIQQQKGQAEKKELQHKIDEMEEKEQELQAKIEALQADNDFTNERLTALQVRLEHL  
QEKTTLKECSSLADRRAASNQSGRRNKAFKRFVFCFSMFFDSSFG

**Important features of the protein:****N-glycosylation sites.**

amino acids 98-102, 271-275

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 138-142, 267-271

**Amidation site.**

amino acids 273-277

**Tropomyosins proteins.**

amino acids 169-217

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**FIGURE 27**

GAACCTGGCGCCGCCGAACTGATCGCGCCTAGTCCCACGCCTGTGCTAGTGAGCCGGA  
GCCGGCGACGGCGGCACTGGCGCCGGCCTGCAGGAGCCCACGGGTCTGCCATGGGG  
AGTGACGCGCTGCACCCGCTGTTCCGGCAGCGGCAGACATGAGGAGACCCCGCACAGG  
GGCAGCGGGCGGCGGCTCGTAGGCCGGGATGGGAGGAGAAATACGGCGGGACGTGCTGGCCG  
GCCCGGGCGGCGGGCGGCCCTGGGCCGGACGTACCCAGCGCTCGATTAAACAAATATA  
TTGTGTTACTATGTTCACTAAATTGGAGGCTGTGGACTTTCAATCATGATCTCC  
TAAAAGCTGTTCACATTGTCAGTTCACTTTATATTAAAACCTGGGACTGCATTGGGATGG  
TTTGTGTTCAAAGCCATTCTCTGGAAAACATTACCAAACACCAGTGGATCAAATAT  
TTAACACATGCGAGTTGCTGGGTGATTATTCACTCTGTGGTTTTGGCCTCACTTTGTG  
GACCACTAAGGACTTGTGCTGATATTGAGCACAGTGATATTGTGTCATTCACACTCAGTG  
TTTGTGTTCAACAGTTCTGGAGGAGGACAGCAAAGACAAGGGGAGCTGCTTTTCAATTG  
CTGTGATCTGTTATTGCTTTGACAAATGATGATCTCATGGCTAAAATGGCTGAACACCCCTG  
AAGGACATCATGACAGTGCTCTAACATGCTTACACAGCCATTGCCCTTAGGTGTGG  
CAGATCACAAGGGTGGAGTATTATTGCTAGTACTGGTTGTGAAAGTTGGTTTCATA  
CAGCTTCCAGAAAGCTCTGTGCGACGTTGGTGGAGCTAAACGTCTCAAGCTTATCTCATC  
TTGTTCTGTGCTCTGTGCCATTGGTCATTGTTCTGTGACAACAGTGGAGTAAAG  
TGGAGTCTGGTTCTCATTATGCTGCAACGGTTATCTTTGTGATGATCCTGG  
ATTTCATCGTGGATTCCATTGTCAGTCAAATGGAAGTTCCAATGTGCTCGTTATGGAT  
CCTTCCCATTGGATATTAGTGTCTCTTTGAAATTGGACACATCCAATAACAGACC  
AGCTTGGGCTATGAACAAAGCAGCACACCAGGAGAGCACTGAACACGTCTGTGGAGGAG  
TGGTAGTGAGTGCTATATTCTCATTGCTGCCAATATCTTATCATCTCCCTCAAGAGAG  
GACAAAAAGGTACCCATTGGATATTCTCTGAGAACACCTCTTATAACTCATGGGTG  
ATGCTTTCAGCATAGCTCAATGATCCCTAGGTTATTAGGAATCACTAAAACAAATT  
TTGAGGAGAGTGACTCTAGGCAGATCTTACTCTGTGCTTGAATCTGCTTTACCTTG  
TGGAAATTATTCTATGGCGTGTGACCAATAGTCGGGCTGATCTGGATGGATTCCACATGC  
TTTTGACTGCTCTGCTTACTGCTGCAACGGTTCTGTGCTGCTGATGAGTAGGTGGAAAGCCA  
CTCGGATTTCTCTATGGGTACGGCCAATAGAAATTCTGTCTGGGATTATTAAATGGACTTT  
TTCTAAAGTAATAGCTTTGTGTTATGGAGTCAGTGGCTAGATTGATTGATCCTCAG  
AATTAGACACTCACATGTTAACACCAGTCTCAGTTGGAGGGCTGATAGTAAACCTTATTGTA  
TCTGTGCCATTAGCCATGCCATAGCCATGCCATGGAGCTCTCAAGGAAGCTGCACTCAT  
CTGATCACAGCCATTCACACCATATGATGGACACAGTGACCATGGCATGGTACAGCCACG  
GATCTGGGGTGGAGGCATGAATGCTAACATGAGGGGTGATTCTACATGTTGGCAGATA  
CACTTGGCAGCATTGGTGTGATCGTATCCACAGTTCTTATAGAGCAGTTGGATGGTTCATCG  
CTGACCCACTCTGTTCTCTTACTGCTATATTAAATTCTCAGTGTGTTCCACTGATTA  
AAGATGCCAGGTTCTACTCCTGAGATTGCCACAGAATATGAAAAAGAAACTACATATTG  
CTTAGAAAAGATACAGAAAATTGAAGGATTAATCATACCGAGACCCCTCATTTGGCGTC  
ATTCTGCTAGTATTGTCAGGAAACATTCAATACAGGTGACATCTGATGTGCTAGAACAAA  
GAATAGTACAGCAGGTTACAGGAATACTAAAGATGCTGGAGTAACAAATTAAACATTCAAG  
TGGAAAAGGAGGCATACTTCAACATATGCTGGCTAACAGTACTGGATTTCATGATGTTCTGG  
CTATGACAAAACAAATGGAATCCATGAAATACTGCAAAGATGGTACTTACATCATGTGAGATA  
ACTCAAGAATTACCCCTGGAGAATAACAAATGAAGATTAAATGACTCAGTATTGTAATATTG  
CCAGAAGGATAAAAATTACACATTAACTGTACAGAACAGAGTCCCTACTACTGGATCAAGG  
AATCTTCTGAAGGAAATTAAATACAGAACATTAATGGTAAAAAAA

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**FIGURE 28**

MEEKYGGDVLAGPGGGGGGLGPVDVPSARLTKYIVLLCFTKFLKAVGLFESYDILKAVHIVQFI  
FILKLGTAFFMVLFQKPFSSGKTITKHQWIKIFKHAVAGCIISLLWFFGLTLCGPLRTLLLFE  
HSDIVVISLLSVLFTSSGGGPAKTRGAFFIIAVICLLLFDNDDLMAKMAEHPEGHHDSALTH  
MLYTAIAFLGVADHKGGVLLVLALCCKVGFHTASRKLSVDVGGAKRLQALSHLVSVLLCPW  
VIVLSVTTESKVESWFSLIMPATVIFFVMILDFYVDSICSVKMEVKARYGSFPIFISALL  
FGNFWTHPITDQLRAMNKAHQESTEHVLSGGVVSAIFFILSANILSSPSKRQKGTLIGYS  
PEGTPLYNFMGDAFQHSSQSIPRFIKEYSLKQILEEESDRQIFYFLCLNLLFTFVELFYGVLTN  
SLGLISDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGFINGLFLIVIAFFVF  
MESVARLIDPPPELDTHMLTPVSVGGLIVNLIGICAFSHAHSHAHGASQGSCHSSDHSHHHMH  
GHSDHGHGHSGHSAGGGMNNAMRGVFLHVLAIDLGSIGVIVSTVLIEQFGWFIADPLCSLSTA  
ILIFLSVVPLIKDACQVLLRLPPEYEKELEKIALEKIQKIEGLISYRDPHFWRHSASIVAGTI  
HIQVTSVDVLEQRIVQQVTGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMESMK  
YCKDGTYIM

**Important features of the protein:****Signal peptide:**

amino acids 1-46

**Transmembrane domains:**amino acids 59-77, 101-119, 150-167, 205-223, 239-258, 267-284,  
305-324, 343-360, 421-440, 452-469, 486-505, 522-539, 592-612,  
621-641**N-glycosylation site.**

amino acids 721-725

**Glycosaminoglycan attachment site.**

amino acids 143-147

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 225-229

**Tyrosine kinase phosphorylation sites.**

amino acids 750-758, 756-764

**N-myristoylation sites.**amino acids 14-20, 46-52, 102-108, 112-118, 144-150, 317-323,  
347-353, 369-375, 372-378, 437-443, 462-468, 529-535, 549-555,  
553-559, 579-585, 582-588, 583-589, 584-590, 605-611, 737-743**Multicopper oxidases protein:**

amino acids 561-569

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**FIGURE 29**

GGCACGAGGGCAGGATATTAGAAATGGCTACTCCCCAGTCATTTCATCTTGCAATCTGCA  
TTTAATGATAACAGAATTAATTCTGGCCTCAAAAGCTACTATGATATCTTAGGTGTGCCAA  
AATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTCACAAGTGGCATGAAGTACCACCTG  
ACAAAAATAAGAGCCCGGATGCTGAAGCAAATTCAAGAGAGATTGCAGAAGCATATGAAACAC  
TCTCAGATGCTAATAGACAAAAGAGTATGATACACTTGACACAGTGCTTTACTAGTGGTA  
AAGGACAAAGAGGTAGTGGAAAGTTCTTGAGCAGTCATTAACTTCATTTGATGACTTAT  
TTAAAGACTTGGCTTTTGGTCAAAACAAAACACTGGATCCAAGAAGCGTTGAAAATC  
ATTTCAGACACGCCAGGATGGTGGTCCAGTAGACAAAGGCATCATTCCAAGAATTTCTT  
TTGGAGGTGGATTATTTGATGACATGTTGAAGATATGGAGAAAATGTTCTTTAGTGGTT  
TTGACTCTACCAATCAGCATACAGTACAGACTGAAAATAGATTCATGGATCTAGCAAGCACT  
GCAGGACTGTCACTCAACGAAGAGGAAATATGGTTACTACATACACTGACTGTTAGGACAGT  
AGTTCTTATTCTATTCTCACTAAATCCAACTGGTTGACTCTTCCTCATTATCTTGATGCTAA  
ACAATTTCTGTGAACATTTGACAAGTGCATGATTCACTTAAACAATTGATATAGCTA  
TTAAATATATTTAAGGGTTTTTTTGACAAATTCAACATTCAACGAGTAGACAAAATGCT  
AATTATTCCTGATTAGGAAAGTTCTTAAAAAACACGTAATTTGCCTAGTGCTTTCT  
CTACCTGCCCTGGGCTCACTAATATCACCAGTATTACCAAGAAAATATTGAGTTACCT  
GATTAAACTTAAAGTTAATTGAGATTAAATTGTGTGAACCTAATGATTTGCAGTGAA  
ACCTTACTAATTCAAAGTGCATGTTCTATGACATCTGTGACTTGCCTTGAGACTGTACAT  
GAAACTGTATAATTGAGTCATTCAAGTAAAGGAGAACAGTATCTGGTTAATTGCTACTGAAAG  
GTTGAGAAAGGAATGGTTGATATTACACAGCGCTGTGCCTTCTACAGTAGAAACTGGGTT  
AAAGGAAATGGTTTATTGCCCATAGTCATTAGGCTGGAAAAAGTTGAAAACCTAACGAAA  
TATTGCCAAGAGATTGTTATGTGTTGGTCCAGCCTAAAATGATTTGTAGTGTGAAATC  
ATAGCTACTTACATAGCTTTCATATTCTTCTAGTTGTTGGCACTCTAGGTCTTAGTA  
TGGATTATGTGTTGTGTGTAGTTATCCTCTCTCATCTTATCTAGAGATTGACT  
GATACCTCATTCTGTTGAAAACCAGCCAGTAATTCTGTGCAACCTTACTATGTGCAATAT  
TTTAAATCCTGAGAAATGTGCTTTGTTGGATAGACTTATTCTTAGTTCTGCACT  
TTTCCACATTATACTCCATATGAGTATTAATCCTATGGATACATATTAAAACAAGTGTCTCAT

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**FIGURE 30**

MATPQSIFIFAIICILMITELILASKSYYDILGVPKSASERQIKKAFHKLAMKYHPDKNKSPDA  
EAKFREIAEAYETLSDANRRKEYDTLGHSAFTSGKGQRGSGSSFEQSFNFDDLFKDFGFFG  
QNQNTGSKKRFENHFQTRQDGSSRQRHHFQEFSFGGLFDDMFEDMEKMFSFSGFDSTNQHT  
VQTENRFHGSSKHCRTVTQRRGNMVTYTDCSGQ

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Nt-dnaJ domain signature.**

amino acids 27-59, 66-90

**Glycosaminoglycan attachment site.**

amino acids 96-100

**N-myristoylation sites.**

amino acids 32-38, 99-105, 102-108, 126-132, 211-217

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**FIGURE 31**

AAAGTTACATTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGTTTG  
GCAGAAAGGAGGGTGCCTCGGAGCCGCCCTTCTGAGCTCCTGGGCCGGCTCTAGAACAAAT  
TCAGGCTTCGCTCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCTGAG  
ATGGACAGAATGCTTATTTGGAAAGAAACAATGTTCTAGGTCAAAC TGAGTCTACCAAATG  
CAGACTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTCTAGTGGTTTCTACGCA  
TTGATTCCATGTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTCTGTGA  
CTCTCAACCAACATGAAGCATCTCTGATGTGGAGCCCAGTGATCGCGCCTGGAGAAACAGTG  
TACTATTCTGTCGAATACCAGGGGAGTACGAGAGGCCGTACACGAGCCACATCTGGATCCCC  
AGCAGCTGGTGCCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATCACGCCACT  
GTGCCATACAACCTCGTGCAGGGCCACATTGGCTCACAGACCTCAGCCTGGAGCATTCTG  
AAGCATCCCTTAATAGAAACTCAACCATCCTACCCGACCTGGATGGAGATCACCAAAGAT  
GGCTTCCACCTGGTATTGAGCTGGAGGACCTGGGCCCCAGTTGAGTTCTGTGGCTAC  
TGGAGGAGGGAGCCTGGTGCAGGGAACATGTCAAAATGGTGAGGAGTGGGGTATTCCAGTG  
CACCTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCAGACATTGTGAAGGCC  
ATTGGGAGGTACAGCGCCTTCAGCCAGACAGAACATGTGTGGAGGTGCAAGGAGGCCATTCCC  
CTGGTACTGCCCTGTTGCCTTGTGGCTTCATGCTGATCCTGTGGCGCCACTGTT  
GTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTGTTGCCCTGGTGGCCTCCCAGACACC  
TTGAAAATAACCAATTCAACCCAGAAGTTAACAGCTGCAGAAGGGAGGGAGGTGGATGCCTGT  
GCCACGGCTGTGATGTCCTGAGGAACCTCCTAGGGCTGGATCTCATAGTTGCGGAAGG  
GCCAGGTGAAGCCGAGAACCTGGCTGCATGACATGGAAACCATGAGGGACAAGTTGTGTT  
TCTGTTCCGCCACGGACAAGGGATGAGAGAACAGTAGGAAGAGGCCCTGTTGTCTACAAGTCTAG  
AAGCAACCATCAGAGGCAGGGTGGTTGTAACAGAACACTGACTGAGGCTTAGGGATGTG  
ACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACCTGGAAAAGTGACTTCATCCCT  
TCGGTCTAAGTTCTCATCTGTAATGGGAAATTACCTACACACCTGCTAAACACACACAC  
ACAGAGTCTCTCTATATACACACGTACACATAAACACCCAGCACTGCAAGGCTAGA  
GGGAAACTGGTGACACTCTACAGTCTGACTGATTGAGTGTGTTCTGGAGAGCAGGACATAATG  
TATGATGAGAATGATCAAGGACTCTACACACTGGGTGGCTTGGAGAGGCCACTTCCCAGAAT  
AATCCTTGAGAGAAAAGGAATCATGGAGCAATGGTGTGAGTTCAAGCCCAATGCCG  
GTGCAGAGGGAAATGGCTAGCGAGCTCTACAGTAGGTGACCTGGAGGAAGGTACAGGCCACA  
CTGAAAATGGATGTGCATGAACACGGAGGATCCATGAACACTGTAAGTGTTGACAGTGTG  
TGCACACTGCAGACAGCAGGTGAAATGTATGTGTGCAATGCGACGAGAACATGCAAGTCAGTA  
ACATGTGCATGTTGTTGCTCCTTTCTGTTGGTAAAGTACAGAACATTGCAAATAAAA  
AGGGCCACCCCTGCCAAAAGCGGTAAAAAAAAAAAAAA

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**FIGURE 32**

MQTFTMVLEEIWTSLFMWFYALIPCLLTDEVAILPAPQNLSQLSTNMKHLLMWSPVIAPGET  
VYYSEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDDITATVPYNLRVRATLGSQTSAWSI  
LKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPFELVAYWRREPGAEEHVKMVRSGGIP  
VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVLALFAFVGFMLILVVVPL  
FVWKMGRLLQYS CCPVVLPDTLKINTSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-44, 134-138

**Tissue factor proteins.**

amino acids 92-120

**Integrins alpha chain proteins.**

amino acids 232-263

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**FIGURE 33**

GAGACACGCGAGCGGGAGACCTCCAAGGCAGCGAGGCATCGGACATGTGTCAGCACATCTGG  
GGCGCACATCCGTCGAGCCGAGGGAGATTGCCGAAACAATTCAAACACTGCGATATTGATCT  
TGGGGGTGACTGTCCCTGGCCGGCTGCGGGGGAGTGCAGTGCACTCGCTCGGAAGTG  
TGTGCGAGTGTATGTGTGTGCCGTGCGGCTCCCCCTTCCCCCGTTTCCCCTCGA  
GTGATGCACTTGAATGAGAATCAGAGGATGAAATAGTCTGGGAGGTGCTTTCTTCA  
AGCCAATTCATCGTCTGCATATCAGCTAACAGAATTACCAAAAATCCATGAAGGCTGGT  
GGCATACAAGGAGGTGGTCCAGGGAAAGCTTGTCCAGTTCTCTTCTGGGATTGGTGA  
CTCAGCTTGAATCTTGTCTGTGGGAAACGGCAGTCGCCAGTCAACATAGAGACCAGTCA  
CATGATCTCGACCCCTTCTGACACCTCTCGCATCAACACGGGGGAGGAAGGTCA  
GACCATGTACAACACTGGAAGACACGTATCCCTCGCCTGGACAAGGAGCAGTGG  
ATCTGGAGGGCCCAGTACAGCAGGCCCTCTGGGAGGATCCGACTACACTTGGGAGTGA  
GGACAGCCAAGGGTGGAGCACCTCTCAATGGACAGGCCCTCTGGGAGGTGCAGCTCAT  
CCACTATAACCATGAGCTATATACGAATGTCAAGAAGCTGCAAAGAGTCAAATGGATTGGT  
GGTAGTTCTATATTTATAAAAGTTCTGATTCAACACCATTCTTAATCGAATGCTCAA  
CAGAGATACTATCACAAGAATAACATATAAAATGATGCATATTACTACAGGGCTTAATAT  
AGAGGAACTATATCCAGAGACCTCTAGTTCACTACGATGGTCGATGACTATCCCACC  
CTGCTATGAGACAGCAAGTGGATCATAATGAACAAACCTGTCTATATAACCAGGATGCAGAT  
GCATTCCCTGCGCTGCTCAGCCAGAACCCAGCAGTCAGATCTTGAGCATGAGTGA  
CTTCAGGCCTGTCAGCCACTCAACAAACCGCTGCATCCGACCAATATCAACTCAGTTACA  
GGGGAGGACTGTCACAAACAAACGAGGCCAGAAGCTCAGTATAGAGTAAATGAATGGCTCCT  
CAAGTAGGAACAAAGCCAAGAAGAATCCCACCTCAGTGAATGCTACAACGTGAATTGACG  
TAACCTAGAATGCCCCCTCTGCTCTCTCCTTCTTCCCCAAGCCTCATTCTT  
GGGATTGGCCCTTCTTCTGAAAGTGTCTGCGAAACCATGGCAGAGGAATACATCTCAC  
ACATACTCACAAACACACACACAAGCACTGCAACATACATAACAAACACATGCAAACATAC  
CACACACACTCTTCAACCTCCATCATGGGAAGTCAGGTTCAAGAAACAAAAGTCTCAT  
TCATAAGAGGTCTAGAAGAAAATAACCAAGTTAACCTGATTCAATTGATACCGTTCT  
GAACATAAAATCTACCCAAATGAGACTTTCAGCCTTGACATACAAAATTCTC  
GAGAGGAGAAAATACAGCTCTGATGCCATCAAACGGACTTGCATCAAGTAATT  
GTCCTAGGATCCTTGAGGGTGTGGTAGCAGGTGAGCAGGACAAAGTTGACCAAGGACACT  
ATTCTAGATTATGATTCTCTGTTACTCAACAATTACAAAGAAAAAGGGACAGACATTG  
AAGAGCTACACATTGTATATATCACCACAGACTATAAGGAATGAAATTAT  
GTCACATATCTGAGTAGGATTGCAAGATCAGAAATGATCCATTGCTGTTCTTGT  
CAAAGGTCAACATTGTGTTGGTTATTGTTACCGCTCAAAATGTGTTAACGAGTTAAT  
TTCATTCTGCTTGGCTGTTACTCAACAAATTACAAAGAAAAAGGGACAGACATTG  
GCATTCTTGATTCACTTGTCCCTCATCTACATGTTGTCAGGCAGCTTAC  
TGAGTTGTCAGGAATGCATTGCTAAGCAAGTATGACTTAATTCCACTCCATGGC  
TCAATCATTACATGAGGTGAGCTCAGCCTGAGATAGCAGGCGACAGACTTCTGC  
AAACTGCCATGCCCTGTGATGCTCCGTGAAGGAATGCACTTGCCTGTAAGTTCTGG  
GAAAGGGGTATGTTCTCCAGGTGCAGCCAGTCTCACAAAGTACAAAGCAATGC  
CTTTCTGTTATAATGGTCACTCACTGTGTTGGTTACTGTCAAGAAATCAATAATGTG  
TTAACAAAGTTA

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**FIGURE 34**

MEIVWEVLFLLQANFIVCISAQQNSBKIHEGWAYKEVVQGSFVPVPSFWGLVNSAWNLCSVG  
KRQSPVNIEETSHMIFDPFLTPLRINTGGRKVSGTMYNTGRHVSRLDKEHLVNISGGPMTYSH  
RLEEIRLHFGSEDSQGSEHLLNGQAFSGEVQLIHYNHELYTNVTEAKSPNGLVVVSIFIKVS  
DSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFITYDGSMTIIPPCYETASWII  
MNKPVYITRMQMHSRLLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTNINFSLQGKDCPNNA  
QKLQYRVNEWLLK

**Important features:****Signal peptide:**

amino acids 1-20

**Eukaryotic-type carbonic anhydrases proteins.**

amino acids 126-162, 220-269, 43-91

**N-glycosylation sites.**

amino acids 116-119, 168-171, 302-305

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**FIGURE 35**

GTCGGAACCCCTCAGGCCACCTCGGGAGTCCTGGGTCCAGAGGGTGTCCCTGTACCCCTTCAC  
 ACAGGACCCCTACTCTGCAGGGATAAGCCAGCTGCCTGCAGCCTAGGGTCCAAGGAGGCTGCTGA  
 TTGTGGCCACAGCCTCATCTGAACGCAGGAGACCAGGATACCGAGGCACCGATCCCCTCTGTG  
 CCCTGGGAGCCCAGTGTCCCAGTCACCCCAAGGGCTGAGGTCTGCCTGAGTCGGGCTTCGT  
 TGGTAGGACCACGGGGCAGGGAATGTGAGCGCCATCGAGTCACGGTGTCCCTAGTGGTCAAGGCC  
 GACTTGGCAGGGCCTCCGGCAGGTGGGCCAGCAGCCCCAGCCATCCACCAATGGTGGTGGCACA  
 AGGAGGTATTCAAGGCTCCAGGCCAGGTGGGCCAGCAGCCCCAGCCATCCACCAATGGTGGTGGCACA  
 CCCCACCGCCACTGCCACCACGCCACTGCCACTGTACGGCTCATCGCCTTCTGACGGAGGTATCGAC  
 AGCACCCACTGCCCTCGGTGTGCCCTGCAGAACCGGTTCATCTACTGCAACGACCGGGACTCAC  
 ATCCATCCCCGAGATATCCTGATGACGCCACCCCTCACCTGCAGAACAAACAGATCAACAACG  
 CGGCATCCCCCAGGACCTCAAGACCAAGGTCAACGTGAGGTCAACCTATAACGAGAATGACCTG  
 GATGAGTTCCCCATCAACCTGCCCTCGCTGACCTGAGGACAACAATGTGCGCAC  
 CATTGCCAGGGACTCGCTGGCCGATCCCGCTGCTGGAGAAGCTGACACTGGATGACAACACTCGTGT  
 CCACCGTCAGCATTGAGGAGGACGCCCTGCGCACAGCAAACAGCTCAAGCTGCTCTCCGTGAGCCGG  
 AACCACCTGAGCAGCATCCCCCTGGGCTGCCGACACGCTGAGGAGCTGCCGTGGATGACACCG  
 CATCTCACCCTCCGCTGATGCCCTCAAGGCCAACAGCTGCCGCGGCTGGTGTGGACGGTA  
 ACCTGCTGGCAACCAGCGCATGCCGACACCTTCAGGCCCTACAGAACCTCACAGAGCTCTCG  
 CTGGTGCAGCAATTGCTGGCCGCCCCCTCAACCTGCCGACAGCAAACAGCTCAAGCTGCTCTCCGTG  
 GCAGGACAATGCCATGCCACATCCCCATCACACGCTGGCAAGATGCGTGAGCTGGAGCAGGGCTGG  
 ACCTGCTCAACAACAACCTGACCACGCTGCCCGGGCTGTTGACGACCTGGGAAACCTGGCCAG  
 CTGCTGCTCAGGAACAACCTGGTTTGTGGCTGCAACCTCATGTGGCTGCCGACTGGTGAAGGC  
 ACGGGGGCCGTGGTCAACGTGCGGGCCTCATGTGCCAGGGCCCTGAGAAGGTCCGGGATGGCA  
 TCAAGGACATTACAGCAGGAGATGGCAGAGTGTGAGACGGGGCGCAGGGCGGTGGCAATGCG  
 GCTGCCAAGACCAACGGCCAGCAACCACGCCCTGCCACCACGCCAGGGTCCCTGTTACCTCAA  
 GGCCAAAAGGCCAGGGCTGCCCTCCCCACTCAACATTGACTACCCATGCCACGGGTGATGGCG  
 CCAAGACCCCTGCCATCCACGTGAAGGCCCTGACGGCAGACTCCATCGCATTGCGAAGGCCACG  
 CTCCCCCTCTTCCGCTCAGTTGGCTGCCCTGGCCACAGCCCAGCCGTGGCTCCATCAC  
 GGAGACCTGGTGAGGGGACAAGACAGAGTACCTGCTGACAGCCCTGGAGGCCAACCGGGCAGC  
 TCATCTGCTGATGGTACCATGGAGACCAGCAATGCCCTGGAGCTGCTGACAGCCCTGGAGGCCAAC  
 GCAGAGACAGCCGACAGCTATGCCCTACCAACACTCAACCAGGAGCAGAACGCTGGCCCATGGC  
 GAGCCTGCCCTGGGGCATCATGCCGGGCACTGGCTCTGGCTCTCCCTCTGGCTGGGG  
 CCATCTGCTGGTACGTGACCCAGGCTGGGAGCTGCTGACCCGGAGAGGCCAACCGGGGAGC  
 AGGAAAAAAGGATGACTATATGGAGTCAGGGACCAAGAAGGATAACTCCATCTGGAAATCCGGG  
 TGGGCTGAGATGCTGCCCATCAACCGTACCGGCCAACAGAGGAGTACGTGGTCCACACTATCTCC  
 CCTCCAAACGGCAGCAGCCCTGCAAGGCCACACACCATGGCTACGGCACCACGCCGGCTACCGG  
 GACGGGGCATCCCCACATAGACTACTCTACACATGATGCCGCCACCCGGCTGCCCGCCTCA  
 GCCCGACTGCCCTGGCTGGCATGTGGCTTGGCCAGCCCTGCTGCAATCCAAGAGAGCAAGGAAGA  
 GAAATTCCATGGGTGACTTCTCCGAGAAAGCAAAGTTGGGAGGGCTGACGATTGAGAAC  
 CAACAGTGACAATTTTTAAAGAATAGAAGGAGGGAGGGACTAAAATAATATTGCA  
 GAGGAGAGGCCAACCGGGCTGGGGTGG  
 GTTTTTTTTTCCCCCTGAACCTGGAGGATACTACCTGTACAAACATCTGTGGACACTCATGCTCT  
 GTTCAAGGCCATCAAAGGAACCGCCAGGGAGAAGCAGCCGGCTCTCAAAGCTCCACGCCAGCTCTC  
 CCGCCACTGCCACTCGCTGGCGACCGATGGAGGGTTTCAAGGCTCTCACAAAGGAGAGAGGGAG  
 AAAAGATTTGCCCTGGAGGATATGGTCTGAAATCTCTCCCTGGTTATTCCATACCATTCCCT  
 TGCAGATTGAGAAACATGGCATCTTCACTGCAATTGAAACAATCATGTAGTCGATTA  
 AAAACAACCTTTTCTAGGCTGAAGCCCTCTTCAGTTCCATGCACCAAGCCTCCGTAGAAGGCC  
 GCGGAAGCCGTAGCTTCCCTGCCACCTGGAGGTGCATCTGTCTGCCTGTATCCCTGCGGGTG  
 TCTCTAAGTACAGATGGTAGATAGAGGCCACATGCACGGTCTTACCGTTCTGGGTAGTTCTT  
 ACCATTCCCTGAACAAATAGAATGTGAAAGTGTAAAAAA

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**FIGURE 36**

MVVAHPTATATTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRCNDNG  
FIYCNDRGLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNQVIYLYENDLDEFPINLP  
RSLRELHLQDNNVRTIARDSLARIPLLEKLHLDNSVSTVSIEEDAFADSKQLKLLFLSRNHL  
SSIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIADDTSRQLQNLTE  
LSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLDSLNNNLTTLPRGLFD  
DLGNLAQLLL RNNPWFCGCNLMWL RDWVKARA AVVNVRGLMCQGPEKVRGMAIKDITSEMDEC  
FETGPQGGVANAAKTTASN HASATT PQGS LFTL KAKRPGLR LPDS NIDYP MATGDGAKTLAI  
HVKALTADSIRITWKATLPASSFRLSWRLGHSPAVGSITETLVQGDKTEYLLTALEPKSTYI  
ICMVTMETS NAYVADET PVC AKAETAD SYGPTT LNQE QNAG PMA SLPLAG IIGGAVALVLF  
LVLGAICWYVHQAGELLTRERAYNRGSRKDDYMESGTKKD NSILEIRGPGLQMLPINPYRAK  
EEYVVVHTIFPSNGSSLCKATH TIGYGT RGYRDGGIPD IDYSYT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 552-573

**N-glycosylation sites.**

amino acids 249-252, 305-308, 642-645

**Leucine zipper pattern.**

amino acids 182-203, 299-320

**Phospholipase A2 aspartic acid active site.**

amino acids 57-67

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## FIGURE 37

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**FIGURE 38**

MAEPGHSHHLSARVRRRTERRIPRLWRLLLWAGTAFQVTQGTGPELHACKESSEYHYEYTACDS  
TGSWRVAVPHTPGLCTSLSDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYS LGTGIRFDE  
WDELPHGFASLSANMELDDSAEESTGNCTSSKWVPRGDYIASNTDECTATLMYAVNLKQSGTV  
NFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSELNRGNNVLYWRTTAFSVW  
TKVPKPVLVRNIAITGVAYTSECFPKPGTYADKQGSSFKLCPANSYSNKGETSCHQCDPDK  
YSEKGSSCNVRPACTDKDYFYTHACDANEGETQLMYKWA KPKICSEDLEGA VKL PASGVKTH  
CPPCNPGFFKTNNSTCQPCPYGSYNSGSDCTRCPAGTEPAVGFEYKWWNTLPTNMETTVLSGI  
NFEYKGMTGWEVAGDHITYAAGASDNDFMILTLVVPGRFPQSVMA DTENKEVARITFVFETL  
CSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYII EENTTSFTWAFQRTTFHEASRKYN  
DVAKIYSINVTNMNGVASYCRPCALEASDVGSSCTSCPAGYYIDRDGTCHSCPPNTILKAH  
QPYGVQACVPCPGTKNNKIHSCLCYNDCTFSRNTPTRTFNYNFSALANTVTLAGGPSFTSKGL  
KYFHHFTLSLCGNQGRKMSVCTDNVDLRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVS  
SQPVSLADRLIGVTTDMTLGITSPAELFHLES LGIPDVIFFYRSNDVTQSCSSGRSTTIRVR  
CSPQKTVPGSLLPGTCSDGTCDCNFHLWESAAACPLCSVADYHAI VSSCVAGIQXTTYVX  
REPKLCSGGISLPEQRVTICKTIDFWLKVGISAGTCAI LTVLTCYFWKKNQKLEYKYSKLV  
MNATLKDCDLPAADSCAIMEGEDVEDDLIFTSKKSLFGKIKSFTSKRTPDGFDSVPLKTSSGG  
PDMDL

**Important features of the protein:****N-glycosylation sites:**

amino acids 153-156, 390-393, 391-394, 404-407, 544-547, 576-579,  
672-675, 717-720, 947-950

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 15-18, 563-566, 709-712

**Casein kinase II phosphorylation sites:**

amino acids 42-45, 59-62, 81-84, 146-149, 168-171, 282-285, 331-  
334, 340-343, 431-434, 449-452, 465-468, 523-526, 557-560, 761-  
764, 780-783, 835-838, 860-863, 893-896, 949-952

**Tyrosine kinase phosphorylation sites:**

amino acids 50-56, 109-116

**N-myristoylation sites:**

amino acids 77-82, 88-93, 152-157, 268-273, 288-293, 320-325,  
400-405, 405-410, 414-419, 463-468, 599-604, 616-621, 634-639,  
644-649, 839-844, 874-879, 912-917, 916-921

**Amidation site:**

amino acids 707-710

**Cell attachment sequence:**

amino acids 162-164

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**FIGURE 39**

GGGAAGGGGTTCTGGGCTGCCGCAGGCACACAGGCCAGAGCTTCGTGGATACCTGCAGGGCCC  
AAAGGTCCCTCCCTGTTTGAAGAGTGAGTGATGGCTATGAGGTAGCGGCCAGGCTGATCACC  
CCTGCCTGGCTGGAGGCAGAATTCTGTAATCCTCGCCAAGTCTTCTCCAGGCCACTGGTT  
AGCTCATCTCAGCCTCCTCTGGGAGCATCAACACCAACATGGCACAGGGGACTGCAGTGGTGT  
GCTTTGGACCTGTGTACCCACCCAAAGGCTAAAGGCAGAGGCCAGGTGACTTGCAGGGGGTCTCT  
TCTCTAGGATTATCTGTACTTCCCCTCTGCTCTTTACTACGGGAGATCGAGCTAGCTATA  
ACCCACCTTCTTCATGAGAACCAACACTAAATTGAAAATTATCCCAGTGCTGGAGGAGGGC  
AGCAGGTTGAGATTATGTTGGCAGGAAGAATGTTGGCATTGATTGGCACGCAGGGGACGAGAG  
CTGCTTTGTGCTTAAAGGAGCAAGTTACACCCCTGTTAACCTGCCTCAAAGGGACGACT  
CTGTAAGATTCTGCTACTTATTCAAGTTGACACG**ATGCC**TTCACACTCCACCTGAGGTCC  
CGCCTCCCTCTGCCATAAGGAGTTGATTCTACAAAAGAAACCAACATCAGAAATACATCC  
AGCATGGCTGGAGAGCTCCGACCAGCCAGCCTGGTCTGCCAGGTCCCTGCTCCAGCT  
TTTGAAAGATTCTGCCAGGTCAACACTGGTCCTCTACCCCTGCTGGGCCAGAGTGAGCCAGAA  
AAGTGGATGCTGCCCTCAAGGTGCTATCTCAGAGACCAGGATGGCCATCCCCAGTTCTGG  
AAATACGAGTTGGTGCCTGCACCGGTAGCCTGGCTCGTGGAGCAGTACTCGGAGCAGCTG  
AAGGACATGGTGCCTCTCCTGGGCTGCAGCTCTCCCTGGAGGAGGCCTGGAGAAAGCG  
GGGCTCCCAGAAGAGACCCAGCAGGTACAGCCAGGCAGGGTCATACAAGACAACAGTGCCT  
TGTGTTACCCATGCTGGCTCTGCTGCCCTCTGGTGGTCACGATGAGGCCATTCCTCAAGGAC  
AAGCTGGAAGGGCTGGTGGGGCCTGCTGCTCCCTCGGAGGTGAGCAGGGCAACCTGTTCAC  
ATGGGCACCCAGAACTGTTGGGAATCAAAGAGCTTCCAAACCTGCCACGGGATGCCATG  
GTGTGCCCCCAGGGGAGGTTCCAGTGTCTGGCCTCTCCGCTGACCAGTCTGGAGCTGTC  
AGCAGCTGTGAGACCCACTGGCTTGCAGCATCCCAGGCTGCACAGTTATGACTGACCTG  
AAGGATGCAAAGGCTCCACCTGGTTGCTCACCCCCAGAGAGAAATTCAAGAGGTCATCACATT  
TCCCAAGATCCTCTGCACTACAGCATCGCTCAGTCTGCTTCAGAAGATCAGAGAACTA  
GAGTCTATGATCGGCATAGACCCAGGGAACCGGGGATTGGCACCTGCTCTGAAAGATGAG  
CTGCTGAAGGCCTCTCTCGCTGTCCATGCCGCTCAGTGCATCACCAACTGGTTCCCC  
ACACATTCAATCATGAGCCTCCAGAAGAGACAGATGGCCACCCAGGAGCTGTGCTCTGGTT  
GCCTCCTGCAGCCTGGAGAAGGAGGTGCCATAATCGTTGACCAGAGAGCCTGGAACCTG  
CACCAGAAGATTGTAAGATGCTGTGAGCAAGGTGTTCTGAAGACGCAGATCCCAGTATT  
ACTTACCAAGGTGGATCAGTGGAAAGCTGCTCAGGCTTCTGTCAGGATGGGAAATGGGACCCGCAG  
ACACCTAGATTGACCACCTGGTGGCCATAGAGCGTGGGAGAGCTGCTGATGGCAATTAC  
TACAATGCAAGGAAGATGAACATCAAGCACTGGTTGACCCCATTGACGATTTTCTTGCT  
GCGAAGAAGATTCTGGAATCTCATCAACTGGAGTCGGTATGGGAGGCAACGAGCTTGGGATG  
GGTAAAGTCAAGGAGGCTGTGAGGAGGCACATACGGCACGGGATGTCATCGCTGCGACGTG  
GAGGCTGACTTGCCTGATTGCTGGTCTTAAGTGGGAGGCTATGCCCTGGCTGCGA  
CTCTACATCCTGACTCATGTGCTGCTCACAGTCAGTACCTGAGGAAAGCAGTCGGACCCCTCC  
AGGGCACCTGGAGATCAGGCCCTGGACTCAGGCCCTCCGCTGGTCATTAAGGAAGAAAAATG  
CTGGGCATCTGGTGCAGCACAAAGTCCGGAGTGGCGTCTCGGCATCGTGGGATGGAGGTG  
GATGGGCTGCCCTTCCACAACACCCAGCCGAGATGATCCAGAAGCTGGTGGACGTACCACG  
GCACAGGTG**TAA**CCGTCATGTTCCGTGTGAGCAGAGTCCTACCAACGGCAGGTCTGCATC  
CGGGGAGAATGCGAGTCGTTCTGGCGACAATCTGCTAGTAAACACTGGCTTCGGTGAGCAA  
CGAACACTCGCCTGGCCTGGAAACTGCATGCCACTTTCTGGGAGGGGTTAGTCAGGTGCC  
GTGGACAAAGGACAACATTCTCTGGGCTTTAACTTTATTCTAAGACTCTAAAGGCGT  
TGATTCTAACCCCTCCTACTCTGGCTTCTTCAGGCAACCCACGTGGTCTCCTATGAGAACT  
TCTCGACAGTTACTTATGGGACACTGTGAACAATTAACTGCCAGGAGCATGAGAAACA  
AACATTCCCAGGCCATGTAGGATAGGATACTCCAGACTCCAGTCATCCTCCCCCATCCATGGT  
TTCTGTTACTCATGGTTCAAGTTACTCATAGCCAATGCGAGACCAGAAACTAAATGAAAAAA  
TTTCAGAAATAACAACTCTAAGTTAAAAAAAAAA

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**FIGURE 40**

MPFTLHRSRLPSAIRSLILQKKPNIRNTSSMAGELRPASLVLPRLAPAFERFCQVNTGPL  
PLLGQSEPEKWMMLPPQGAISETRMGHPFWKYEFGACTGSLASLEQYSEQIQLKDMVAFFLGCSF  
SLEEALEKAGLPRRDPAHSQAGAYKTTVPCVTHAGFCCPLVVTMRPIPKDKLEGVRACCSL  
GGEQQPVHMGDPELLGIKELSKPAYGDAMVCPGPVEPVFWPSPLTSLGAVSSCETPLAFASI  
PGCTVMTDLKDAKAPPGLTPERIPEVHHISQDPLHYSIASVSASQKIRELESMIGIDPGNRG  
IGHLLCKDELLKASLSLSHARSVLITFGPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAI  
IVDQRANLHQKIVEDAVEQGVLKQTQIPILTYQGGSVAAQAFLCKNGDPQTPRFDHLVAIER  
AGRAADGNYYNARKMNICKLVDPIDDLFLAAKKIPGISSTGVDGGNELGMGKVKEAVRRHIR  
HGDVIACDVEADFAVIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQAWTQAL  
PSVIKEEKGMLGILVQHKVRSGVSGIVGMEVDGLPFHNTHAEMIQKLVDVTTAQV

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 358-378, 517-539

**N-glycosylation site.**

amino acids 28-32

**Tyrosine kinase phosphorylation site.**

amino acids 444-452

**N-myristoylation site.**amino acids 98-104, 102-108, 123-129, 149-155, 181-187, 190-196,  
238-244, 308-314, 399-405, 413-419, 448-454, 477-483, 482-488,  
487-493**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 233-244, 531-542

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**FIGURE 41**

CTTT CCTG TTTATCCG CAGCC TTTCTT CTTGAGTTAGTAAAGATTATTCTGTAA CCTG  
ACACTCATCTGCCCTTG CAGTTGCCAGCCATATTCCCATGTGATTCCC ACTGGATCCAG  
GCCCCATCCGGCTGGCAGGAGGGGCTCTGACGTACAGGTTGAAATCAGAAGTCTGTGAGA  
GCGCGGGAGTGCATGGCAGCTCTGGGTCCAGACCTGGCCGACCCCTCTGCTTCACCTCAG  
CTCTGCTGCTCCTCTACTCTTGGGTGAGATCCCTTGGAGCCACAGCGAGGAACCCTGTGGT  
CCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGCCCTTTCTGTCAAAGCCTGCCCTC  
GGGCTCTGCTCACCTCTGGT GACCCTCCAAGATGCCCTGCCCTCAGTTCCCTCATGATCT  
GCCCTCTGCCCTCTAGCCACAGCCTCTAGTACACTTAGCAATAACCACCAACTAGTT  
AGAGTTCCCCACTCACCAAGCAAGACATGCAGTTCATGCCCTGTGCCTCGCTCATGCTGT  
TTCTTCCGACTGGAATGCCCTCCCTGCTCCTCCTGCCTTGCTGCCTGGCAAGTTCATCTCT  
CACGATCCCCCTCAAAGGCCCCCTCCTCCAGGAAGGCAACCCCTGTGCCCTCCCTCAGGCT  
ACCTCTGCACTTGTCAATGCTCTCTGTGGCACTTATCACACTGTATTTACTTGTAA  
TGTTTGCTCCCTCTAGACTGTTGAATCCTTAAGGGCATGGACTGTATCTTATGCATCTG  
TATTTCTGCGCCTAGCACGGTGCCTAGCACACAGTAGGCGCTCAATAATGTTGAATGAATGA  
ATGATTT

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**FIGURE 42**

MQFHASVPSLMLFLPTGMPSPAPPALS A QVHLSRSPQR PPPPGRQPLCSPPGYLCTL SMLL  
LWHL SHCILLVYMFVSPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Microbodies C-terminal targeting signal.**

amino acids 81-83

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**FIGURE 43**

GTTCACAAAGGATGATATGAAGACTTCCCTGAAGAAAGTTGTGAAGGGACCTCCTACGAGA**TG**  
**GATGCAGTGTGTCCC**CATGTTGCCACCCCTGCATGTCATCTCAATGCGCTGCA  
TGGTCCAGTTGTGGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGAAAGATT  
TCAAAGAGGAAGGGCTGCTGGGATTCTCGTTGGATTAAATCCCTCACCTCTGGCGATGTGG  
TTTCCTGTGGGCCTGTAACCTGCTGGCCCACTTCATCAATGCCTACCTGGTGGATGACAGCT  
TCAGCCAGGCCCTGCCATCCGGAGCTATAACCAAGTTGTGATGGGATTGCACTGAGCATGC  
TGACCTACCCCTCCTGCTAGTTGGCGACCTCATGGCTGTGAACAACACTGCGGGCTGCAAGCTG  
GGCTCCCCCTTACTCCCCAGTGTCAAATCCTGGATTCACTGCTGGAAGTACCTGAGTGTGC  
AGGGCCAGCTTCCGAGGCTCCAGCCTGCTTTCCGCCGGTGTCACTCAGGATCATGCTTG  
CCCTGGAG**TAAC**CTGAATCATCTAAAAAACACGGTCTCACCTGCCACTGTGGGTGAGGCCT  
GACCACCTTGGGACACCTGCAAGACGACTCCAACCCAAACAACCAGATGTGCTCCAGCCCA  
GCCGGGCTTCAGTTCCATATTGCCATGTGTCTGTCCAGATGTGGGTTGAGCGGGGGTGGGG  
CTGCACCCAGTGGATTGGGTACCCGGCAGACCTAGGGAAGGTGAGGCAGGGTGGGAGTTGG  
CAGAATCCCCATACCTCGCAGATTGCTGAGTCTGTCTGTGCAAGAGGCCAGAGAATGGCTT  
ATGGGGCCCAGGTTGGATGGGAAAGGCTAATGGGTCAGACCCACCCGTCTACCCCTCC  
AGTCAGCCCAGGCCCATCTGCAGCTCAGCTGGGAGCATTCTCCTGCTTGTACATAGG  
GTGTGGTCCCTGGCACGTGGCCACCATCATGTCAGGCCTATGCTAGGAGGCAAATGGCAG  
GCTCTGCCGTGTTTCTAACACTACTTTCTGATATGAGGGCAGCACCTGCCCTGAATG  
GGAAATCATGCAACTACTCAGAATGTGCCTCCTCATCTAATGCTCATCTGTTAATGGTGA  
GCCTCGCGTACAGGATCTGGTTACCTGTGCACTGTGAATACCCAGAGGTTGGCAGATCAGT  
GTCTCTAGTCCTACCCAGTTAAAGTTCACTGGTAAGATTGACCTCATCTCCGCAAATAAA  
TGTATTGGTGAATTGGAAAAAAAAAAAAAAA

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**FIGURE 44**

MMMQCVSRMLAHPLHVISMRCMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGDV  
VFLWGCNLLAHEFINAYLVDDSFSQLAIRSYTKFVMGIAVSMLTPFLLVGDLMAVNNCGLQA  
GLPPYSPVFKSWIHCWKYLSVQGQLFRGSSLFRRVSSGSCFALE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 51-72, 97-114

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 160-163

**N-myristoylation sites.**

amino acids 34-39, 100-105, 123-128, 165-170

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**FIGURE 45**

GCTCACTCTTGGTCCACACTGCCTTATGAGCTGTAACACTCACTGGGAATGTCTGCAGCT  
TCACTCCTGAAGCCAGCGAGACCACGAACCCACCAGGAGGAACAAACAACACTCCAGACGCGCAG  
CCTTAAGAGCTGTAACACTCACCGCGAAGGTCTGCAGCTTCACTCCTGAGCCAGCCAGACCAC  
GAACCCACCAGAAGGAAGAAAACCTCAAACACATCCGAACATCAGAAGGAGCAAACCTCGTGACA  
CGCCACCTTAAGAACCGTGACACTCAACGCTAGGGTCCCGGGCTCATTCTGAAGTCAGTG  
AGACCAAGAACCCACCAATTCCGGACACGGCAAAGTAACATCCTAGACATGGCTTTAGAGATC  
CACATGTCAGACCCCATTGCGCTCATCGAGAACCTTAATGAGCAGCTGAAGGTTAATCAGGAA  
GCTTGGAGATCCTGCTGCCATTACGCAACCTGTAGTTGTGGTAGCAGATTGTGGCCTCTAT  
CGCACTGGCAAATCCTACCTGATGAAACAAGCTGGCTGGGAAGAACAAAGGGCTCTGTGCA  
TCTACGGTGCAGTCTCACACCAAGGGAAATTGGATATGGTGTGCTCATCCAACGGCCA  
AATCACACATTAGTTGCTGACACCGAGGGCTGGAGATGTAGAGAACGGTGAACAACAAG  
AATGATACTTGCAGATCTTGCACTGGCACTCTTACTGAGCAGCACCTTGTGTACAATACTGTG  
AACAAAATTGATCAGGGTGCTATCGACCTACTGCACAATGTGACAGAACTGACAGATCTGTC  
AAGGCAAGAAACTCACCTGACCTTGACAGGGTGAAGATCTGCTGACTCTGGAGCTTCTTC  
CCAGACTTAGTGTGGACTCTGAGAGATTCTGCTTAGGCCTGGAAATAGATGGCAACTGTC  
ACACCAAGATGAATACTGGAGAATTCCCTAACGCCAACAGCAAGGTAGTGATCAAAGAGTCAA  
AATTTCAATTGCCCCGTCTGTGTATACAGAACGTTCTTCCAAAAAGAACATGCTTATCTT  
GACTTACCTGCTCACAAAAAGCTTGCCTAACATTGAAACACTGCCTGATGAGCTAGAG  
CCTGAATTGTGCAACAAGTGACAGAACATTCTGTTCTACATCTTAGCCATTCTATGACCAAG  
ACTCTCCAGGTGGCATGGTCAATGGATCTCGTCTAAAGAACCTGGTGCTGACCTATGTC  
AATGCCATCAGCAGTGGGATCTGCCCTGCATAGAGAACATGAGCTCTGGCCTGGCTCAGAGA  
GAGAACTCAGCTGAGTGCAAAAGGCCATTGCCACTATGACCAGCAAATGGCCAGAAAGTG  
CAGCTGCCATGGAAACCCCTCAGGAGCTGGACCTGCACAGGACCAGTGAGAGGGAGGCC  
ATTGAAGTCTTCATGAAAAACTCTTCAAGGATGTAGACCAAAGTTCCAGAAAGAACATTGGAG  
ACTCTACTAGATGCAAAACAGAACATGACATTGAAACGGAACCTGGAAAGCATCCTCGGATTAT  
TGCTCGGCTTACTAAGGATATTTGGTCTCTAGAAGAACAGTGAGCAGGAAATTAT  
TCTAACCCAGGAGGCCATAATCTCTCATTCAAGAACAGAACACTGAAGGCAAAGTACTAT  
CGGGAGCCTCGGAAAGGAATACAGGCTGAAGAACGTTCTGCAGAAATATTTAAAGTCCAAGGAG  
TCTGTGAGTCATGCAATATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAGAACAGAAA  
GAGGCACAAGTGAAAGCAGAACGCTGAAGCGAAAGGTGGCGGCGATTCAAAGG  
CAGAACCGAGCAAATGATGCAAGGAGAGGGAGAGACTCCATCAGGAACAAAGTGAGAACAAATGGAG  
ATAGCCAAACAAAATTGGCTGGCAGAGCAACAGAAAATGAGGAACAAACAGATGCAGGAACAG  
GCTGCACAGCTCAGCACAACTTCAAGCTCAAATAGAACGCTTCTCAGTGAGCTCCAGCAC  
GCCAGAGGGCTTTAATAACGATGATCCATGTGTTTACTCTTAAAGTGTAAATATGGAGT  
TTCCTTTTTACTCTTGTCACTGATGACACAAACAGAAAAGAACACTGTAGACCTTGGGACAA  
TCAACATTAAATAAACTTATAATTATTAAA

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**FIGURE 46**

MALEIHMSDPMCLIEFNNEQLKVNVQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAKKNK  
GFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLSSTF  
VYNTVNKIDQGAIDLLHNVTTELTDLLKARNSPDLDRVEDPADSASFVPLVWTLRDFCLGLEI  
DGQLVTPDEYLENSLRPKQGSQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQQKLAQLETLP  
DDELEPEFVQQVTEFCSYIFSHSMTKTLPGGIMVNGSRKLNVLTYVNAISSGDLPCIENAVL  
ALAQRRENSAAVQKAIAHDDQMGQKVQLPMETLQELLDLHRTSEREAEVFMKNSFKDVQSF  
QKELETLLDAKQNDICKRNLEASSDYCSALLKDIFGPLEEAVKQGIYSKPGHHNLFIQKTEEL  
KAKYYREPRKGIQAEEVLQKYLKSKEVSHAILQTDQALTEKKKEAQVKAEEAKAEAQRL  
AAIQRQNEQMMQERERLHQEQVRQMEIAKQNWLAEQQKMQEQQMQEQAQLSTTFQAQNRSL  
SELQHAQRRAVNNDDPCVLL

**Important features of the protein:****Transmembrane domains:**

amino acids 31-49, 114-131

**N-glycosylation sites.**

amino acids 90-94, 144-148, 287-291, 563-567

**N-myristoylation sites.**

amino acids 45-51, 283-289

**Prenyl group binding site.**

amino acids 583-588

**ATP/GTP-binding site motif A (P-loop).**

amino acids 45-53

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**FIGURE 47**

CACTCATTCAAAGGGTCTCTCAAGGCATGGTAATGTGCAAGGAGGTGATACCTAAAT  
GAATGACAAAAGAACATGCTCTGCTTTGTGTCTCCTACATTTAGACATTGTTGTT  
TCTCTGGTAGCCTTAAATTCTTGAAGGCCAGGACCAGTCTCACTTACCTTGTTCC  
ACTAACTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAAGCCTGTGAAATAAGTGT  
CTATTCTAGCATATTATTCTGAGATTAAATGATAGATTAGTGAATGAGATTCCATT  
TTCAAATACAGCAAAGCATAACTATTCATTCAATTCAACTTCATTCTCAAA  
ATTAGGTCTGAGTTAACAATAATTACCTTGAAATGTGTGGTTATTGAGGCAATCAGGT  
GGTACATTGAGCTCTCAGCCAGAGTTGTTCTGGAATTGATTCCATTGCATTGATT  
TTTGTCTCAGAACGCCAGGTTCCATGAAAAATCATTCCCACCTGAATTGGCTGTGATT  
TTGCTCGTTAAAGTAAAGGAAGCCTTGGTTCTAGTCTGCAAACACTACACTGAACGG  
GACAAGTTTGTAGAGTAATGGCTGGAAAAGAGGAACCTTCATTATTACAGAACTCA  
AAAACAAAGGCCCTCCAGCCACCTGGAGATTTGTTGCAGACACCAGCCTGGCTCTGTCTT  
TATGCCTAACAAATTGAGCATCCAGTCTTCTTGCTGGGACATTGCTCAGCTCTGCAAGGG  
GAAAAGAGGGAGAAAGCCAGAGCTGCCAGGCTCTTGCACTGGGCCGGGGAGGGTTCC  
GAAGCAGGTGCTCTGGCTCTTGGTACGTGAGGCTCGGAGCTGCCTCTCCTCTGACCC  
CAGGCTCACCAGTTGCTCCAGGAGTATTGAAAACATACCCAGTGCTCTCAAGCAC  
CCACTGCTTAGAGGGCCAGATTCTTCCCTTGCAGAGCTGGAGACTGCATCG  
GGCATCTGGTGTAAACTAACAGGAAACTGACTAAAGGTCCACAGTGCTCATTGTGAGA  
CTAGCTGCCCTCCGATGGGTCTGATTATCAGTGGTCCAGTGCAAGGGCTGTCACAAAC  
AGGCCTCACTCCTGGGGCTTCCATGGAGGTGGCTTTACTCTACATGGAAA  
TGAECTCTGCAAGCCACAGAACACAGTCATTCTGAATTATCCCAGTCTCATGCGCCTG  
GATTCCCTCAGATGCCTTATATCTTGTGCAAAGTTGTCTAAATTGGTCCAGCTCCA  
AGCCTTGCCTTGGCCTTGGAAAGTATTGTTGATGAGTCGTCTGTCATTATTCTCA  
AAATGATTGCTTTGTTCTTCATTCCATTCCACCCACATATACACACATGCTTCTT  
AACTTAGGGATTACATGCCAATAAACTATTGTTGAAAATGCACTAAACTATCGCAAAGAC  
GAAAATTACAGGCTGAACCGTTGTAAGTCCATATGCTCCTCAACTTACATGTGT  
TATGCCCAAATAAGTCCATCGTCAAGTTGAAAATCAAGCCATCTTAGGTTGAGGAC  
CATTTGTTGTACCTCAAAGATGTCAATTAAACATACTCCCTAGCTTTCTTTACT  
TTTATTTGAAGTAATTATAGAATCACAGAAAGTTGCAAAAAAA

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**FIGURE 48**

MGALIISGSSAGPVTQASLPPWGLSHGRCGFLLYMEMTLCSHRTQSFSELSQSLMRPGFLQM  
PYISCAKLSKIWFPAASKPCLLAFLEVFLLMSRLSLFSKMICFLFLSFLFPPHIYTHAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 88-107

**Casein kinase II phosphorylation site.**

amino acids 47-50

**N-myristoylation site.**

amino acids 24-29

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**FIGURE 49**

GGCTTCTACAGTCCACAACACCACCGCCCCAGGCCAGCAGAATGAGCCAGTGAGTGCCCCGGCTCCAGTT  
TGGCTTTGCTATGACAACGTGCCACTGCAGCGGTCTCTTGGGAAGGCTGTGTGGGCCAGCCCAGCCATGC  
CTACCCCGTGCCTGCCTGCCCAGTGCCTCATGGCTTGTGCAGACTGGCTGCCGTGGTACTTCGTTGC  
CTCTGGGCCAATGTAACCGCTTCTGGTATGGCCTTGTGCAGACTGGCTGCCGTGGTACTTCGTTGC  
GTGCATGAGCAGCTGCCAGGGATCTCTCCTAGGGCCCCCTGTCCTCCCAGCCTGGGCTTCTGGAAAGGGACCAACCA  
CACGGATGGTGGCGCAGCAGTCTGCAGGGAGCAGGAACCCAGCAGCACAGGACAGGGGCCGGTGCAGAG  
AAAGCCCTGGCCTTCTGGTGGTCTCTGGCGCAAGACCAACAGCCTGGGCCAGGGGCCACACCCAGGC  
CTTTGGAGAATGGCATGGGGCAGGAGCTGGTCCAGGGCCCTGGACTGGTGGAGATGCCGGATCACCGC  
GCCACCCCTCCACAGCTCTCTACAGATCTCACTTCCACCTCTCAGGATTAGCTTGGCAGGTGTGGAGCCCT  
CGTTGGTGCAGGCCAGGGCTGGCAGTGGTGCAGCTCTCTGCTCAGACGACACTGCCCGGAATCCCAGGCTG  
CCTGGCAGAAAGATGGCATGGCCAGGCCATCTCTGCAGCAGGACAGCCTGGCAGCTGGCAGGATCCCTGATCATCCACC  
CCCTGCAGGCAGGGACGCGGGCACCTACAGCTGTGGCAGCACCCGGCCAGGCCGACTCCAGAAGATCCAAC  
TCCGCATTATAGGGGTGACATGGCGTGTCTGAGGCTGAGCTGGGGCTTCTACACCTGTGCGCTTCAATG  
CTCAGGACTTGGCCAAGCGGGCTGCTGGGCCATCCCCCTTCAACACCCACAGCCTGCAAACA  
GGCTGCGTTGGACAGAACAGCCCCGGGGTGGATGCCAGTCCAGGCCAGGGGATCCGGATGACCTGCGTG  
CCGAAGGCTTCCGCCAGGCCATCGAGTGGCAGAGAGATGGCAGGCTGTCTCTCTCCAGACACCAGCTGC  
AGCCTGATGGCTCCCTGGTATTAGGCCAGTGGCTGAGAAGATGGGGCTTCTACACCTGTGCGCTTCAATG  
GGCAGGGACGAGCACCGATGGTCCAGCTCAGAGTCTGGGGGAGCTGACAATCTCAGGACTGCCCTACTG  
TGACAGTGCAGGGGTGATACGGCTATTGTTGAGGCTATTGTTGAGGAAATGTAACATCAGGTGGTCCA  
GGAACGGGCTACCTGTGCAAGGCTATTGTTGAGGCTATTGTTGAGGAAATGTAACATCAGGTGGTCCA  
TGCGGGCCAGGGATAGGGCTCTACATGTGCACTGCAGTGCCTACAGGGGAGCCAGCAGTCAGCCGAGCACCGAGG  
TGAAGGTGGTCTACCAGCACCCACCGCCAGCCCAGGGACCCCTGGCAGGGACTGCGTCGACCAAGCCAGACTGG  
CCAACGTGATTGATCTGCAAGGCCAGTTGTGGCAATGAGTATTACTCACGCTCTGCTGTGCCAGCTGTT  
CACGTTCCACGCTCACGCCATCTGCCAGTAGGGATGAAAGGCTAGTCCAGCCCAGTCCAAAATAGTT  
CATAGGGCTAGGGAGAAGGAAGATGGACTCTGGCTTCTCTGGCTGGAAAGGGAGTTATCTCTGGAA  
CATATTAGCTTCAAAACCCACCCAGTGGTCTGGCTACACGGCAGCCAGTCCACAGGCTTCTCTGTAGCCT  
TCAGCAGTGGTCTGATCTGACATAACACAGGCTGCTGTTCAAGAAGGCAATCTGTTGGATAAGAAAAAA  
CCTTACTTTACAGCTCCCTTATAATTGTTACACAGGAATAGTTAAATGCAATTGTTGTTGTTTTGAG  
ACGGAGTTCACTCTGTTGCCAGGCTGGAGGGCAATGGCGCATCTCAGCTACTGCAACCTCCGTCTCTGG  
GTTCTGATTCTCTGTGTCAGCCTCTGAGTAGCTGGGATTACAGATGCCATCACATGCCCTGGTAATT  
GTATTTTAGTTGAGATGGGGTTGCCATGTTGGCAGGCTGGTCTGAACTCTGACCTCAGATGATCTGCC  
GCCAGCTCCCAAGTGTGGGATTACAGCAGGCCACGCCAGCCATCAATGCAATT  
TTTTTGAGACAGAGTTCCGACTCTGCCAGGCTGGAGTACAATGGCGATCTGGCTCACTGCAACCTCC  
ACCTCTGGGTTCAAGCGCTTCTCAGCCTCAGCCTCTGAGTAGCTGGGATTACAGGATGTGCCACCATGCC  
GGCTAATTGTTGATTGGGAGACGGGTTCTCCATGTTGGCAGACTGGCTTGTGAACTCCGACCTCAG  
TAATCCGCCGCCCTCCGCTCCAAAATGCTGGGATTAGAGGTGTGAGCCACTGTGCCAGCCATCAATGTT  
TTAAAGCTAGCTGTCAGGGTCACTTAATTAAAGCTGGCAGGGAGATGTGTAATGATTCAAAGTTAACACC  
TGTTGTTCTAAAGGGCATGCAAGTCTGCTGTATCAGGGAGTATTCTGTGCTAAAATCAGCGATGGTCA  
TTGCTCTAGTCTCTCCTCTAGGCAGTGCATCAGTCAGCTCTAAATCTGGTGCAGAGGGTTAACAGCATA  
ACCCCTGGGAAAATGGAATAGTTAAAGACCTAAATAGGGATTGGGATGAAACAGCTGCACTGACT  
GTTATCTGAGCATGAAAGAAACTGAAACGCTCCTTACGTCAGGATGTGGACCTTGAAGCCCTCTGAGGCCAC  
ATGCAAATCTGGCTGTGACGGTCACTGACACCTGTGTAAGAGCTGACAGGCCAGCCTGCTCTGACAGTCA  
GAGGCCCTCTCTCTTAAAGTAGGAATCTGTAAGCAAATGTTGCTGCCAAAGACAAATCAGACTGTCAGTCA  
TTAAAAACAGCATTAGCAGGATGAGGATAGCAATGGGAAGGGTTGGGCAATGCACTGAAACAGGGAAATGGCTT  
CAGAAATGGTTGAGGTGGAAAGACAACATTCTCATCTCAGGACTCTAATTCTGATGCTAAAAGAAGAGG  
CATGGATTCTATGAGCTTCAAGTCCCTTCACTTAAACCTTCTACAAATCTTACAGAGGACTGCCAGTAGAG  
AAGGTTATTCTGGACACAGGAAGACGGGCAATTACAGGGACCAAAAGCTGAAAGGTGACTTTATTACCAACA  
CACTGGCTGGAAAAGGGACAAACACATCACGGGTGAGTGATACTTCTCAGTCTCTACTCATTCAACAAAGG  
AAATGTGGCTGGGAGGGTCTTTTCTTAATACTGGAAAATATTGAAAGACATCCATGTTCACTTATG  
GCTGGTTTGTATAGAAATTGGAAAATAAGGCCACTTTTG

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**FIGURE 50**

MGPVVPSLGLLEGAPTRMVAAVLQASRN PASTGQGPRCRESPGLLVVSGGKTNSLGQGRPPT  
PRPLENGHGRSLGPGLDWVEMPDHQRHPSTAPPTDLTSHLSRISLAGVEPSLVQAALGQLV  
RLSCSDDTAPESQAAWQKDQPISSDRHRLQFDGSLIIHPLQAEDAGTYSCGSTRPGRDSQKI  
QLRIIGGDMAVLSEAELS RFPQPRDPAQDFGQAGAAGPLGAIPSSH PQPANRLRLDQNQPRVV  
DASPGQRIRMTCRAEGF PPPAIEWQRDGQPVSSPRHQLQPDGSLVISRVAVEDGGFYTCVAFN  
GQDRDQRWVQLRVLGE LTISGLPPTVPEGDTARLLCVVAGESVNIRWSRNGLPVQADGH RV  
HQSPDGTLIYNLRARDEGSYMC SAYQGSQAVSRSTEVKVVSPAPTAQPRDPGRDCVDQPELA  
NCDLILQAQLCGNEYYSFCCASC SRFQPHAQPIWQ

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Tyrosine kinase phosphorylation site.**

amino acids 392-400

**N-myristoylation sites.**amino acids 9-15, 50-56, 112-118, 146-152, 173-179, 195-201,  
220-226, 229-235, 280-286, 306-312, 336-342, 397-403**Myelin P0 protein.**

amino acids 153-182

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**FIGURE 51**

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCGTATCTGC  
TCTCCTGAAATAATTCTGGAGTCATGCCTGAAATGCCAGAGGACATGGAGCAGGAGGAAGTTA  
ACATCCCTAATAGGAGGGTCTGGTTACTGGTGCCTGGGCTTCTGGCAGAGCTGTACACA  
AAGAATTCAGCAGAATAATTGGCATGCAGTTGGCTGTGGTTAGAAGAGCAAGACAAAAT  
TTGAACAGGTTAATCTGTTGGATTCTAATGCAGTTCATCACATCATTGATTTCAGCCCC  
ATGTTATAGTACATTGTGCAGCAGAGAAGACCAGATGTTGAGAAAATCAGCCAGATGCTG  
CCTCTCAACTTAATGTGGATGCTCTGGGAAATTAGCAAAGGAAGCAGCTGCTGTTGGAGCAT  
TTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTACAGAGAGGAAG  
ACATACCAGCTCCCCTAAATTGTATGGCAAAACAAAATTAGATGGAGAAAAGGCTGCTGG  
AGAACAACTAGGAGCTGCTGTTTGAGGATT CCTATTCTGTATGGGAAGTTGAAAAGCTCG  
AAGAAAGTGTGACTGTTATGTTGATAAAGTGCAGTCAGCAACAAGTCAGCAAACATGG  
ATCACTGGCAGCAGAGGTTCCCCACACATGTCAAAGATGTGGCCACTGTGTGCCGGCAGCTAG  
CAGAGAAGAGAATGCTGGATCCATCAATTAGGGAACCTTCACTGGTCTGGCAATGAACAGA  
TGACTAAGTATGAAATGGCATGTGCAATTGAGATGCCTCAACCTCCCCAGCAGTCACTTAA  
GACCTATTACTGACAGCCCTGTCTAGGAGCACAACGTCCGAGAAATGCTCAGCTTGACTGCT  
CCAAATTGGAGACCTTGGGCATTGGCCAACGAACACCATTGCAATTGGAATCAAAGAATCAC  
TTTGGCCTTCCTCATTGACAAGAGATGGAGACAAACGGTCTTCATTTAGTTATTTGTGTTG  
GGTTCTTTTTTTAAATGAAAAGTATAGTATGTGGACTTTCAAGTAAAGAACAAAGGAAATA  
GTTTGTATGAGTACTTAATTGTGACTCTTAGGATCTTCAGGTAAATGATGCTCTGCACT  
AGTGAATTGTCTAAAGAAACTAAAGGGCAGTCATGCCCTGTTGCAGTAATTTCCTTTA  
TCATTGTTGTCCTGGCTAAACTTGGAGTTGAGTATAGTAAATTATGATCCTAAATATT  
TGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTCAGATGAAATTGTCATTCTCGTAAC  
CTCCATATTTCAGGATTTGAAGCTGTTGACCTTTCATGTTGATTATTAAATTGTGTTG  
AAATAGTATAAAATCATTGGTGTTCATTATTGCTTGCCTGAGCTCAGATCAAATGTTG  
AAGAAAGGAACCTTATTGGCAAGTTACGTACAGTTTATGCTTGGAGATATTCAACATGT  
TATGTATATTGGAACCTCTACAGCTTGTAGCCTCCTGCTTTATAGCAGTTATGGGAGCAC  
TTGAAAGAGCGTGTACATGTATTTCTAGGCAAACATTGAATGCAAACGTGTATTT  
TTAATATAAAATATAACTGCTTTCATCCCATGTTGCCGCTAAGTGTATTTCAATGTTG  
GTGGTTATACTCATAATAATGGGCCTTGTAAAGTCTTGCACCATTCATGAATAATAATA  
TGTACTGCTGGCATGTAATGCTTAGTTCTTGTATTTACTTCTTTAAATGTAAGGACC  
AAACTCTAAACTAATTGTTCTTGTGCTTTAATTAAATTACATTCTCTGATGTA  
ACATGTGATACATACAAAAGAATATAGTTAATATGTATTGAAATAAACACAATAAAATT

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**FIGURE 52**

MPEMPEDMEQEEVNIPNRRVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKEQVNLLD  
SNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAAQLNVDAAGNLAKAAAAGAFLIYISSD  
YVFDGTNPYYREEDIPAPLNLYGKTLDGEKAVLENNLGAAVLRIPILYGEVEKLEESAVTVM  
FDKVQFSNKSANMDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKYEMAC  
AIADAFNLPSHRLPITDSPVLGAQRPRNAQLDCSKLETLGIGQ RTPFRIGIKESLWPFLIDK  
RWRQTVFH

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 105-127

**N-glycosylation site.**

amino acids 197-201

**N-myristoylation site.**

amino acids 303-309

**Short-chain dehydrogenases/reductases family proteins.**

amino acids 18-30

## **FIGURE 53**

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**FIGURE 54**

MLLISLLAAGLMHSDAGTSCPVLCTCRNQVVDSSQRLFSVPPDLPMDTRNLSLAHNRITAV  
PPGYLTGYMELQVLDLHNNSLMELPRGLFLHAKRLAHLDLSYNNFSHVPADMFQEAGGLVHID  
LSHNPWLRRVHPQAFQGLMQLRDLDLSYGGLAFLSLEALEGLPGLVTLQIGGNPWVCGCTMEP  
LLKWLRLRNRIQRCTADSQLAECRGPPEVEGAPLFSLTEESFKACHLTLDYLFIAFVGTVVS  
IASVATNFLLGITANCCHRWSKASEEEEI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation sites.**

amino acids 52-55, 81-84, 107-110

**Tyrosine kinase phosphorylation site.**

amino acids 148-154

**N-myristoylation sites.**

amino acids 11-15, 263-268

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 175-185

**Leucine zipper pattern.**

amino acids 77-98

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**FIGURE 55**

GGCTGCGCCCAGGCCGGCGGGCCAGCAGCTGCGAACCGCCGGCGCACCAACCTGTTCCGC  
CCGGGGACTTCCCCGGCGGGCTCAGAAGTGTGGGTGCGTCCTGGCTTCCCTGGCGTCA  
GCGACCCAGGTAACTCCTCCACTGCTGCGTGCGTGCAGGCCCTGCGTGTGAGAGCCACG  
TGTGCCGCGCTTGGCACAGCCTGGAAAGTCAGGACCCGACGCCAGCAGAGCAGAAACCT  
TACAGAAACATGAAGCCCTAACCATCTGCTACTCAGTTATTGGGGCTGACGGCGGCTTCTA  
GAACATCCAGGTCTGAGATGCGAGAACTCATCCTGTAGTCACAGATGGAGTCCAAAC  
AGCCAAGCAGATGTAAGGCCGTGCTGTGGCTGAGGCCCTGAATAACAGAAGGGTCACTTTC  
TTAGTGGCAAAGAGCAGTTGACATTGATGCTAATTATTGAACACGACCAGTCATTAA  
CTGAGCTGAGTGGAAACACTGACCATAGAAGATCAAGCCAAATGAGGGATTGCAAATTTC  
CTGATTCTTTGAATTAGGATTCCAGATGGGGCCTATTCTACAGCCCCAACATTCTAT  
AGCCGTTATCACTGCCATCACCACTGCCACCAGCATTTGAGATTCCACCCCTGCTCCC  
CAGAGACTCCTGCTTGAAGTGAGCAGAAAGGAAGCTCAGAAAAAAATCTCTAGTGGTGGC  
TGCGTCGCTCCAGACAATCGGAATCTGCCTTCACCACCATGGGCTGGCTTTCTAAAGGT  
TTTGTGGCGGGAGTGAGTTCTCAGGATTCTTATCCTCTTGAGATTGGCATCAGTGG  
GAAAACAAGAGGACAGAAGCCAAACTTGTGATTATTGGCCATGACATGGGTGGGTGA  
CCTGGGAGCAAACCTGGCAGAAACAAAGGACACTGCCAACCTTGATAAGATGGCTTCGGAGGG  
AATGAGGTTGTGGATTCCATGCAGCTGCCTCACCTGTCACCCCTCCGGGCTTCTTGCT  
CACCGGCCGGCTTGGCTTCGCAATGGAGTCACACGCAACTTGCAGTCACCTCTGTGGGAGG  
CCTCCGCTAACGAGACCACTTGGCAGAGGTGCTGCAGCAGGGTTACGTCACTGGGAT  
AATAGGCAAATGGCATTTGGACACCACGGCTTATCACCCCAACTTCCGTGGTTGATTA  
CTACTTGGAAATCCCATAAGCCATGATATGGGCTGTACTGATACTCCAGGCTACAACCACCC  
TCCTGTCCAGCGTGTCCACAGGGTGATGGACCATCAAGGAACCTCAAAGAGACTGTTACAC  
TGACGTGGCCCTCCCTTTATGAAAACCTAACATTGTGGAGCAGCCGGTGAACGGCAG  
CCTTGGCCAGAAGTATGCTGAGAAAGCAACCCAGTTCATCCAGCGTGCAAGCACCAGCGGGAG  
GCCCTTCTGCTCTATGTGGCTCTGGCCACATGCACGTGCCCTAACCTGTGACTCAGCTACC  
AGCAGCGCCACGGGGCAGAAGCCTGTATGGTGCAGGGCTCTGGAGATGGACAGTCTGGTGG  
CCAGATCAAGGACAAAGTTGACCAACAGTGAAGGAAAACACATTCCCTGGTTACAGGAGA  
CAATGGCCGTGGCTCAGAAGTGTGAGCTAGGGCAGTGTGGGTCCTTCACTGGATTG  
GCAAACCTGTCAAGGGGAAGTCCAGGCAAGCAGACGACCTGGGAAGGGAGGGCACCGGGTCCC  
AGCACTGGCTTACTGGCTGGCAGAGTTCCAGTTATGTCACCAGCAGTCCTGTTAAGCGT  
GCTGGACATTTTCAACTCTGGTAGGCTGGCCAGGCAAGCTAACCTCAAGGACAGGGCCTT  
TGATGGTGTGGACGTCTGGAGGTGCTTGGCCGGTCACAGCCTGGCAGGGTGTGTT  
CCACCCCAACAGCGGGCAGCTGGAGAGTTGGAGCCCTGAGACTGTCGGCTGGAGCGTTA  
CAAGGCCTCTACATTACGGTGGAGCCAGGGCGTGTGATGGAGCATGGCCTGAGCTGCA  
GCATAAGTTCTGATTTCACCTGGAAGACGATACCGCAGAAGCTGTGCCCTAGAAAG  
AGGTGGTGGAGTACCGAGCTGTGCTGCCAGGTCAAGAAAGGTTCTTGCAGACGTCTCCA  
AGACATTGCCAACGACAACATCTCCAGCGCAGATTACACTCAGGACCCCTCAGTAACCTCTG  
CTGTAATCCCTACCAAATTGCCTGCCGTGCAAGCCGAT**TAA**CAGACCCAATTTTATTCCAC  
GAGGAGGAGTACCTGGAATTAGGCAAGTTGCTTCAAATTTCATTTCACCCCTTTACAA  
ACACACGCTTACTGTTAGTCTGGAGTTAGTTGGAGTTAGCCTGCAATCCCTCTGTA  
TCCTGTCCCCCTCCACGCCGACCGAGAGCAGCTGAGCTGCGCTGGCTGGGAGGTG  
TGCCTTAATGGGAAGCACACGGGTTGGAGTCAGGCACAGGTGCCAGCTCCAGCTTTGAAC  
TTGGGCAATTGTTAACCTAACCTGCAAGTTGAGTTGAGGGTAAATAAAGGCATACATGAA  
AATGCCTGGCAACTTAAAAAAAAAA

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**FIGURE 56**

MGWLFLKVLLAGVSFSGFLYPLVDFCISGKTRQKPNFVI ILADDMGWGD LGANWAETKDTAN  
LDKMASEGMRFVDFHAAASTCSPSRASLLTGRGLRNGVTRNFAVTSVGGPLNETTLAEVLQ  
QAGYVTGIIIGKWHLGHGHSYHPNFRGF DYYFGI PYSHDMGCTDTPGYNHPPCPACPQGDGPSR  
NLQRDCYTDVALPLYENLNIVEQPVNLSLAQKYAEKATQFIQRASTSGRPFLLYVALAHMHV  
PLPVTLPAAPRGRSLYGAGLWEMDSLVGQIKDKVDHTVKENTFLWFTGDNGPWAQKCELAGS  
VGPFTGFWQTRQGGSPAKQTTWEGGHRVPALAYWPGRVPVNTSTALLSVLDIFPTVVALAQA  
SLPQGRRFDGVDVSEVLFGRSQPGHRLFHPNSGAAGEFGALQTVRLERYKAFYITGGARACD  
GSMVPELQHKFPLIFNLEDDTAEAVPLERGGAEYQAVLPEVRKVLADVLQDIANDNISSADYT  
QDP SVTPCCNPYQIACRCQAA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 353-373

**N-glycosylation sites.**

amino acids 117-120, 215-218, 356-359, 397-500

**N-myristoylation sites.**

amino acids 12-17, 33-38, 52-57, 97-102, 101-106, 113-118, 158-  
163, 328-333, 388-393, 418-423, 435-440, 436-441

**Amidation site.**

amino acids 382-385

**Sulfatases signature 2.**

amino acids 129-138

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**FIGURE 57**

TGGACAAGACACCTCCAGGAGCCCAGCTCACAGCCACCAGTACCTTCTTCAGGACAAGCTGG  
GGGCCTCCATGGGCCCTGAGGGCCAGGGCCAGGGCGTGGGCACAGACT**ATGGT**GAGACACC  
AGCCCCCTGCAGTACTACGAGCCACAGCTGTGCCCTCCTGCCTCACGGGCATCTACGGCTGCC  
GTTGGAAGCGCTACCAGCGCTCCCATGATGATACCACACCAGGGCACAGCGCCATTCCCTGCATG  
TGGGGGCTGTGGCAGCAGTCACCATGCTCTCCTGGATCGTGGCAGGACAGTCGCCGTGCAG  
AGCGGACCTCCTCCCAGGTGACCATTCTCTGTACCTCTCACCGTGGTGTTCGCCCTCTACC  
TGGCCCTCTCACCATCTCCTCTCCGCATCATGGAGAAGAAAGACCTCGGCCCAAGCCTG  
CTCTCATTGGCACCGCGGGGCCCCATGCTGGCTCCAGAGCACACGCTCATGTCCTCCGGA  
AGGCCCTCGAGCAGAACGCTGTACGGGCTCCAGGCTGACATTACCATCAGCCTGGACGGCGTGC  
CCTTCCTCATGCATGACACCACCCCTGCGCGCACCACCAACGTGGAGGAGGAGTCCCGGAGC  
TGGCCCGCAGGCCCTGCCTCATGCTTAACCTGGACACCCTGCAGAGACTCAACGCTGCCAGT  
GGTCCCTGAAGACTGACCCCTCTGGACAGCCAGCTCCCTGTACCCCTCCGACCACAGAGAGG  
CCAGAACCAAGCTCATCTGCGCAGAGCTCCTGGAGCTGGCCAAGGGCAATGCCACAC  
TGCTGCTCAACCTGCGTACCCGCCCCGGAGCACCCCTACCGCAGCAGTAACTCAACGTGA  
CTCTGGAGGCCGTGCTGCACTCCGGCTTCCCCCAGCACCAAGGTATGTGGCTGCCCTAGCAGGC  
AGAGGCCCTGGCGGAAGGTGGCTCCCGTCCAAACAGACATCAGGCTCCAAGGAGGCAG  
TCGCCAGCCTGCCAGAGGCCACATCCAGCGCTGAACCTGCGCTACACTCAGGTGTCCCGCC  
AGGAGCTCAGGGACTACCGCTCTGGAACCTGAGTGTGAACCTCTACACAGTCAACGCACCGT  
GGCTCTCTCCCTGCTGTGGTGTGCGGGGTCCCATCGTCACCTCTGACAACCTCCACACCC  
TGTCCCAGGTGCCCTCCCCCTCTGGATCATGCCCGGACGAGTACTGTCTCATGTGGGTCA  
CTGCCGACCTGGCTCCTCACCCATCGTGGCATCTCGTGTCCAGAAGTGGCGCTGG  
GTGGCATACGGAGCTACAACCCCTGAGCAGATCATGCTGAGTGTGCTGCCGTGCGCCGACCAGCC  
GGGACGTAGCATGAAGGAGAAGCTATTCTCAGAGATCAGGATGGTAGAGGTCT  
CCGATGTGCTCTCGTATGTCAGACAACAGTTATGACACATATGCCAACAGCACGCCACCC  
CTGTGGCCCCCGAGGGGGTGGCAGCCACACCAAGACCTCATAGAGCGGAGTGGCGT**TAGC**  
TGAAGACATGTCTGCTCCACCTGTACCTGACACAGAACGCTGGGAGGCTAGGGAGGCTGGTGG  
AAAGTGTCTGAACTCGGAGTGTCTGGGAGCGGGCTCACAGCCTCTGTGGCTCCAGCC  
CCTTGTCAAGCCGAGCCTCTTGAGGGGACTCCCTGTCTCTGAGGGCCAGCTGGGCCAGG  
ACTCCATCCTTCAGATGCCCTGCAAGGCCTGGGCTCCTCTGGGAAGTATGGGCCTAGGG  
CTTGGTCCCCCTTCTGAGGCCCTCCTGTATCCGACCTGGAAAGCTTGTGGCTCATGG  
GCCATGCCATACCCCTGTGGCAATGGAGTGTGGATGCTCACCTGTGCCATCTGTCTCCT  
GTCTGTGCCAGGAGGCACCTGAGTTCTGTGTTATCTGCCCAAGGGCTGGGCCAGGCC  
TCTACCTGAAGCAACTCTGCTCTCCGTAGTCTCAAAGCACAAGGAGGTTAGCCAGGAG  
GAAGCCAGCTGCAATGTGGAGACACGTCCCTCCCCAACCCACCTCATGCCACCGCCAACCC  
CCTGCCCAAGGAGCGGGCTGAGCCACGTCCCTAGGAGCAGCTGGAGATGGCCAAAAGAGTG  
AGCTCAGGACTACTGGATCCCATGCCAGGTGTCCAGCAGACCTCAAGGAGGACGGTCACCT  
AACCCAGGAGTCCACAGACTGATGTGACCTCAGGTTCCACATCAGTGGCCACAGGGCAGGGC  
CCACCTGGTAGAGTGTCTGGATATGGCAGGGTGTGTGGCTAAGTGGCCTGAACAG  
AGGGAACCTAGGCCCTGGCCAATGTGATTAAAGCTGCCATCTTGAAA

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**FIGURE 58**

MVRHQPLQYYEPQLCLSCLTGIYGCRWKRYQRSHDDTPGTAPFLHVGAVALVMLSIVAGQ  
FARAERTSSQVTILCTFFTVVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGAPMLAPEHTL  
MSFRKALEQKLYGLQADITISLDGVFPLMHDTLRRTTNVEEFPELARRPASMLNWTTLQRL  
NAGQWFLKTDPFWTASSLSPSDHREAQNQSICSLAELLEAKGNATLLNLRDPPREHPYRSS  
FINVTLEAVLHSGFPQHQVMWLPSRQRPLVRKVAPGFQQTSGSKEAVASLRRGHIQRLNLRYT  
QVSROELRDYASWNLSVNLYTVNAPWLFSSLWCAGVPSVTDNSHTLSQVPSPLWIMPPDEYC  
LMWVTADLVSFTLIVGIFVLQKWRLLGGIRSYNPEQIMLSAAVRRTSRDVSIMKEKLIFSEISD  
GVEVSDVLSVCSNDSYDTYANSTATPVGPRGGGSHTKTLIERSGR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 47-61, 77-93, 335-350, 380-399

**N-glycosylation sites.**

amino acids 182-186, 217-221, 233-237, 255-259, 329-333, 462-466

**Tyrosine kinase phosphorylation site.**

amino acids 130-139

**N-myristoylation sites.**

amino acids 21-27, 48-54, 294-300, 404-410, 442-448, 473-479

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**FIGURE 59**

CCTGAGCAAACACAGCAGCCCGAGTGTCCCAGGCCAAATGCTGAGAACGTCCACTCCTAA  
TCTGTGTGGTGGTCTGCATTGCCGGGCCCCCTGGCTCTCTCTGGCATTCTCTGCCTCTGCCT  
CATATTCTTGTAGGGCAGGTGGGCTTGCCTGCAGGGACACCCCCAGTGCCTGGATTACGGGCC  
CCCTTCCAGCCCCCTGCACCTTGAGTTTGCTCTGACTATGAGTCCTTCGGCTGCTGTGA  
TCAGCACAGGACCAGCCGATCGTCCCCGGTACTGGGACATCATGGAATATTTGATCTGAA  
GAGACATGAGCTGTGGAGATTACATTAAAGACATCCTTGCCAGGAGTGCTCGCCCTACGC  
AGCCCACCTCTACGACGCCAAAACACCCAGACGCCCTCCGGAATCTCCCAGGCCCTGCTC  
TGATTACTGCTCTGCCTTCATTCTAAGTCACTCAGCCATTCCCTGCTGACCAATGACCG  
CGGCCCTCAGGAGTCTCATGGAAGGGACGGTACCCGCTTCTGCCACCTCCTGGACCTTCTGA  
CAAGGACTATTGCTTCCCTAATGCTCTGAGGAACGACTATCTCAACGCCACCTGGGATGGT  
GGCCCAAGATCCTCAGGGCTGCCTGCAGCTGCCTGAGCGAGGTGGCAACGGGCTGAGGAA  
CCCCGCTCCATGGTCCATGCTGGGAGGGCACCCATCGCTTCTTGTGCGGAGCAGGTAGG  
AGTGGTGTGGGCTACCTCCCTGATGGGAGTCGCCTGGAGCAACCCCTCCTGGACCTCAAGAA  
CATCGTGTGACCACCCATGGATGGGGATGAGAGAGGGCTTCTGGGTTGGCTTTCACCC  
CAAATCCGCCACAATCGCAAGTCTATATTATTATTGTGCTGGACAAGAAGAAGGTAGA  
AAAGATCCGAATTAGTGAGATGAAGGTTCTGGGCTGATCCTAACAAAGCTGACCTGAAATC  
AGAGAGGGTCATCTGGAGATTGAAGAACCGCCTAACCCATAATGGCGGACAACCTCTTTT  
TGGCCTGGATGGCTATATGTACATATTCACTGGGACGGGGACAGGGCTGGAGATCCCTTGG  
CCTGTTGGAAATGCTCAGAACAAAAGTTCCCTGCTGGGAAAGTTAAGGATCGATGTGAA  
CAGGGCAGGCTCACATGGCAAGCGGTACCGAGTCCCCTCGGACAATCCATTGTTCTGAGCC  
AGGGGCCACCCGCCATCTATGCCCTATGGGATCAGGAACATGTGGCGTTGTGCTGTGGACCG  
AGGGGACCCATCAGCGCCAGGGCGAGGGCGATATTGTGCGGACGTGGCCAGAACAG  
GTTTGAAGAGGTTGACCTCATTTGAAGGTGGAAACTATGGCTGGAGAGCAGAACAGGAGGTT  
TGCATGTTATGACA~~AAA~~ACTTGTACAATGCCCTTGGATGATGTTCTGCAATCTATGC  
TTATGCCATGCAGTGGGAAGTCAGTCAGTGGAGGTATGTCTATCGTGGTTGTGAATCCCC  
AAATCTCAATGGCTGTATCTTGGAGACTTCATGAGTGGTCGACTATGGCTTGCAGGA  
AGATAGAAAAAACAGAAATGGAAGAACGAGGATCTTGCCTGGCAGCACACGTCCCTGTG  
CTTCCCAGGGCTGATCAGCACCCATAGCAAGTTCATCATCCTTGTGAAGATGAAGCAGG  
GGAGCTGTATTCCTGGCACCTTACCAAGTGCCTATGCACCACGTGGATCTATTACAA  
GTTTGTGACCCCTCAAGGGAGCACCCCCAGGCAAGTGCACATACAAGCCAGTGGCGTGG  
AACCAAGAGTAAGCGGATCCGTTAGACCAACTGCCAAGACAGTGGACTGCTAAAGGA  
ACAATCAGAGAACGCTAGAAAATCTCAGTGCAACCTTAGCTCTGGCCAGGCCAGGG  
TTTGTCTGAGAAAGGCTCCTCCAAGAAGCTGGCTTCTCCTACAAGCAGCAAGAACATGG  
AGGGCCTGGTACAAAGAAGAAAGCCAGAGTGGGGCCCCACGTCCGCCAGGGCAAGAGGAGGAA  
GAGCCTGAAAAGCCACAGTGGCAGGATGAGGCCATCAGCAGAGCAGAACAGCAGTGGCAGAAG  
TCTCCCTTGACCTATTGGTCAAGGTGGCGACAGGGTGACGTGAGAGAGGAGGCCACCTCAT  
CAAATGAAAGTCACTGCTGAATAAGACCTTAGAAGTCTGGGAAGCCAGGGTAGAGGTGGGC  
AGGGCGGTTTCCCTCCCTGGGAATCTGCTGTACTGAATAAAATGACACCTTCTCT  
GTATGCACTGCTCTGTGGGAGACCATATCCCAGATTGCTGGTGCACCTGGTTATGGTAAGC  
ACTAGTCCATGAGCCTGCTTGGAAATCACACTGGATGTCTCCGTTTGTCTTGTAAATGCCTAC  
AACCTGAGGTAATAAAATCAACATTTGCTCA

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**FIGURE 60**

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGVGLLQGHPOCLDYGPPFQPLHLEFCSD  
YESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCGYIKDILCQECSPYAAHYDAENTQTPL  
RNLPGLCSDYCSAFHSNCHSAISLLTNDRGLQESHGRDGTRFCHLLDPDKDYCFPNVLRNDY  
LNRHLGMVAQDPQGCLQLCLSEVANGLRNPVSMVHAGDGTHRFFVAEQVGVVWVYLPDGSRLE  
QPFLDLKNIVLTTPWIGDERGFLGLAFHPKFRHNRKFYIYYSCLDKKKVEKIRISEMKVSRAD  
PNKADLKSERVILEIEEPASNHNGGQLLGFLDGMYIFTGDGGQAGDPFGLFGNAQNKSLLG  
KVLRIDVNRAKGSHKRYRVPSDNPVSEPGAHPIAYGIRNMWRCAVDRGDPITRQGRGRIF  
CGDVGQNRFEVDLILKGGNYGWRAKEGFACYDKLCHNASLDDVLPIYAYGHAVGKSVTGGY  
VYRGCESPNLNGLYIFGDFMSGRLMALQEDRKNNKKWKKQDLCLGSTTSCAFPGLISTHSKFII  
SFAEDEAGELEYFLATSYPSSAYAPRGSIYKFVDPSSRAPPGKCKYKPVVRTSKRIPFRPLAK  
TVLDLLKEQSEKAARKSSSATLASGPAQGLSEKGSSKKLASPTSSKNTLRGPGTKKKARVGPH  
VRQGKRRKSLKSHGRMRPSAEQKRAGRSLP

**Important features of the protein:****Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 17-36

**N-glycosylation sites.**

amino acids 372-376, 480-484

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 645-649, 699-703

**Tyrosine kinase phosphorylation site.**

amino acids 81-89

**N-myristoylation sites.**amino acids 11-17, 37-43, 156-162, 165-171, 357-363, 365-371,  
368-374, 408-414, 459-465, 548-554, 557-563**Amidation sites.**

amino acids 391-395, 696-700

**Cell attachment sequence.**

amino acids 428-431

**Leucine zipper pattern.**

amino acids 25-47

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**FIGURE 61**

CTCCATTAAACCACCAAGCTCCCCAAGCCACCCCTCAGCC**ATGAAGTTCTGCTCCTGGT**  
CTTGGCAGCCCTCGGATTCCCTGACCCAGGTGATCCCAGCCAGTGAGGTGGGTCAAATGTGT  
GAGTAACACCCCAGGATACTGCAGGACATGTTGCCACTGGGGGGAGACAGCATTGTTCATGTG  
CAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTCCTGCCAAGCCTGACCTACCACAGCT  
CATCGGTAACCACTGGCAATCAAGGAGAAAGAACACACAAAGGAAAGACAAGAAGCAACAAAC  
GACCGTAACATCA**TAATA**ACCACTGCTATGCCCTCACCAACTCAGAGAAATATCATTCCAC  
AGTTCCAATTCCCTACATTGCTGAGTACTAGCCAAGGCTCCTTTATGGGGCAGATATCT  
ATAGCCAACCCAAAACTTCTGTCTTCTATCATTCTGTCAATTCTCATCTAGTAACAAATTGGAG  
TTTGTATCTATCTTACGAGAACATCATGCAGATTGTCCACAGGGGATCTGTCAAGTTG  
GGTCCTCCAAATGAAAATGTCAAGACAGAATTGGACATGCAAAAGATTGACTGGAGAACAC  
ACCTCTGATGGACAAAGGTGAGACAGAGCAGCCACAGGCAGGGAGAGCCTTCAGACTGCAACG  
CTGGCCTGATACGTGTCAAAGGAGAGAGGGATAGAGGAGGATTGAATAGAAGGAGACTAACAC  
TGCAGCTCTAAGAAAGTCTCAGCCAAACAGATGGGAGGCCAAAGCAAGGCTTGCCCTCAG  
AGGAGCTCACGCAGGGCAGGAATAGCCAGGTTCTCATATCCAGGGTTCAGACTGGCTGAG  
AACAGCCCTGGAGAACATGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCACC  
AACTATCCCCTGAAGCAAGTTCTTGTAAAGGAAATCTAACAGTGCACCCCATGGCTGCC  
ACGGAGTATAAGGAGGGAGAACAGGAGCTGAAAGTCTAGGTTGGCAGCTAGGTAGACTGA  
CTTGTGAGGTATTATTATTGAGTAACAAAGCAGACAGAACATAGCCACCATTGG  
TAGTACACCCAAAAGCAAGGATGGCATGATGCTGGTGACTIONGCTAACAGTGCCTACTCATGGTGT  
CAAATTGGCATAATCCTCTGGAGCTGTGGAAATAAGCACAGAGAACGAGACTCTAAT  
TGCTTAATCCACTAAACATTACTCTGGAAATTGGCTCATCATAAATTATCCAAGAGAACAG  
CAAAGTTATGGCACAAAGGTTCCATATAATTATTATAAATGCTGAGAAAATGAAAAAA  
TCTAAATGGTAAATATACTAATGCCATCTATAAATACAAACAAATAGAACATGTTATAGAA  
TAATGGAACATAATAACATTATTCAAATTGCTATTGCTATAGTGTCAAATTGTCTCCT  
TATATGATACAAAACATGAAAATTATGACTTTTGTGAAAGCAGAATTATGCA  
TAAATTCCCTTACAGTTGATGCCATTAGTTTATATAACATTATTGACACGTACTGA  
CTTCTATCTGAGAAGAACAAACAAACACTCAGGCCTAAATAATTAAAAACGTCCTAAAAA  
CTAGCAAACCAAGATAAGAAAAGATGTTAATGCCATTCCCTAACCTATGCTTAGACCAAAAT  
TAATTCTAGATGGTTAAAATGACAGTGTAAAGTAAAGTATTAAAAGATTGTGTGGTCAAA  
TATTCAATTAAAGAGCAAGGAAATTCTTATAAATATAACAATAGAGGCAGAACATGTAAGA  
ATAAAATTGATTAGGTGGTATTAAATATTAAGTTCTTATGTATGTCAAAGATATCATTGAA  
ATTCCATCCATCTTATTGGTATTGCAGGAGTTGCTATTCTTTGTTATAAATACTCTTCGT  
CATATGAATAGTATTCAATTGTATACTGGTTGATGGACATTGGGTTGTTCCAGTTA  
TGGCTATTACAAATAAGCTTCTATGAACATTATGTACA

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**FIGURE 62**

MKFLLLVLAAALGFLTQVIPASAGGSKCVSNTPGYCRTCCHWGETALFMCNASRKCCISYSFLP  
KPDLPLIGNHWQSRRRNTQRKDQQTTVTS

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 1-22

**N-glycosylation site.**

amino acids 50-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 79-82

**N-myristoylation site.**

amino acids 23-28

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**FIGURE 63**

CGGGAGCGCCTGGGAGAGGAGAAGGAGCCGACCTGCCGAGATGGGAGGCACCGGCACCTGGC  
GCTGCTGCTGGCGCTGGCGCTGCTCCTGCTGCTGACGCTGGCGCTGTCCGGGACCAGGGCCCG  
AGGCCACCTGCCCGGGCCCACGCCGCTACCACTGCTGGAAACCTCCTGCAGCTACGGCC  
CGGGCGCTGTATTCAAGGCTCATGCCGCTGAGTAAGAAGTACGGACCCGGTGTTCACCATCTA  
CCTGGGACCCCTGGCGCCTGTGGTGGTCTGGTGGGAGGGCTGTGCGGGAGGGCCCTGGG  
AGGTCAAGGCTGAGGAGTTCAAGCAGGGGGAAACCGTAGCGATGCTGGAAGGGACTTTGATGG  
CCATGGGGTTTCTTCTCCAACGGGGAGCGGGTGGAGGCAGCTGAGGAAGTTCACCATGCTTGC  
TCTGGGGACCTGGGATGGGAAGCGAGAACGGGAGGGAGCTGATCAGGCCAGGGCCCGTG  
TCTGGTGGAGACATTCCAGGGGACAGAACGGGAGGCCATTGATCCCTCCCTGCTGCTGGCCA  
GGCCACCTCCAACGTAGTCTGCTCCCTCCTCTTGGCCTCCGTTCTCCTATGAGGATAAGGA  
GTTCCAGGCCGTGGTCCGGCAGCTGGTGGTACCCCTGCTGGGAGTCAGCTCCCAGGGGGTCA  
GACCTACGAGATGTTCTCCGGTCTGCGGCCCTGCCAGGCCACAAAGCAGCTCCCTCA  
CCACGTCAGCACCTGGCTGCCCTCACAGTCCGGCAGGTGCAGCAGCACAGGGGAACCTGGA  
TGCTTCGGGCCCCGACGTGACCTGTCGATGCCCTCTGCTGAAGATGGCACAGGAGGAACA  
AAACCCAGGCACAGAACATTACCAACAAGAACATGCTGATGACAGTCATTATTGCTGTTGC  
TGGGACGATGACGGTCAGCACCGCGCTATACCCCTGCTCTGATGAAATACCCCTCA  
TGTCCAAAAGTGGGTACGTGAGGAGCTGAATCGGGAGCTGGGGCTGGCCAGGCACCAAGCCT  
AGGGGACCGTACCCGCCCTCCCTACACCGACGCCGTTCTGCTGATGAGGCGCAGCGGCTGCTGGC  
GCTGGTGCCCATGGAAATACCCCGCACCCCTCATGCCGACCCGCTCCGAGGGTACACCC  
GCCCGAGGCACGGAGGTCTCCCCCTCTGGCTCCATCCTGCATGACCCCAACATCTCAA  
GCACCCAGAAGAGTTCAACCCAGACCGTTCTGGATGCAGATGGACGGTTAGGAAGCATGA  
GGCGTTCTGCCCTCTCCTTAGGGAAGCGTGTGCTGCCCTGGAGAGGGCTGGAAAAGCGGA  
GCTCTCCTCTTCACCACCATCTAACGCTTCTCCCTGGAGAGGCCGTGCCGCCGG  
CACCTGAGCCTCAAGCCCACCGTCAGTGGCTTTCAACATTCCCCAGCCTCCAGCTGCA  
AGTCGGTCCCACTGACCTTCACTCCACACGAGACATGAAGGAAGGCAACTTGGAAAGTG  
GTGGGTGCCAGGACGGTGCCTCCAGCCTCAACAGTGGCATGGACAGGGTTAATGTCTCCAG  
AGTGTACACTGCAGGCAGCCACATTACACGCCCTGCAAGTTGGTTCCGGAGTCGTCCACGG  
CCCCACGCTCACTGACTCATGCTGTAAGATGCACAACCGCACACCCATACAAACTACAA  
GGGCCACAAAGCAACTGCTGGTTAGCTTCCACAGACATAATATGTCATCTGCAATCAC  
AAGCACATAGCCAGGTAAACCAACTCCCCTGGATCTGCAAGCCCACACGTGGAGTCGTGGC  
TGTACCTTCACAAGCCACAGAACGCCACACATGTTACAGCTCACAGGCCCTCTCCATT  
ATCGAACTTCTCAGTGTCCCTGTCCCTGGCTGCCAGGGAACAGCATGCCCTCCGG  
GTCATGCCACCCAGAGACTGTCGCTGTCTATGGCCCCAACTCATGCTCCCTCTTGGCTACA  
CCACTCTCCAGCCTGTGACCCAGCTGCAACACACCCCAACCAACTTGTCCACACAGCTAC  
CCACGTACAACATCGTCCTGGCTCCCCAGAGTATCTTCCCACTGAGACACGCCGCCACAG  
AGGCACAGTCCCAGCCACCTGCAACTGCGAGCCCTCAGTCACCCCTTTTAAGCACCCTGA  
TTCTACCAAATGCAAACACATCTGGGCTGCGATTATGCACAGAGACTTGGACATACGAGGA  
CCCTCAGACCGGAGGAACACCTGCCAACCCCAACACGTGCTTATGTAACCACGTGGAAAGCG  
GCCCTGCTGCCCTCCACACACATACACACTCACTGATCTACAGCCCTGTTGGCGTCA  
GAGTCCCCACTAGACCCAGTGGAAAGGGTTAGAGACCAAGTAGGGGCCAGTTCCAATTCA  
CTGTCAGGGAGTGAGCCGGATCTGACGTTCTTGTGACTTAAGGGTCCGGTTGGAAATTAAA  
GTTGTTCTGGCCTTGTAGCTAAAAAA

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**FIGURE 64**

MEATGTWALLALALLLTLALSGTRARGHLLPPGPTPLPLGNLLQLRPGALYSGLMRLSKK  
YGPVFTIYLGPWRPVVLVGQEAVREALGGQAEEFSGRTVAMLEGTFDGHGVFFSNGERWRQ  
LRKFTMLALRDLGMGKREGEELIQEARCLVETFGQTEGRPFDPSSLQAQATSNVVCSLLFGL  
RFSYEDKEFQAVVRAAGTLLGVSSQGGQTYEMFSWFLRPLPGPHKQLLHHVSTLAFTVRQV  
QQHQGNLDASGPARDLVDAFLLKMAQEEQNPGTEFTNKNMLMTVIYLLFAGTMVSTTVGYTL  
LLLMKYPHVQKVWREELNRELGAGQAPSILGDRTRLPYTDALHEAQRLLALVPMGI PRTL MRT  
TRFRGYTLPQGTEVFPLLSILHDPNIFKHPEEFNPDRFLDADGRFRKHEAFLPFSLGKRVCL  
GEGLAKAELFLFFTILQAFSLESPCPPDTLSLKPTVSGLFNI PPAFQLQVRPTDLHSTQT R

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 294-313

**Glycosaminoglycan attachment site.**

amino acids 99-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 128-132

**N-myristoylation sites.**

amino acids 51-57, 109-115, 115-121, 188-194, 207-213, 257-263,  
284-290, 339-345, 370-376, 444-450

**Amidation sites.**

amino acids 140-144, 435-439

**Leucine zipper pattern.**

amino acids 32-54, 39-61

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 433-443

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**FIGURE 65**

CGGACCGCGTGGGGCCGTATGCGCGCTCTGTGGAGTGCACCTGGGGTTGGGGCACTGTGCC  
CCAGCCCCCTGCTCCTTGGACTCTACTTCTGTTGCAGCCCCATTGGCCTGCTGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTACCTAACTGGCTGGCCCCCTGCAGAACCTGCTTC  
ATATAACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCCACAGCACCCGTAGCATCAACTGGAGCCTCTGC  
TATCCCTGAGCCCAGTGGGGCCTGATGGTGCTCCATAAGGACAGCATTCAAGTGGGGCCTCTGG  
CCCTTGTGTTTACCAAGGCTGCTTGAGTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTGGAAGACCATATCCTCCATACTCCTGGCCATTCTCTTGAACAACATCACTGATT  
CATTGGATCCTGCCACCTGAGTGCCACATTCAAGGCCACCCATGAACGACCCCTACCAGGA  
CTTTGCCAATGGCAGCCTGGCCTCAGGGTCCAGGCCTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGAAACGTTCCCTGTTGGCTGGAGGTAGCCACATTGGCCAGGGCCCTGACT  
GCCCTCAATGCAGGAGCAGCACTCCATGACGATGAATATGCACCGGCCGTCTCAGTTGG  
ACCAGCTACTGTGGGCTCCCTCCATCAGGCTTGCACAGTGGCACCAGTGGCTTACTCCC  
AGAAGCCGGGGGCCGAGAATCAGCCCTGCCCTGCAAGCTCCCTTCTCATCCTGCTTAG  
CATACTCTCTTCCCCAGTCACCCATTGTCAGGCCCTTGGTCCCAGAATAACTCTGTG  
CCTTCAATCTGACGTTGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGCTTCCAGTGGACGGCTTGTCCCCACTAGTCCTGGCA  
TCATGGCAGTGGCCCTGGGTGCCCTGGGCTCATGCTGCTAGGGGGGGCTTGGTTCTGCTGC  
TGCACCAAGAAGTACTCAGAGTACCAAGTCCATAAATTAAGGCCGCTCTGGAGGGAAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTGGAGCATCAAGTTCCAGCC  
GGCCCTTCACTCCCCATTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGCTTCTTCATACTTGTGGGGACTTGGAGGCAGGGACAG  
GGCTATTGATAAGGTCCCCTGGTGTGGCTTGCATCTCCACACATTCCCTGGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTACAGGGAAAAAA

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**FIGURE 66**

MRGSVECTWGWGHCAPSPLLWTLLLFAAPFGLLGEKTRQVSLEVI PNWLGPLQNLLHIRAVG  
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAKPLGRPPYPSLADFSWNNITDSLDPATLSATFQGHPMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGSLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPVLGIMAVAL  
GAPGLMLLGGGLVLLHHKKYSEYQSIN

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234,  
333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**Casein kinase II phosphorylation sites:**

amino acids 151-155, 249-253, 255-259

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern.**

amino acids 371-393

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**FIGURE 67**

CGGGACAGGCGCGTGAGGCCACAACACATGGTGTATCTTGTGGCTATCTTCCCTGCTCTGCCACGCCGGGT  
 CTGGAGAAGGGGTTTCAGCCCCAGGACATTACTGAGAGTCGGCAATATTGGGAGCCGCGATGTTCCCCCTTCG  
 GGCCTGTGGTGGCTGGCGCTCTAGGAGTGGCGGATCATGCCGGAGCCGCTGGGTGGAAAGGACTGCCAACGTGACGAC  
 CGCTCACCAAGTTCGGGACTGCCCTACAAAGAGTTGCGTGGGTGCCGAAGGACTGCCAACGTGACGAC  
 GCTTAGTCTGTCCCGAACAAGACTGTGCTGCCGGCGGGGCTCGCCACGTACACAGGTACCGTCAAC  
 GTGGCTGGCACAATGAGGTGCGCACCGTGGAGGCCAGGCGACTGCCGTGCTGAGTCAGCTCAAGAACCTCGA  
 TCTGAGGACACAACCTCATATCCAGCTTCCGTGGAGCGACCTGCGAACCTGAGCGCGCTGAGCTGCTCAAAT  
 GAACCACAACCGCCTGGGCTCTGCCCGGGACGACTCGGTGCGCTACCCGACCTGCGTCCCTGCGCATCAA  
 CAACAACCGGCTGCGTACGCTGCCCTGGCACCTTCGACGCCCTAGCGCGCTAGCGCGTACACTGCAACTCTATCA  
 CAATCCCTTCACTGCCGTGCCCTTGTGGCTGAGGCCCTGGCGAGCACCCGGGTGCTTACCCGA  
 GCCCGACTCCATTGCTGTGCCCTGCCCTCCCGCGCTGAGGGGTGCCGTGAGCCCTGCCCGCCCTGCCCTG  
 TGCACCGCCCAGCGTGCATCTGAGTGGCGAGCCACCGCTTGAAGCACCCGGCACCCACTGCCCGAGGACTGGC  
 GTTCGTTTACACTGCATGCCGACGGCCACCCACTGCCCTGCCCTGCAATGGCAACTTCAGATCCCCGGTGGCAC  
 CGTAGCTTAGAGCCACCGGCTCTGAGCGGGGAGGAGCACGGGGTTGGGGCGGAGGAAGGAGAGGGAGAAGGAGA  
 TGGGGATTGTGCGAGACCAAAACGCCGACTCCAGCACCCGCTGGCCGGCCCCAGCCACACC  
 GCGCTTCTGGCCCTCGCAAATGGCTTCTGGTGGCTTCTGGTGGCTACAGTGGCAAGGGAGGGCGGCT  
 CCGTGACACAATGAGCTGGCGCCAACCTACGTCATACTGCCCTGCCCTGAGCGCAACGTCACAGCAAGGGCCCG  
 CGCGCCTGGCGCCGGGGAGAACCCGACGGACAGGGCCGACCTCTGAGCGCAACGTCACAGCAAGGGCCGG  
 CAACAGCGCTGCTGCCCTCAAACCCGAGGGCAAATCAAAGGCAAGGCCCTGGCAAGGTGAGCATTCTCGGGGA  
 GACCGAGACGGAGCCGGAGGAGGACACAAGTGAGGGAGAGGGAGGCCAGAACAGATCTCGGGGACCCGGG  
 GGAGCAGCGCTGTGCGAACCGGGACCCCTCGGTACGTTCTAACACCGCTTAACCAGCGCTAACAGCGCAGAGCTAA  
 GCCGCACGTCTCGAGCTGGCGCTATCGCGTGGATGGCGAGGGCGAGGCCGAGGGCGGGTGAGCTGACTCGCT  
 GGCTGCCGCTGGGGCTGGGGCGGGGGCTGGCGAGGGCGAGGCCGAGGGCGGGTGAGCTGACTCGCT  
 CTATCTGTCCAGCGGGGGCGCGCGAGCTGAGTGGCTCCCGTAGAGGAAGGCGTCAACGCCCTACTGGT  
 CCGGGCTGCCGGGTACCAACTACTCCGTGTGCCCTGGCGCTGGCGGAAGCTGCCACGTGCAAGTGGT  
 GTTTCCACCAAGAAGGAGCTCCATCGCTGCTGGTACAGTGGCAGTGGCTATTCTCTGGTCTGGCCAC  
 AGTGCCCTCTGGCGCCGCTGCTGCCATCTGCTGGCTAAACACCCGGCAAGCCCTACCGTCTGATCTGCG  
 GCCTCAGGCCCTGACCTATGGAGAAGCGCATGCCGAGACTTCGACCCGCTGCTTGTACCTGAGTCCGA  
 GAAAAGCTACCCGGCAGGGAGACCCAAGTGGGACCTCGAGAGAGGGAGGCCAGAGGAGCTGGCAAGTGG  
 CGCGGAGAGGGAGACCCAAGTGGGACCTCGAGAGAGGGAGGCCAGAGGAGCTGGCGCTGCTACTGGTGGAGTCCC  
 GTCCAAGGCAACCAAGAGGAGTTCGAGGCGGGCTCTGAGTACAGCGATGCCCTGGCCCTGGCGCCAGGG  
 CAACATGCCCAAGGAGATAATGCAACTACAGGAGCAGGGCAGGGCTAACCTCCGGCTCCGGCCATT  
 CCCGACCTCCACCTAGGGTGCCTGGGAGCAGCAGTCTAGGGCTGGCAGGACTTATGCCCCGTCCTCCAAACCTTC  
 ACCTACTCCTCCCCCTACTACTCCCAACCTTGACTACCAGGGACTCTATTAGGGAGTGGGGGATTTACCA  
 GTCCCTGCTACCCACGGCTGCCATTCTCCCTGCCGGCTGAATCCCCCTCCCCGCAAGCACAGTGTATCTTAC  
 CCCATGCAAGACTCCACCCGAGACGGTGGCGATATCTATGCTCCCTCATTCCCGTGCATATCTGCAAAAT  
 CCACCCGGCAGCCGGCCACCGTGGGCTGGAGGCCAGGGAAACGAGCGAAGACTTGGAAACCTCGCGTAA  
 CGCGGTGGTTGGGGCCAGCAAGGCCAGGGCTGGAGTCTGCCCTGGGAGGCTGGCTCTCAAGGG  
 TTTCTTCTTTTTTATTTTTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT  
 CAGGCTGGAGTGCAGTGGCGCAGTCTGGCTCACTGCACTTCCGGCTCCGGGCTTAAGCGATTCCTGCTC  
 AGCTGCTCTAGTAGCTGGACTACAGGCGCGGCCACCCAGCTAATTTCTTATTTTATAGAGACGG  
 GTTTCAACCATGTTGCCAGGATGGCTGGATCTTGCACCTCAGGTGATCCATCTGGCTCTGGCTCTCAAAGTG  
 CTGGGATTAACAGGGCTGAGGCCAGGGCTGGAGTCTGCCCTGGGAGGCTGGCTCTGGGAAATCGAGTGT  
 TGCAACCCCTAGTTTATGGAGCTGGCT  
 CCTTGGCGCTGAGCTGTGGACTTGGCTGCGGGCAATTCTGTTGCTGCTGCTGCTGCTCTCTCTCTCT  
 CGGCCAACAGCGCCGCTCCCGGGCTCCACCGACCCAGACCCCTAGCTGAGGCCGGAGGGGGAGGG  
 GACTGTGGCTCCGGCTCTCTGGAGGGCTGCCCTAGTCGACAAAGCCTGCTCGTACTGTG  
 GACTGTGCGACGGGATCCGGATGGAGCGAGCCCTCCGCTCTCGCTCTGGCTCTCGCTGCC  
 CGCCCCCTGCTTCCGGGGAAATCGTGTGGCTGCCGGCGTGAGTCCTGACAAGCGTGCCCTGAGGAGAAAAGTC  
 TGTGTCTGTGAAGTGTGACCGTGTAGTGTAGGGGGCGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGG  
 GAGGGGGCGGGCGCGGGACTCGGGGGGGGTCTTTTCCATTGAAAAGAAAAGCGTGGGGGGGGGGGGGGGG  
 GGAGTTCACTCTGGGATCAGCCCTCTCCGCGAAGCGCAGCACAAGCGGGCCCTGGGACGGAGTAGCCCC  
 GGAGCCCCGTGCCCTTCTAAACCGTCTGTATGCAAGTCATAAAACAAATCGATTGAAA

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**FIGURE 68**

MFPLRALWLVWALLGVAGSCPEPCACVDKYAHOFADCAYKELREVPEGLPANVTLTLSANKITVLRRGAFADVTQVTSWLHNEVRTVEPGALAVSQLKNLDLSHNFISSFPWSDLRNLSALQLLKMNHNRLGSLPRDALGPDLRSLRINNNRLRTLAPGTFDALSALSHLQLYHNPFHCGCGLVWLQAWAASTRVSLPEPDSIACASPPALQGVPVRLPALCAPPSVHLSAEPPLAEGTPLRAGLAFVLHCIADGHPTPRIQWLQIPGGTVVLEPPVLSGEDDGVGAEEGECEGDGDLLTQTQAQTPTPAPAWPAPPATPRFLALANGSLVPLLSAKEAGVYTCRAHNEGANSTSIRVAVAATGPPKHAPGAGGEPDGQAPTSERKSTAKGRGNSVLP SKPEGKIKGQGLAKVSILGETETEPEEDTSEGEAAEDQILADPAEEQRCGNGDPSRYVSNHAFNQSAELKPHVFELGVIALDVAEREARVQLTPLAARWGP GP GAGGA PRPGRRPLRLYLCPAGGGAAVQWSRVEEGVNAYWFRGLRP GTNYSVCLALAGEACHVQVFSTKKELPSLLVIVAVSVFLLVATVPLLGAACCHLLAKHPGKPÝRLILRPQAPDPMEKRIAADFPRASYLESEKSYPAGGEAGGEEPEDVQGEGLDEDAEQGDPSGDLQREESLAACSLVESQSKANQEEFEAGSEYSDRLPLGAEAVNIAQEINGNYRQTAG

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 587-610

**N-glycosylation sites.**

amino acids 52-55, 121-124, 337-340, 364-367, 474-477, 563-566

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 397-400

**Casein kinase II phosphorylation sites.**

amino acids 19-23, 202-205, 289-292, 246-249, 411-414, 431-434, 433-436, 440-443, 544-547, 583-586, 650-653, 700-703

**N-myristoylation sites.**

amino acids 15-20, 48-53, 165-170, 296-301, 351-356, 362-367, 390-395, 419-424, 514-519, 536-541, 557-562, 561-566, 610-615, 661-666, 716-721

**Amidation site.**

amino acids 522-525

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 10-20, 603-613

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**FIGURE 69**

GGCGGCGGGAGCAGCGAAGGGGGCGGCAGGGATCCTCCAGGCTGCCGGCTGGGAAGGCGTGGG  
CGACCCGGTGTGCGCGCCCAGAGCCCCGCGTTCAGCCCTAGGGAAGGAAGCCAGTGAG  
GGAAGTTCTCCATGAATGTACGTACAATGATGATGACCGACCAATCCCTGGAACTGCCA  
CCATTGCTAACCGAGAGGGTAGCCATGATGCCCACTTGGTGAATGGAGATGCAGCTCAGCAT  
GTTATTCTCGTTCAAGTTAACCAAGGTGAGACTTCACAATAAGAGCAGAGGATGGAACACTT  
CAGTGCATTCAAGGACCTGCTGAAGTTCCCATGATGTCACCCAATGGATCCATTCCCTCCATT  
CATGTGCCTCCAGGTATATCTCACAGGTGATTGAAGAGATAGTACTGGAGTCCGGGGTGGT  
GTCACACCCAGTCTCTGAGTGTATCCCCAAGCTACCCCTCAGCCATGTCCTCAACCCAT  
CATCTCCCTCCCTATCTGACTCACCATCCACATTATTCATAACTCACACACGGCTTACTAC  
CCACCTGTTACCGGACCTGGAGATATGCCGCCTCAGTTTTCCCCAGCATCATCTCCCCAC  
ACAATATATGGTGAAGAAATTATACCATTATGGATGTCAAGCTACATCACCGAGAA  
GACCAGTACAGCAAGCCTCCGACAAAAAAACTGAAAGACGCCAGATCGATGCCAGAACCGC  
CTCAACAGCCCTCTCTTCTATCTACAAAAGCAGCTGCACAACAGTATAATGGCTATGGG  
AAGGCCATAGTGGTGAAGTGGCGAGGCGGAGCGGTAGTGGTCCCGAATTAGAAAACA  
GAGCGACGAGCAAGAAGCAGCCAAAGTCGAATGATTGAGACTTGCAAGAATATGAGTTGGAA  
GTAAAGAGGGTGAAGACATTCTTCGGAATAGAGAAACCACAGGTTCTAATATTAGGCA  
AGAGCAGTTGTGTTGCTCTGGCTCCCCCTGTTGGACTTCTGTGGACCCACAGTGGCTT  
TCCTTCCCTACAGTTACGAGGTGGCTTATCAGACAAAGGACGAGATGGAAAATACAAGATA  
ATTTACAGTGGAGAAGAATTAGAATGTAACCTGAAAGATCTTAGACCAGCAACAGATTATCAT  
GTGAGGGTGTATGCCATGTACAATTCCGTAAGGGATCCTGCTCCGAGCCTGTTAGCTTCA  
ACCCACAGCTGTGCACCCGAGTGTCTTCCCCCTAAGCTGGCACATAGGAGCAAAGTTCA  
CTAACCTGCAGTGAAGGCACCAATTGACAACGGTTAAAATCACAACACTACCTTTAGAG  
TGGGATGAGGGAAAAGAAAATAGTGGTTCTAGACAGTGCTTCTCAGGAGCAGAAGCACTGC  
AAGTTGACAAGCTTGTCCGCAATGGGTACACATTCAAGCTGGCGCTCGAAACGACATT  
GGCACCAAGTGGTTATAGCCAAGAGGTGGTGTGTCACACATTAGGAAATATCCCTCAGATGCCT  
TCTGCACCAAGGCTGGTTGAGCTGGCATCACATGGGTCACTGGCAGTGGAGTAAGCCAGAA  
GGCTGTTCACCGAGGAAGTGTACACCTACACCTGGAAATTCAAGGAGGATGAAAATGATAAC  
CTTTCCACCCAAAATACACTGGAGAGGATTAAACCTGTAAGTGTACTGTAAAAATCTAAAAGAAGC  
ACACAGTATAAATTCAAGGTGACTGCTTCTAATACGGAAGGAAAAGCTGTCCAAGCGAAGTT  
CTTGTGTTGACGACGAGTCCTGACAGGCTGGACCTCCTACAGACCGCTTGTCAAAGGCCA  
GTTACATCTCATGGCTTACTGTCAAATGGATCCCCCTAAGGACAATGGTGGTTAGAAATC  
CTCAAGTACTGCTAGAGATTACTGATGGAAATTCTGAAGGTGAAGTTTTGGCAATTGTTT  
ATTCAAATCAAATGCAAGCTCTGTTCTAATATAGTAAATGTCTTATAGTAATAGTGA  
AATCATAATTCTAAAGATAGAATTATTACAAATAACAAACTTACTGACATATTGGCAG  
TTTTCTATTCAACACAGCACCAGAGATCAGAGTCACTTGAAACTTACATTGTGTTATT  
TAACAATTCTGTATCTTCTTCACTGGTGTGTTGTTGTTGTTCTTGTGTTCTTGTGTTCT  
TTGGTTGGTTGTTGTTGAGATACGATCTCTGTCACACAGGCTGGAGGG  
AGTGGCACAGACATGGCCCATGCACTGTCAGACTCCTGGCTTAAGTGA  
ACTCTCTGCCACA  
GAAGATGAGGAAGAATACATTTCATAGTGA  
TGGGCTCAAGCAACCCCTCCACCTGGCCTCCAAAGTGTGGGACTATAGACATG  
AAATCACCACACTCAGCTTCCATGTCTTTTATGA  
ACTAGGGTCTAATTAAATCAGATAAATT  
TGGTATTTCATCTCTAACATTGCCATATGTTCTGGAAATTCTTATAAGCAGCGAGAGTG  
GTGGCTCACGCTGAGTCCCAGCACTTGGGAGGCTGAGGTGGTGGTCAGGAGATCAAGACC  
ATCCTGGCCAACATGGTGAACCCCCGCTCTACTAAAAAATACAAAATTAGCTGGGTGTGGT  
GCAGGCACCTGAGTCCCAGCTACTTGGGAGGCTGAGGCAGAAGAATTGCTTGA  
ACACCCAGCAG  
GCGGAGGTTGCAGTGAGCTGAGATTGCCACTGCACTCCAGCCTGGTACAGAGTGAGACTC  
TGTCTCAAAAAAA

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**FIGURE 70**

MMMTDQIPLELPPLLNGEVAMMPHLVNGDAAQHVILVQVNPGETFTIRAEDGTLQCIQGP  
PMMSPNGSIPPIHVPPGYISQVIEDSTGVRRVVTPQSPECYPPSYP  
SAMSPTHLPPYLTHH  
PHFIHNSHTAYYPPVTGPGDMPPQFPQHHLPTIYGEQEIIIPFYGMSSYITREDQYSKPPHK  
KLKDRQIDRQNRLNSPPSSIYKSSCTTVNGYGKGHSGGSGGGSGSGPGIKKTERRARSSPK  
SNDSDLQEYELEVKRVQDILSGIEKPQVSNIQARAVVLSAPPVGLSCGPHSGLSFPYSYEVA  
LSDKGRDGKYKIIYSGEELECNLKDLRPATDYHVRVYAMYNSVKGCSEPV  
SFTTHSCAPECP  
FPPKLAHRSKSSLTLQWKAPIDNGSKITNYLLEWDEGKRNSGFRQCFFGSQKHCKLTKLC  
PAM  
GYTFRLAARNNDIGTSGYSQEVCYTLGNIPQMPSAPRLV  
RAGITWVTLQWSKPEGCSPEEVIT  
YTLEIQEDEDENDNLFHPKYTG  
EDLTCTVKNLKRSTQYKFRLTASNT  
EGKSCPSEVLV  
CTTSPDR  
PGPPTRPLVKGPVTSHGFSVKWDPPKDNGGSEILKYL  
LEITDGNSEGEVFGNCFIQIQ

**Important features of the protein:****N-glycosylation sites.**

amino acids 69-73, 254-258, 401-405

**Glycosaminoglycan attachment sites.**

amino acids 229-233, 234-238, 236-240

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 416-420, 535-539

**Tyrosine kinase phosphorylation site.**

amino acids 319-326

**N-myristoylation sites.**amino acids 52-58, 227-233, 228-234, 230-236, 231-237, 232-238,  
235-241, 239-245, 402-408, 610-616**Amidation site.**

amino acids 414-418

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 290-301

**ATP/GTP-binding site motif A (P-loop).**

amino acids 546-554

**CUB domain proteins profile.**

amino acids 294-301

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**FIGURE 71**

AAGTCATTCA GTGGATGTGATCTGGCTCACAGGGGACG **ATGT** CAAGCTTCCCTGGCTCCTCTCAGCCTTGTT  
GCTGTA CTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTGGACAAGTTAACACAGCGAA  
GACCTGTTCTATCAAAGTTCACTTGCTTCTGGAATTATAACCCAATTACTGAAGAGAAATGTCCAAAACATG  
ATAATGCTGGGACAATGGCTGCCCTTTAAAGGACAGTCCACACTTGCCAAATGTATCCACTACAAGAA  
ATT CAGAATCTCACAGTCAAGCTCAGGCTCAGGCTCTCAGCAAATGGGCTCTCAGTCTCAGAAGACAAG  
AGCAACCGTTGAACACAATTCTAAATACAATGAGCACCATCTCAGTACTGGAAAAGTTGTAACCCAGATAAT  
CCACAAGAATGCTTATTACTTGAAACCAGGTTGAATGAAATAATGCAACAGTTAGACTACAATGAGAGGCTC  
TGGGCTGGGAAAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTATGAGAGTATGTGGCTTGAAA  
AATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGATTATGGAGAGGAGACTATGAAGTAAATGGGTA  
GATGGCTATGACTACAGCCGCGCCAGTTGATTGAAGATGTGGAACATACCTTGAGAGATAAACCTTATAT  
GAACATCTCATGCTATGTGGGCAAAGTTGATGAATGCTATCCTCTATATCAGTCAATTGGATGCCTC  
CCTGCTCATTTGCTGGTGAATGTGGGTAAGTTGGACAAATCTGACTCTTGACAGTCCCTTGACAG  
AAACCAAACATAGATGTTACTGTGCAATGGGACAGGCCATTGGGACAGAGAAATATTCAGGAGGCGAG  
AAGTTCTTGTATCTGTTGGTCTTCTTAATATGACTCAAGGATTCTGGAAAATTCCATGCTAACGGACCCAGGA  
AATGTTAGAAAGCAGTCTGCCATCCCACAGCTGGGACCTGGGGAAAGGGCAGCTCAGGATCTTATGTCACA  
AAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGCATATCCAGTATGATATGCCATATGTCGA  
CAACCTTTCTGCTAAGAAATGGAGCTAATGAGGATTCCATGAAGCTGTTGGGAAATCATGCACTTCTGCA  
GCCACACCTAAGCATTAAACATGGCTTCTGTACCCGATTTCAGAAGACAAATGAAACAGAAATAAAC  
TCCCTGCTCAAACAAAGCACTCACGATTGTTGGGACTCTGCCATTACTACATGTTAGAGAAGTGGAGGTTGAGT  
GTCTTAAAGGGAAATTCCAAAGGACAGTGGATGAAAAGTTGGGAGATGAAGCGAGAGATAGTTGGGTG  
GTGGACCTGTGCCCATGATGAAACATACTGTGACCCCGATCTGTTCCATGTTCTGATGATTACTCATTC  
ATTGATATTACACAAGGACCCATTACCAATTCCAGTTCAAGAAGCACTTGTCAAGCAGCTAACATGAAGG  
CCTCTGACAAATGTGACATCTCAAACCTACAGAAGCTGGACAGAAACTGTTG**TAAGAAATACCTCAAATGTT**  
GAACCTCTCTAGTATTCA GTATTACTCATTCCATGCCATTGTTGATTGATTTCTTGTAAAAAGAAA  
ATTTTATGGCTCAAATGTCTCATTTACAAACCAAACATTTAATTGTTGTTGAGCAGAGGAACTAGACCATAAC  
AACATTTGGGTGGGCCACCTCTTCTCCATCATAACTACAGCCCTCTTCTGTAATTGGAAAGGAAAGAG  
CGGTTTGGGTGGAAATATATGTTAATATGCACTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTT  
AGAAGAAACCATAGATCATAGATGAAATATATGACATCTGGAACCCCTCAAAGGCCCTGAACCCCTTTTT  
TGTGTTGCAATATGTCAGGCTGGAAAATCAGAACCCCTGGACCCTAGATTGAAAATGTTGAGGAGCAAGAA  
CATGAATGTAAGGCCACTGCTCAACTACTTGAGCCATTATTCACCTGGCTGAAAGGACAGAACAGAAATTCTT  
TGTGGGATGGAGTACCGACTGGAGTCCATATGCAAGACCCAAAGCATCAAAGTGGAGGATAAGCTAAAATCAGCTC  
TTGGAGATAAGCATATGAACTGGACAAATGAAATGTAACCTGTTCCGATCATCTGTTGATATGCTATGAGGC  
AGTACTTTAAAAGTAAAAAAAGATGATGTTCTGAGGCTGGGAGGATGTCAGCTGCTAATTGAAACCAA  
GAATCTCTTTAATTCTGTCACTGCACCTAAAGATGTTCTGAGGTTGATTTGTTGATGAAATGTTAATTCTGTT  
CCATCAGGATGTCCCGAGCGTATCAATGATGCTTCCCTGTAATGACAACAGCCTAGGTTCTGGGATAC  
AGCCAACACTTGGACCTCTAACAGCCCCCTGTTCCATATGGCTGTTGAGGTTGATGGAGTGA  
TAGTGGTTGGCATTGTCATCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAAATAAGCAAGAACGG  
AAAATCCTTATGCCCTCATGATAATTGAAAGGAGAAAATCCAGGATTCCAAAACACTGATGATGTTCTGAG  
CCTCTCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
AAAATATAAGATGATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
ACATGGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
CTGTTCTTAAATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
TAATCTAAATGTAATGTCGTGAAATTCTGAAGTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
TGTATGAAATGATGATGCTGAGGATGACATGCTTCTTCACTGGGATCAGGAGGAGGAGGAGGAGGAGGAG  
TGCATTAGCTCACTTCACTTAACTGCAAGGATGACATGCTTCTTCACTGGGATCAGGAGGAGGAGGAGGAG  
TGGTGAATTGCTACAGTGTGATGTTGGAACTGATCATGCTTCTTCAAGGTGACAGGCTAAAGAGAGAAGAATC  
CAGGGACAGGTAGAGGACATTGCTTCACTTCAAGGTGCTGATCAACATCTCCCTGACAACACAAAAC  
GAGCCAGGGGCCCTCGTAACCTCCAGAGCATGCCGTGATAGAAACTCATTTCTACTGTTCTCTAATGTGGAGT  
GAATGGAAATTCCAACGTGATGTTGACCCCTGAAAGTGGTACCCAGTCTCTTAAATCTTGTATTGCTCACA  
GTGTTGAGCAGTGTGAGCACAAAGCAGACACTCAATAATGCTAGATTACAAA

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**FIGURE 72**

MSSSSWLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNNTNITEENVQNMN  
NAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTI  
YSTGKVCNPDPNQECLLLEPGLNEIMANSLDYNERLWAWESEWRSEVGKQLRPLYEEYVVLKNE  
MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY  
PSYISPIGCLPAHLLGDMWGRFWTNLYSLTPFGQKPNIDVTAMVDQAWDAQRIFKEAEKFF  
VSVGLPNMTQGEWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH  
IQYDMAYAAQPFLRNGANEFGHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLK  
QALTIVGTLPTYMLEKWRWMVFKEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLF  
HVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLL

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 53-57, 90-94, 103-107, 322-326, 432-438, 546-550

**N-myristoylation sites.**

amino acids 260-266, 286-292, 395-401

**Cell attachment sequence.**

amino acids 204-207

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 371-381

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**FIGURE 73**

CCCACCGCGTCCGAGCGGGGTGGACAAGTGGCGTGTGCTGCACCCCGAGGGAAAG**ATGAACG**  
GGACCGGAACTGGTGTACCTGGTGGACGTGCACCCAGAGGACCAGGCAGGCCAGGA  
AGACCTATGCCATGGTGTCCAGCCACTCAGCTGGCATTCTCTGGCTTCAGAACTGGTGGAGT  
CCCAGTGGACATGAGGAGATCATTAAGGTGTACTTGAAGGGAGGTCTGGAGACAAGATGA  
TTCACGAGAAGAATATTAACCAGCTGAAGAGTGAGGTCCAGTACATCCAGGAGGCCAGGAACCT  
GCCTACAGAACGCTCCGGGAGGGATAAGTAGCAAGCTTGACAGGAACCTAGGAGATTCTCTCC  
ATCGACAGGAGATAAGGTGGTGTAGAAAAGCAAATGGCTTAGTCAGAGTCCCACAGCCC  
TGTACAGCAGCCCCACCTGAGGTGGACACCTGTATAAATGAGGATGTTGAGAGCTTGAGGAAGA  
CGGTGCAGGACTTGCTGGCCAAGCTTCAGGAGGCCAACAGCAGTCAGACTGTGTGG  
CTTTGAGGTACACTCAGCCGGTACCAAGAGGGAAAGCAGAACAAAGTAATGTGGCCCTTCAGA  
GAGAGGAGGACAGATGTCCAGAG**TGATTGGAGAATGTCCTGGGGAAATGAAGTCCTTCCACA**  
AACACAGCTCAGTTCTAGCAACAAACTGTTTTCTACTTGCTCCATCTGCAGCCTACG  
CTGCCCTGGCCTCTGCAGACAGATAGTGGGTTACCTGGCAAGGCCTGGTGAGAGCCAGTGA  
ACCTAACGCTTGTACTGGTGGCCTTGTCTTTCTGGGGAGGGAAATGTACATTCA  
GCCTTTGCGGAAAAATTCTCTAGGGCTACAGACAGTCATGTGTGACTTCTCTGCTGTGAA  
AACTCCCAGAGTCTTTAGGGATTTCCTAAAGGTGTACCAACCAGGCACACCTCAGTCTTCT  
TGACCCAGAGCCTGAAACTGTTTCACTGGGTTCCACCAGTCCCAGCAAAATCCTCTTGTAA  
TTTATTTGCTAAGTTATTGGGGTTTGCTTACATCTCATGATTGATATAATACCAAAAGTTCT  
TATAGCCTCTCTGCAGTATTGGGATTGCTTGAACCCGGAAAATGTTCCATTAGGCTT  
GTTAATGTCAGAGTGCACACTATTATGAATCTTCTCCCTTCTGCCTGTTCTCT  
CTTTCTCCTCAAACCTGCTCTGCAGCTAAGGAAGGTGAGTCTACTTCCCTGAGGTTGG  
GTCAGAGTATATGTTGGAGAAAGAGGGCAATCAGGACTCTCTGGACCCAGATGAGTT  
CTTCACTAGCCCTCTGAACCCCTTGCCTCCATAATTGGTCTTTATCCTGGCTCTGAATGACC  
CTGCAGGTCATCATGGTTCTTTTTATTGTTTTCTGAGACAGAGTCTCACT  
CTGTCACCCAGGCTGGAGTCAGTGGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCGGAT  
TTAAGCGATTCTCTGCCTCAGCCTCCGAGTAGCTGGACTACAGGTGTGCCACCACGCCTG  
GCTGATTTGTATTTAGTAGAGATGGGTTCAACCATACTGGCTAGGCTGGTCTCGAATT  
CCTGACCTCAGGTGATCCACCCACCTCGGCTTCCAAAGTGCTAGGATTATAGGCTTGAGCTA  
CTGCGCCCGGCCATGGTCTTTCTTAGGGCTTCTACAGCCTGAGAAGTAGATAGGC  
ATCAGAGTATGGTACTATAGGAATCAGAAAAATTCAAAACAAATGTGGATTAAAGTGTGTTAGGC  
TCTATGTGGCTACGCAGCCAGAATCCTAAGTCTGTGTTCTGTCTCAAGACTGGCT  
CACATTCTGGCTTGTCCATAACAATGCTCTGGGATTTCAGGGAGTCCCTCATTGTAAAAT  
GAGGGGGTCAGAGCAGGTGATATCCATGTTCTCCCTTCTGATATTGTTGTCTGTGGCATA  
TTCTTTGTATGGCGAATTAAATAATTATATTAAATGTGTCA

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**FIGURE 74**

MNGTRNWCTLVDVHPEDQAAAGRKYAMVSSHSAGHSLASELVESHDGHEEIIKVYLGRSGD  
KMIHEKNINQLKSEVQYIQEARNCLQKLREDISSKLDRLNLDSDLHRQEIQVVLEKPNQFSQSP  
TALYSSPPEVDTCINEDVESLRKTVDQLLAKLQEAKRQHQSDCVAFEVTLSRYQREAEQSNVA  
LQREEDRCPE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-39

**N-glycosylation site.**

amino acids 2-6

**Amidation site.**

amino acids 21-25

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## FIGURE 75

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**FIGURE 76**

MLKKMGEAVARVARKVNETVESGSDTLDLAECKLVSFPIGIYKVLNVSGQIHLITLANNELK  
SLTSKFMTTFSQLRELHLEGNFLHRLPSEVSALQHLKAIDLRSRNQFQDFPEQLTALPALETIN  
LEENEIVDVPVEKLAAMPALRSINLRFNPLNAEVRVIAPPLIKFDMLMSPEGARAPLP

**Important features of the protein:**

**N-glycosylation sites.**

amino acids 17-21, 47-51

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**FIGURE 77**

ACCAACAAGCAATCGTTCATGAGAAAGCCGTGCACCCGCTGCAGTTGGGCCATGTTGGTCCGATCGTATTCCAC  
TAGGTCCCCATTGTACACCAAGTACTGTCCCCTCGCTCCAGCAGATGCCCTGCAGCCTTCACCTCTCAAGCAG  
GGTGGTGTGAGTGCCTGCTTCCCTCCAGCAGATGCCCTGCAGCCTTCACCTCTCCAGGCTGCTGGGGAGGCACCCCCCGGGGTGGAGAA  
AAAGCCGGCTGGCCTCGGAGGTGGTCTGGCCCCCGCCCCACCAGACTCCCTCCAGGCTGTTCTGCTCGGTCAA  
GGCTCCGGCGGCAGCAGCGCAGGCAGCAACGTAAGCGGATGCTCTCCAGGCTGTTCTGCTCGGTCAA  
ATGGCTGAGCTGGTACATCTCGCTCCAGGTTAGGAGATCTCGCGGCGCTCTATGAACGACTGCCGTAGTTCTG  
GTAGACGTTGCGCTTCAGGTTCTGCGCCGCTCCTCCGCAGCGCCTGGATGCGCTGCCGTGCTCTGGAGGTC  
CCGGTCCCCATCCGACTGCTGAGAGCTGCTCACGTAACAGCGCCTCAAACACCCCTGACTCCAGCTGCC  
ACGCAGCGGCTGCCACTGTCGACATGCCATGCCATTCTCCGGTCTCACGCACACTGTCACTA  
TCGGCGCGCAGCGCCGCCGCTGCTAGACCCACCAAGGCCAACCCAGCTCCGGCTGAGGAAGCAGGAATG  
GGAACGAGACGAGTACGCCCTGCCGGCTGAGCGTACAGACACTGCCCTGCCAGTGAGGCGCAGACA  
TTGCGCTCGCGCAGCAATGCCATCGGTTAACAGCGTACGCCAGATGAGTATTGCGGAAGTGAGGGGAGGGAGA  
GGCGAGAGAAATTTCGGTACTGCGCATGAAACCGAGCGTACGTTGAGGTTGAAATAACCGGCAAAGACTAAAG  
GCTGAAACTAGCTTCTGAAAGCTTCGTTAGGGCCGAGCCCTGTGAGGCCAGGTTCTGCCACTAGGAGGTG  
CATGCTGACTGTTTTAAAGCCCTAGAACATCTGGCTTGGCTTGGGTAAGCTCGTCTCGTTCTCAA  
GCCGTTTCCCGAACTCTCGCCGGATTGACGGGCCGCTCGAGAGCCGGCATCTCTAGGAGCTAGCTGGT  
CTCGCTAGGCGCTTGGGTCGGCGTAACTGGGAGCCAGCCTGACGCCGGGACCCGCTGTGATCTG  
GCAACGATGGATGATGACTGTGATGGCTGGGCTTGGAGGAGTGGAACTTGCAAGGAGGCGGAGCGCAG  
CATGCCAGGAGTCCCTGCTGACTGGAGCTGGCTGGAGTGGGACTTGCAGGAGGCGGAGCGCAG  
TTTGTTCAGTTAACGACCAATTCTCTGGGCCAGCTGGAGGCGCTGAGGTGAAGTGGAGCGTGCAGGACTG  
CTGTGTGCTGGGATATGCGACTATGAAAGGGAGGGTGGATGTGTTCATCCGTCAGCGAACCCCTTTGAAG  
TTGAGGCCAAGAAAGGATCTGTAGAGACCCCTCTGCAATGAAATGATACATGCCATTATTTATGACTAAAC  
GACAAAGACCGAGAACGGCATGGCCAGAATTGTAACATATGCATCGCATCACGCCACTGGAGGCCAAT  
ATAACGGTATACCATACTTTACGATGAGGTGGATGAGTATGGCGACACTGGTGGCGTGCATGGCCGTG  
CAGCACAGGCCACGGTATGGCGTACTGCAACAGAGCTAACAGGGAACCTCTGCTCATGACTATTGGTGG  
GCTGAGCACCAGAAAACCTGTGGAGGCATTACATAAAATCAAGGAACCGAGAGAAATTACTCAAAAAAGGCAAA  
GGAAAGGCAAAACTAGGAAAGGACCGATTTGGCGCAGAGAATAAGGTACCTCTGTATATTCTGATT  
TTTATGTCACCATAGCTATGATGTAAGACAAACTGTCCTCAGAGAACTGGTATTAAAGATAAACTTAAGGATC  
GTTTCTGTTGAGAAGTCTCAAGTGTAGACTTAAGGAAAAAACTCCACTGTCATGAAATGATGGTAGGAAAC  
AGACTTTGCTCTGTACAGAAGTAAGTAAAAGTAGGAATAGTTCCATGGATATTGTTATTTTATTAACCTTTT  
CAGTTCTTTTATTCAAAGAAAACAAAATTCAATCTGTGATAATATTGAGGTAAGTCCCTTCCATCTG  
CTCACTGAGTTATTAGGAAACAGAACGGAAAAGATTGTCAAAATAAAAACAATAATTCAAGTAACATGCCGG  
AATATACTGCTTAACACCCCTCTATCAGCTGGATTCTATCCAAGTGTACTTATGATGATGTATGTTCA  
TTCAAAGAATGGGAAAGGATATGACATATTGCGACTTCTGAGGTTACTTCATTCAGGTTACCTTCCCTGTGAAG  
TTCAGAGTTACTGAAGATGCTTCCCTGGAGTTGACCCAAGAACATAGGTTATATTCCCAAATCTT  
TAATTATTGAGTGAAGAGCTATAGTGAATTGATGAAAGACCGTATCTCATTTCTGTGAGTAGAAGGAAA  
GATAAGAATGAGGAGCAGATTTCCTCTGAAATTACACATAAGGACACTAACAGAATTTCAGGTAATG  
TGCCTTGTGGCTTGGCATGATAAGATTCTTATTAAATATGAGAGAAATTGTTTATCCTTATATT  
CTCTCAATATCAGAACCTCTGAAATTGAGATTGCCCTCCCTCCATTAAAGGATTGATGGATGTAAGATGGA  
ATAAAATACAGTCTTCAATTGAGAAAATCTGACATTAGTTAATGTTACTGTATTCTTGGAGTTGA  
GGCACTTACATAACAACTTCTTGTCTTTGGAGATAAAACCAACAGAGGTGAGGCCAGCTAGTAATCC  
TTTGTGGAAAGGATATGTTAGGAGAACAGCAATTACCTTCACCTGGAAACTGATCACTTCACATGCC  
ATTAATAAAACCAAGATCTTTAAATCAAACACCAATTGCTGAAAGACCTAATTCTAAATCAAGGTG  
AAATTGAAACAGAACAGATGGTTCAAGTAAAATTCTCATCTGGCTCCCTGCTGTTAGTAACAGTCACCCAAATGTT  
CTAAGCAACTACTTCTTAGAGTATCATTGCAACAAAAGGCTTCAAGAGGTGTAATGGATCTCAAGGATA  
AGTGTAAACAGTTGGCAACATCCCTAAAACCTGAGTCTGATGCCATCCAGGATGTGAGTGGTCTGAAGAT  
TCCCTAAAGAAATTCTCAAAAGTAACCGAATCAGCATTGCAACAGAGGTGAGTGGTCTGAAGAT  
ACATTCCCAAATAAACGACCTAGGCTAGAAGATAAAAAAAA

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**FIGURE 78**

MDDDLMLALRLQEEWNLQEAEERDHAQESLSLVDAWEVDPPTPDLQALFVQFNDQFFWGQLEA  
VEVKWSVRMTLCAGICSYEGKGGMCIRLSEPLLKLRPRKDLVETLLHEMIHAYLFVTNNKD  
REGHGPEFCKHMHRINSLTGANITVYHTFDEVDEYRRHWWRCNGPCQHRPPYYGYVKRATNR  
EPSAHDYWWAEHQKTCGGTYIKIKEPENYSKKKGKAALGKEPVLAENKGTFVYILLIFM

**Important features of the protein:****Signal peptide:**

amino acids 1-41

**N-glycosylation sites.**

amino acids 148-151, 217-220

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 184-187

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 121-124, 154-157, 187-190, 192-195

**Tyrosine kinase phosphorylation site.**

amino acids 211-218

**N-myristoylation sites.**

amino acids 59-64, 85-90, 146-151

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 108-117

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**FIGURE 79**

CGGACGCGTGGTGGCAACCAGGAGAACGCCAAACTGGTCCCCGGCTCGCGGAGTGCGCTGCG  
AGCGGTGCTATGGCGCTCTATGAGGTCTTCTCACCAGGCTGAGCGCAGTTACCGCCGG  
GCTCTGCTCCAAGCCGCGCTGTTCTGCTGCTGGCGCTGCGCTACGTACATCCCAGGCG  
GCTGGTGGCCTCCGGAGCCACGGGTTTGGCTGAAGCGGAGCAGCTACGAGGAGCAGCCGAC  
CGTGCCTTCCAACACCAGGTGCTGCTCGTGGCCCTGCTCGGACCCGAAAGCGGACGGTTCT  
CGCCTGGAGCACGTTCCCGCTTCACCGGCTGCAAGGGGATCGCCTGCGCTCCCGCTCGT  
TTCGACTAGAGAAGAACAGGAACAGGATGGGAAGACGGACATGTTACATTAAAGCTGGA  
GCTTCCCTGCAGTCCACGGAGCACGTTCTCGGTGTGCAGCTCATCCTGACTTTCTCCTATCG  
ATTACACAGGATGGCGACCCCTCGTGATGCAGAGCATGGCGTTCTCAGTCCTCCTTCTGT  
CCCGGGATCCCAGTTACGTGAACGGAGACCTGAGGCTGAGCAGAAGCAGCCGCTGAGCTG  
TGGTGGCCTAGATGCCGATAACACATATCCGTGATCAACGGGACCAAGCCCCTTGCCTATGA  
CTACGACCTCACCCATATTGTTGCTGCCTACCAAGGAGAGAACGTTACCAACCGCCTGAATGA  
TCCCAACCCCATCTGGCTGGTGGGCAGGGCCGAGATGCTCATTGTTGATTAATGCTATCAT  
CCGATACCCCTGTGGAAGTCATTCTTATCAGCAGGATTCTGGGAGATGGTAAAGTTGCCCTG  
GGTACAGTATGTCAGCATCCTGTTATCTCCTCTGGGTGTTGAAAGAATCAAGATCTCGT  
GTTTCAGAATCAGGTGGTACCACCAATTCCGTGACAGTGACGCCCGGGAGACTTGTGAA  
GGAGCACTTACTAGAAAGGCCATTCTGAAGACTCAGCAGGACCGTGGCTGCCCTATTGTC  
ATCTCTGGGAACATCTTAGGACCTTTGAAAGAGGCCAGCGGACACCTGCGGGCTGTGTC  
TTTCCTCAGAGACAACGGTTCTTCCGGTTTGCTCTACACAGTCCGTATCTCAGAGCT  
CCTGAGAATTGTCAGGGACTAGTTGTTGAAAGGTCTGAGAGTTCTGGAGGCTATAATTAG  
CTTTTGGGTTTCTTCTTGCTTAGCCTGAATTTCAGGAGAAAATTGCACTGAGTCAGTTCA  
ACATCTTGGAAAGAGTCCCATTCTCTGGTCAAGCAGAGACTTTCTCTGTTGAAC TGAGAAC  
ACACTGTGCAATTCTTCTCTGTTGAGGCCACTCTTACTCTTTCAAGGGCTCTTGAC  
AAACATGCCAATCACTAGCACTTGCACCCCTGGGCTTCTCCATTCCATTACAGCTTGAC  
TTTCCAGAGCTGAGGCCTTAACTGGAGACCTGGAGGGCAGGGCCAAGGGCAAGGGCCGCA  
TTAGCACAGGCAATCAGGGAGGGCCGCTGAAGGACACTGGACCGTCCACCTGCCCAAGGCCA  
ACAGTCAGTCATGTCATCAGCTCAGCTGAGCAGCCCTGGATTTGCCGTACTGTGACTGG  
GCTCTTGCCTATTTCCTCTGTCGTGCCCCCTGGATGGCAGGCTGAAGTCAGAGGGCT  
GTTTCATTCTCAGCCCCCTCAGCAGCACTGGGAGAAAGCATTGTCACAACAGGTTCTTC  
TGGCCCTCACCAACAGCCTGGGCACTGGCCCTCCTCCTGACAGCCCTCCCCCTTCC  
GCAAAGGACAGGGCGACAGGGTTGGTGTGGATTGGCTCCGCTGCCGTACAACCACAAG  
TTTATTGGAAAGCTAGCAGGGAAAGCCAGCGGCTGGCGTTCCCTGACTAAGGAACAGGGT  
CCCATCAGAGTGGGCGGGCAGCTTGGGAAGGACACAAGAACGAGTAAGAGTGTAAAGAGGA  
TGCTGGCCTGGCAGGCCAGTCCAGCCTGGCCACTAGCAGAATACCAAGCAGTCCAGTGGATT  
ACCCTCGTGGCTAAGCAAGTGTCTGCAGGAGCAGAGATGGCTGGAAAGGGGCTCTGCACACGG  
AAGATGGCTTGTCAAGCCATTCACTCAGGATGTGGCAGTCTCCTCCAAGAACACATG  
GAGCTGCTTCTGATCCAAGCAGGTCACTGCCACTGGAAAGGACATGGCCCGGTGATCCATG  
CTTCATGCCACCCAGAAACACACCCCTCAGTGTGCGCTCAGTTACTTGGAGATCAGTTG  
TCGTTTTAGTGTCTCTTCTAGGCTTACTAAACAGTTTGGAAACAAAGCTATTGAAAGTAT  
TCAAGCAGAGGAATTCCCTAACACTGACCCCTGTCTTTTTAATATTCAAGGCTGTTTAT  
ATGCCTAAATTCTTAAGATCTAAACGAAAAATAGTTCTGTTAAATTCAACATAAGG  
CAATGAGATATGAAAGATGACAAGATACGTATAACACATTGGTTGCATCTTATTAAATTATT  
CTAATGCAAATCTGTATAAGAACCCATGATGTTGTAACTTTCTAATTAAATGTTCAAA  
ATGAG

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**FIGURE 80**

MALYEVFSHPVERSYRAGLCSKAALFLLLAAALTYIPPLLVAFRSHGFWLKRSYYEEQPTVRF  
QHQVLLVALLGPESDGFLAWSTFPANRLQGDRLRVPLVSTREEDRNQDGKTDMLFKLELPL  
QSTEHVVLGVQLILTFSYRLHRMATLVMQSMAFIQSSFPVPGSQLYVNGDLRLQQKQPLSCGGL  
DARYNISVINGTSPFAYDYDLTHIVAAYQERNVTTVLNDPNPIWLVGRAADAPFVINAIIRYP  
VEVISYQPGFWEMVKFAWVQYVSILLIFLWVFERIKIFVFQNQVVTTIPVTVTPRGDLCKEHL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 268-284

**N-glycosylation sites.**

amino acids 194-198, 199-203, 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 51-55

**Tyrosine kinase phosphorylation site.**

amino acids 250-259

**N-myristoylation site.**

amino acids 187-193

**Cell attachment sequence.**

amino acids 307-310

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**FIGURE 81**

GCCGGGAGCTTCCCTGATGGTGCCGCCCTCCGAGCGGGGAGGAGCTGCCAGGGCCAGCTGGGCAGGAGCCT  
GGGTCCGCTGCTGCTCTGGCGTTGGGACACACGTCGACCTACAGAGAGGAGCCGGAGGACGGCAGACAGAGA  
AATCTGCTCAGAGAGCAAAATCGCGACGACTAAATACCGTGTCTGAAGTCTTCAGCGAGCTCACCATGCTA  
CAGGAAAAAGTGCTCAAAGGATAATAATTGTTCTTGACATGCCAGAACAGATTACGACGTTGTGCCGA  
GGCTCCCTGTGAACAGCAGTGCACGGACAAGCTTGGCCAGTGTACTTGTATCCGGGATACCGATATGA  
CCGGGAGAGACACCGGAAGCGGGAGAACGCCACTGTCTGGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT  
GTGTGCCACATCTGCATCAATAACCTTGGCAGCTACCGCTGCGAGTGCAGGGAGGCTACATCCGGGAAAGATGA  
TGGGAAGACATGTACCAGGGGAGACAAATATCCAATGACACTGCCATGAGAACGACTGAGAACATGGTAAAGC  
CGGAACTTGCTGTGCCACATGCAAGGAGTTCTACCAGATGAAGCAGACCGTGTGCAGCTGAAGCAAAAGATTC  
TCTGCTCCCAACAAATGCACTGACCTGGCAAGTATATCACTGGTACAAGGTGCTGGCCTCAAACACCTACCT  
TCCAGGACCTCTGGCCTGGCCTGGGGCCAGGGCCCTCCGGCTCACCAAGGACAAAGGGAGGCCAGGCTTCCC  
CCGATGCCAGGCCCTCTGGGAGGGGGCTGTGGTCAACAGGGCTCAATGGGACCCATGGGACCATCTCTGATCTGTC  
CCACATTAAGCAAGGGCGAGGGGGCTGTGGTCAACAGGGCACAGGAAGAGATGGTTCTAAGGGGGAGAG  
AGGAGGCCCTGGGCCAGAGGTCTCCAGGACCCCCCTGGTCTTCACTTCTGACTTATGGCTGACAT  
CCGCAATGACATCACTGAGCTGAGAAAAGGTGTTGGCACCAGACTCTAGGAGATGACATCCAAGAAGAACTGAGAC  
ACCTCAGGAATTCCCAGCTACCCAGAACGCCATGGACCTGGGCTCTGGAGATGACATCCAAGAAGAACTGAGAC  
AAGAGACTTGAGAGCCCCAGAGACTTCAACCAATAGCACATCCAAACACCGTACGCCAAAGGAAGAGAAAGAT  
CAACTCACCTGCAGTTAACCATCTAAAGAGAACGACACTGGAGACCTAGAAAACATACATTTCTTCTC  
TCTTCTCTGACGTCCTCCACTCTCTCCTCAAATACGATGCTATTTCAAGAGTCCCTCTAGGCCTGCAG  
ACATGAGGGAGTGAATTGATTACCTGCTTCACTAAAGAGTCCATTGGGGTGGTTGCATTGTAACTTTT  
TTTACATCTATTTCAGGAATTGGATTAAAGTACTCTCACAGTGTCTTAAATCATAAATTCTGAGTT  
AAATTGGCAGAGTATCAAAAGGGGAAAATGACAAAGTGAAGCTTAAGAAAATGAGGCTACTTCTAAGATGT  
GTGTTACAATAGACCAACTCTTAGTATCAAATTGGGCTCTCAGTTAAAAGGGGGAGGAGACAAA  
CGTGTGATGTGTTGGGAGAATTTCCTGTGCTTCTAGTAGACTTAAATATTGTATCCCTTGTCAA  
ACCTTGTTCACAAATTCAATTAAAGAGAGGAGAACATTGAATGGCTTAGAGAACATAGAAAAGAACATCACAGT  
CATATATTAAGTGTATAGATGCCACATTCTAAATACGGTGTCAAGGTTTCAGCCATGCTTAT  
CTGTAAGTATCTATTAGGGAGAACGATTAACACTCTCTTCAAAACAAAGTGAATGCTGGATTACAT  
TAAACAAATGGGCTCTGTTGCTATAATTAAAGCTTTAATCAACAGTGGAGCTGCTCTATAAAATATA  
GATTATTGTTCAATAAAACTGGCTGAGCTTAGAGAGAGGTGAGAACATTCTGTTCTGAGCAGGTGCCAGAAGG  
TACCATTAGGTGCCATGATCCAGGCTGAACCAATATACAGTGGGCTGAAGTCTGCAAGGAGGGTGTGGCTTGG  
GCTGACCTCACTAATGCCATCAGCAGCGTAGGTAAATTCTCTGGTATTACAAGTTTGTCTGGAGC  
CAACCAAGCTGCCACCAACATATTGAGAGTAATACACTATTGAAAGTTATCTGATGGGAGAAAAAAAATA  
GTGGTTTCTCTGTTGCAAAAACCTCTCTATTCTCATTTTCTTAATTCTTAATTAGTCAAGTTC  
CAGTCTTTAGGCCCTCTTTGATTATTCTCTGATGTGAGAACAGCTCAGAAAAAGGTCTATATCTC  
CACCTCTAGTGAAGTAGTGTCTCAGAGCACCTCTGGGGCAAAAGGGAGCATGTTCTGCCAAGGTT  
GCTGTGGATTCAAGACACCAGGAGCAAGAGACCAAGAGGATGATCTGCTCCCTGTAACTGTTGAGGGCCCT  
CTGTTTCAATGAGCAGCTTATAGGTTACTCACAGTCACTTCTCACTGGACACACAAAGTGGCTTTATCT  
ACCTTGCAGGGAGATTCACTCTCTGCAAATGATGCTCTCACACTCATATTAGCTCATGTTGAAATTCCCA  
TCCTGCCATGCTCTTCCCATTCTTTGGCTTTTGCTCCACCTTTAGCCACATCATTAACCTCACTA  
CTGTGAAAGCTGCTAAAGAAAATCCCTCTGGCCGGGTGTGGTAGGCCACGCCCTCAATCCAGCACTTGG  
AGGCTGAGGCCGGAGAGTACAAGGTCAAGGAGATCGAGAACAGCCTGACCAACATGGTAAACCCCTGTCTACT  
AAAAATACAAAAATTAGCTGGCGTGTGGCACACACCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAA  
TTACTTAAACCTGCAGGGGGAGCCTAGATTGCGCTACTGCACTCCAGCCTAGGCAACAGAGGGAGACTCTGCTC  
ATTAAAAA

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**FIGURE 82**

MVPPPSRGGAARGQLGRSLGPLLLLALGHTWTYREEPEDGDREICSESKIATTKYPCLKSS  
GELTCYRKCKGYKFVLGQCIPEDYDVCAEAPCEQQCTDNFGRVLCTCYPGYRYDRERHRK  
REKPYCLDIDECASSNGTLCAHICINTLGSYRCECREGYIREDDGKTTRGDKYPNDTGHEKS  
ENMVKAGTCCATCKEFYQMKQTVLQLKQKIALLPNNAADLGKYITGDKVLASNTYLPGPPGLP  
GGQGPPGSPGPKGSPGFPGMPGPPGQPGPRGSMGPGMPGPSPDLSHIKQGRRGPVGPPGAPGRDG  
SKGERGAPGPRGSPGPPGSFDFLLLMLADIRNDITELQEKVFGHRTHSSAEEFPLPQEFPSPYR  
EAMDLGSGDDHPRRTETRDLRAPRDFYP

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites.**

amino acids 142-148, 182-188

**Tyrosine kinase phosphorylation site.**

amino acids 125-132

**N-myristoylation sites.**

amino acids 10-16, 143-149, 155-161, 196-202, 250-256

**Amidation site.**

amino acids 299-303

**Aspartic acid and asparagine hydroxylation site.**

amino acids 150-162

**Cell attachment sequence.**

amino acids 176-179

**C1q domain proteins.**

amino acids 247-280

**Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 144-165

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**FIGURE 83**

ATCTGAGTGAGCTAACTGACACAATGAAACTGTCAGGCATGTTCTGCTCCTCTCTGGCTC  
TTTCTGCTTTAACAGGTGTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGTTCCAGG  
ACCCCAGGTCTACTGCACTCGGAATCTAACCCACACTGTGGCTCTGATGCCAGACATATG  
GCAATAATGTGCCCTCTGTAAGGCCATAGTGAAAAGTGGTGGAAAGATTAGCCTAAAGCATC  
CTGGAAAATGCTTGATTAAAGCCAATGTTCTGGTGACTGCCAGCTTGCAGCCTCTT  
TCTCACTCTGCTTATACTTTGCTGGGATTCTTAATTCATAAAGACATACCTACTCTG  
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTCTCTGATTCACTGTCAATAAGTACATTC  
TGCAAAAGCAAAA

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**FIGURE 84**

MKLSGMFLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNPHCGSDGQTYGNKCAFCK  
AIVKSGGKISLKHPGKC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 26-32, 52-58, 56-62, 69-75

**Kazal serine protease inhibitors family signature.**

amino acids 40-63

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**FIGURE 85**

GGAGCAGACACACAGACCCGGGCCGAGGCCCTCTTAGCCCTCGGGAACCGGACAGTTC  
CCCAACTGGGACTCTGGAACCACAGCTCCTAAATCATCAAATTCTCAAGCTTTTTCCC  
TCTCTCGTCCCAGCCATCCCAGTCTTCTCTTTTTTTAACTATTGTTTTT  
TCGCTCTGTCAATTGAAAGTGGTACGCCATTCAATATAAGACTTGGAGGGATTGGGA  
AAGAAAAGAAGAATCTAAAAGAAGAGAAGCGACCGGTGCTTTAAGGGTGTCAATTTC  
AAGAGACGTCTGGGAGTATTTGCTCTGGCGTTGGAGCAACTTCGCGGACAGCGGAGCTG  
CCCAGCATGGATGTTCCAGGTTCACAGGCCTTCTCTGAGAACGACCCGGCTTGAAACG  
TCAGAGCCGGGAGCAAGGCCCGGAGGCTGCTGGAGCTCCGGCGTCCCTCGGCCCTT  
CCGCGCCGCTCGCGCCGGCGCCCTCACCCCCCGCGCCCTCCACCAGTCCCATGC  
AGGCGCCCGGCCGGGGGGCACTCGGCTGCGGCTGATGATGCCCGGGCGCCGGGGGCGCTGC  
GCGAGCCTGGCGCTGCGGATCCTGCGCTGGGGTGGCGCTGGCCCTGCTGTTGCTGACTGC  
CCGCGCTGCGCCCGTGCAGGCGAGAACGACACGGAGCCATCGTGTGGAGGGCAAGTG  
TGGTGGTGTGCGACTCCAGCCGTCGGCGAGGGCGCCGTCACCTCCTCCCTAGGCATCTCG  
TGCCTCCGGCAGGCCAACGGTGGCCTCTCCGCCACGCGGAGCACCACGAGCCGTC  
AGATGAGCAACCGACCATGACCATCTATTGACCAAGGTATTAGTAAATATTGGCAACCA  
TTGATCTGCTTCCAGTATTTGATGACCGAGAAAAGGGATTATAGCTCAGCTTCCACG  
TGGTCAAAGTGTATAACAGACAAACCATCCAGGTAGTTAATGCGAAATGGCTACCAAGTGA  
TCTCGCCCTTGCAAGGAGACCAGGATGTCACCAGAGAACGCTGCTAGCAATGGCGTGTG  
TCATGGAAAGGAAGACAAAGTCATCTCAAACCTGAGAGAGGGCAACCTATGGGGGCTG  
AATACTCCACATTCTGGGCTTCTGGTGTTCCTCTAAAACACAGAGCCCTAGATGGT  
GGGAATGGCAAACCTGGACCCAGGACTCGCCCTTAAACACCCCTGAACCTACTGGAAATTGG  
ACACCTGTTCCAACCTCCGTAGACTGTTGAGTAGAAGAACGATGTTCCCTTGAAACCTCC  
AGTACTTTGTTTGGAAACTTGACAATTCTCGGGAACCTGGCCCTTAATTAGT  
TTTAGATGACAAGGTCTAAGGAGAAATGAAATTATCGATTGAGCAATTGTAACCTGTGATT  
GTAAAGTCATATCGGATTATTGTTGGGACCATGGACCTCTTTGTTGTTGATGTTGATTG  
TCGTCCAACGGAAGGAGAGCTCTGACTCCAGGATGGCTGAGGTGAGTCAGGGCTTG  
AGTAGGAGCCCAGCAAAGAACCACCTGCTGGACAGTCCTGACATGTGTTCTGTGTC  
TATAGCCTTAAGAAAAAGAATGGCTCACTTCATTCTGATTCTCCCCCACCAGTGGCT  
GGGAGGACTTGGGAGGGGATGGGACATTGGAACCTGTCAAGAACGTTATCCAGAGAA  
GCAAATTTCGACGATTGGACTGCAATTGGTATTGTTGTTGTTTCTTGAAAG  
CTTACTTTCTTCCACACTCAGCTCTCCCTCTCAACCCACTTTATTCTGCTGG  
GTTGAGGAGAGAAAATATAGAATTCTGGATAAGACCAACAAAACATTTAAACACT  
GTATGTTGTTAGACGAGACCAAACAAACAAAAGTATCTGTTATCAAAGTAAAGTA  
ACACAATGGACAATTCTGCTTATCTCAAAGAGATTCTAAGATGCACTTAACTTAA  
ATAGCAACCTGCAATTGTTTAATTATAGTCACTTCAAGAACCTGGTGTCTG  
GTGGTCCTGAATCATATAAGTGGTAATGGAAGCTGTAATGACCAAGTCCCCTAAACATA  
TGTCTTGCCACGTGTGACTCTCTGTTGGGTGATTAAATTGATGGACCTCC  
AGTGAGCGCACAGTGATCAGGTGCTTCAAAGCCAACAGACAGCTCCTCTCCGGATC  
CTTTGATCTGCCAGGAAGGGATGCATTGACACTCTCTGCATGCACCTGGGAGAACCCA  
CCTGAAAGTCAGTGGTTAAAGATATTGGTGGAGGTACCCAGGAGCACTGTTACAAATC  
TCTTGTTGGCATCTGTACAACATTAAAGACACAGCTGAGAGGTTGATGGGTGTG  
CATATGCCAAGGAAATGTCATAATCCAAAGCAATCAAAAGGAGACCTCAAACCA  
AATTGTTCTTGTGTAACAAATGTAACCAAAATTGATGATAAAAGTCATAATTAA  
AGAATAAAATGGGTTGATGTCGGAAAAAAAAAAAAAA

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**FIGURE 86**

MQAPGRGPLGLRMMMPRRGALREPGGCGSCLGVALALLLLPACCPVRAQNDTEPIVLEGK  
CLVVCDSSPSADGAVTSSLGISVRSGSAKVAFSATRSTNHEPSEMSNRTMTIYFDQVLVNIGN  
HFDLASSIFVAPRKGIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQDVTRREAASNGVL  
LLMEREDKVHLKLERGNLMGGWKYSTFSGFLVFPL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation sites.**

amino acids 53-57, 110-114

**N-myristoylation sites.**

amino acids 26-32, 27-33, 29-35, 33-39, 76-82, 205-211

**Amidation site.**

amino acids 16-20

**C1q domain signature.**

amino acids 117-148

**C1q domain proteins.**

amino acids 115-149

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**FIGURE 87**

AGGGCCCGGGTGGAGAGAGCAGCCCCGAGGGGGATGGCGGCAGCGTCCCAGCGCCTCTG  
GCTGGCGCTACTGCTGCTGGCACTTGGCAGCAGCGCGGCCGGCTCCGGCGTCTTCC  
AGCTGCAGCTGCAGGAGTTCAACAGAGCGCGCGTACTGGCCAGTGGCGGGCTTGCGAGC  
CCGGCTGCCGGACTTCTTCGGCTGCCTTAAGCACTTCCAGGGCTCGTCTCGCCCGGAC  
CCTGCACCTTCGGGACCGTCTCACCGCGTATTGGCACCAACTCCTCGCTGTCCGGGACG  
ACAGTAGCGCGGGGGCGAACCCCTCTCAACTGCCCTCAATTTCACCTGGCCGGTACCT  
TCTCGCTCATCATCGAAGCTGGCACCGCCAGGAGACGACCTGCAGGCCAGAGGCCTGCCAC  
CAGATGCACTCATCAGCAAGATCGCCATCCAGGGCTCCCTAGCTGTGGTCAGAACTGGTAT  
TGGATGAGCAAACCAGCACCCCTACAAGGCTGCCTACTCTTACCGGGCATCTGCAGTGACA  
ACTACTATGGAGACAACTGCTCCGCTGTGCAAGAAGCGCAATGACCAACTCGGCCACTATG  
TGTGCCAGCCAGATGGCAACTGTCTGCCCTGGACTGGGAATATTGCCAACAGC  
CTATCTGTCTTCGGGCTGTCACTGAACAGAAATGGCTACTGCAGCAAGCCAGCAGAGTGCCCT  
GCCGCCAGGCTGGCACGGCCGGCTGTGTAACGAATGCATCCCCAACATGGCTGTGCCACG  
GCACCTGCAGCACTCCCTGCAATGTACTTGTGATGAGGCTGGGGAGGCCTGTTTGACC  
AAGATCTCAACTACTGCACCCACCACCCCCATGCAAGAATGGGCAACGTGCTCCAACAGT  
GGCAGCGAAGCTACACCTGCACCTGCGCCAGGCTACACTGGTGTGACTGTGAGCTGGAGC  
TCAGCGAGTGTGACAGCAACCCCTGTCGAATGGAGGAGCTGTAAGGACCAGGAGGATGGCT  
ACCACTGCCTGTGCTCTCGGGCTACTATGGCTGCACTGTGAAACACAGCACCTTGAGCTGCG  
CCGACTCCCCCTGTTCAATGGGGCTCTGCCGGAGCGAACCGGGGCCAACTATGCTT  
GTGAATGTCCCCCAACTTCACCGGCTCCAACGCGAGAAGAAAGTGGACAGGTGCAACAGCA  
ACCCCTGTGCAACGGGGACAGTGCCTGAACCGAGGTCCAAGCCGATGTGCCGCTGCCGTC  
CTGGATTACGGGCACCTACTGTGAACTCCACGTCAGCGACTGTGCCGTAACCTTGCGCC  
ACGGTGGCACTTGCATGACCTGGAGAATGGCTCATGTGCACCTGCCCTGCCGGCTCTG  
GCCGACGCTGTGAGGTGCGGACATCCATCGATGCCGTGCCCTGAGTCCCTGCTCAACAGGG  
CCACCTGCTACACCGACCTCTCCACAGACACCTTGTGCAACTGCCCTATGGCTTG  
GCAGCCGCTGCGAGTCCCGTGGCTGCCGCCAGCTCCCTGGGTGGCGTCTGCTGG  
GTGTGGGCTGGCAGTGTGCTGGTACTGCTGGCATGGTGGCAGTGGCTGTGCCAGCTGC  
GGCTCGACGGCCGGACGACGGCAGCAGGGAGCCATGAAACAACCTTGTGGACTTCCAGAAGG  
ACAACCTGATTCTGCCGCCAGCTTAAAAACACAAACAGAAGAAGGAGCTGGAAGTGGACT  
GTGGCTGGACAAGTCCAACGTGGCAAACAGCAAAACACACATTGGACTATAATCTGGCC  
CAGGGCCCTGGGGGGGACATGCCAGGAAAGTTCCCCACAGTGACAAGAGCTTAGGAG  
AGAAGGCGCCACTGCGGTTACACAGTGAAAAGCCAGAGTGTGGATATCAGCGATATGCTCC  
CCAGGGACTCCATGTACCGAGTGTGTGTTGATATCAGAGGAGAGGAATGAATGTGTCATTG  
CCACGGAGGTATAAGGCAGGAGCCTACCTGGACATCCCTGCTCAGCCCCGGCTGGACCTTC  
CTTCTGCATTGTTACA

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**FIGURE 88**

MAAASRSASGWALLLVALWQQRAAGSGVFQLQLQEFINERGVLASGRPCEPGCRTFFRVCLK  
HFQAVVSPGPCTFGTVSTPVLGTONFAVRDDSSGGGRNPLQLPFNFTWPGTFSLIIEAWHAPG  
DDLRLPEALPPDALISKIAIQGSLAVGQNWLLEQTSTLTRLRYSYRVCISDNYYGDNCNSRLCK  
KRNDHFGHYVCQPDGNLSCLPGWTGEYCQQPICLSGCHEQNGYCSKPAECLCRPGWQGRLCNE  
CIPHNGCRHGTCTPWQCTCDEGWGGLFCQDLNYCTHSPCKNGATCSNSGQRSYTCTCRPG  
YTGVDCLELSECDSNPCRNNGSCKDQEDGYHCLCPPGYYGLHCEHSTLSCADSPCFNNGSCR  
ERNQGANAYACECPNPFTGSNCEKKVDRCTSNPCANGQCLNRGSPRMCRPGFTGTYCELHV  
SDCARNPACAHGGTCHDLENGLMCTCPAGFSGRCEVRTSIDACASSPCFN RATCYTDLSTDTE  
VCNCPYGFVGSRCEF PVGLPPSF PWVA VSLGVGLAVLLVLLGMVAA VRQLRLRRPDDGSREA  
MNNLSDFQKDNLIPAAQLKNTNQKELEVDCGLDKSNCGKQQNHTLDYNLAPGPLGRGTMPGK  
FPHSDKSLGEKAPLRLHSEKPECRISAICSPRDSMYQSVC LISEERNECVIATEV

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 530-552

**N-glycosylation sites.**

amino acids 108-112, 183-187, 205-209, 393-397, 570-574, 610-614

**Glycosaminoglycan attachment site.**

amino acids 96-100

**Tyrosine kinase phosphorylation site.**

amino acids 340-347

**N-myristoylation sites.**amino acids 42-48, 204-210, 258-264, 277-283, 297-303, 383-389,  
415-421, 461-467, 522-528, 535-541, 563-569, 599-605, 625-631**Amidation site.**

amino acids 471-475

**Aspartic acid and asparagine hydroxylation site.**

amino acids 339-351

**EGF-like domain cysteine pattern signature.**amino acids 173-185, 206-218, 239-251, 270-282, 310-322, 348-360,  
388-400, 426-438, 464-476, 506-518**Calcium-binding EGF-like:**amino acids 224-245, 255-276, 295-316, 333-354, 373-394, 411-432,  
449-470

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**FIGURE 89**

GTCTCCCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCCTTACCTGGAGAC  
TTGACTCCCGCGGCCCAACCTGCTTATCCCTGACCGTCAGTGTCAGAGATCCTGCAGC  
CGCCCAGTCCCAGGCCCTCTCCGCCAACACCCACCCCTCCTGGCTTCTGTTTACTCC  
TCCTTTTATTATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGCTGTGACCCAAGCC  
GAGCGTGGAAAGAATGGGGTTCTCGGGACCAGGCACTGGATTCTGGTTAGTGCTCCGATT  
CAAGCTTCCCCAACCTGGAGGAAGCCAAGACAATCTCTACATAATAGAGAATTAAGTGCA  
GAAAGACCTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAACATATCCT  
CCAGAAAACAAGCCAGGTCAAGCAACTATTCTTTGTTGATAACTGAACTGCTAAAGGCA  
ATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCAC TGATAAT  
AAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACGTATCGATGATTATGACTCT  
ACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTTCATCAACTAGACGGG  
ACTCCTTAACCGCTGAAGACATTGTCATAAAATCGCTGCCAGGATTATGAAGAAAATGAC  
AGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTGGCCTTATCACAGAAAGCCAA  
GCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAATTAACTCAAAGGAAGCCAAC  
AATTATGAGGAGGATCCAAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCA  
GAGAAAGTGAATGCAATGGCAGCAATTCAAGATGGCTTCTAAGGGAGAAAACGATGAAACA  
GTATCTAACACATTAACCTGACAAATGGCTGGAAAGGAGAACTAAAACCTACAGTGAAGAC  
AACTTGAGGAACCCAATATTCCAAATTCTATGCGCTACTGAAAAGTATTGATTGAGAA  
AAAGAAGCAAAGAGAAAGAACACTGATTACTATCATGAAAACACTGATTGACTTGTGAAG  
ATGATGGTGAATATGGAACAATATCTCCAGAAGAAGGTGTTCTACCTTGAAAACCTGGAT  
GAAATGATTGCTCTCAGACCAAAACAGCTAGAAAAAAATGCTACTGACAATATAAGCAAG  
CTTTCCCAGCACCCTCAGAGAAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAAGCAGCT  
AAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAGATGATAACTCCAACCCAGGA  
GGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTGGAAGCCATCAGAAAAATATT  
GAATGGTTGAAGAAACATGACAAAAGGGAAATAAGAAGATTATGACCTTCAAAGATGAGA  
GACTTCATCAATAACAAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAAGAAGCC  
GAGGCCATCAAGCGCATTATAGCAGCCTGTAAAATGGCAAAGATCCAGGAGTCTTCAAC  
TGTTTCAGAAAACATAATATAGCTTAAACACTCTAATTCTGTGATTAAATTTTGACCC  
AAGGGTTATTAGAAAGTGTGAATTACAGTAGTTAACCTTTACAAGTGGTAAACATAGC  
TTTCTCCCGTAAAACATCTGAAAGTAAAGTTGATGTAAGCTGAAAAAAAAAAAAAAA  
AAA

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**FIGURE 90**

MGFLGTGTWILVLVLPPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEDKIKKTYPPENK  
PGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSG  
LDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTL  
EDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPFKVTPMAAIQDGLAKGENDETVSNT  
LTILTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVK  
YGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEAAKMEK  
EYGSLKDKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKEDYDLSKMRDFIN  
KQADAYVEKGILDKEEAEAIKRIYSSL

**Important features:****N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390**N-myristoylation sites:**

amino acids 143-148, 239-244

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**FIGURE 91**

TGCTCATGGCCCAGGCAAGCCCAGGAGTTGACATTCTGCCAGCCATGGGCCTCACCC  
GCTCTTGCTGCTCCTGGGACTAGAAAGGTCAAGGGCATAGTGGCAGGCCCTCCCTGAGGTGCT  
GCAGGGACCCGTGGGAAGCTCCATTCTGGTCAGTGCACACTACAGGCTCCAGGATGTCAAAGC  
TCAGAAAGGTGTGGTGCAGGGTCTTGCAGGGAGGGTGCCAGGCCCTGGTGCCTCAGCTGTGGA  
TCGCAGAGCTCCAGCGGGCAGGCAGTACGTTCTCACAGACCTGGTGGGGCCTGCTGCAGGT  
GGAAATGGTTACCCCTGCAGGAAGAGGATGCTGGCGAGTATGGCTGCATGGTGGATGGGCCAG  
GGGGCCCCAGATTTCACAGAGTCTCTGAACATACTGCCCCAGAGGAAGAAGAGAC  
CCATAAGATTGGCAGTCTGGCTGAGAACGATTCTCAGACCCCTGCAGGCAGTGCCAACCCCTT  
GGAACCCAGCCAGGATGAGAACAGCATCCCTTGATCTGGGTGCTGTGCTCCTGGTAGGTCT  
GCTGGTGGCAGCGGTGGTGTGTTGCTGTGATGCCAAGAGGAACAAGAATCCCTCCTCAG  
TGGTCCACCACGTCAGTACTCTGGACCGGCTGCTGAATTGCCCTTGGATGTACCAACACATTA  
GGCTTGACTCACCACTTCATTGACAATACCAACCTACACCAGCCTACCTCTTGATTCCCCAT  
CAGGAAAACCTCACTCCAGCTCCATCCTCATTGCCCTCTACCTCTAAGGTCTGGTCT  
GCTCCAAGCCTGTGACATATGCCACAGTAATCTCCGGAGGGAACAGGGTGGAGGGACCT  
CGTGTGGGCCAGCCCAGAACATCCACCTAACAAATCAGACTCCATCCAGCTAACGCTGCTCATCACA  
CTTTAAACTCATGAGGACCATCCCTAGGGTTCTGTGCATCCATCCAGGCCAGCTCATGCCCTA  
GGATCCTTAGGATATCTGAGCAACCAGGGACTTAAGATCTAACATGCCCTAACCTTACT  
AGGGAAAGTGACGCTCAGACATGACTGAGATGTTGGGAAAGACCTCCCTGCACCCAACTCC  
CCCACTGGTTCTTCTACCATTACACACTGGCTAAATAACCTAATAATGATGTGAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 92**

MGLLLLLLLEGQGIVGSLPEVLQAPVGSSILVQCHYRLQDVKAQKVWCRLFPEGCQPLV  
SSAVDRRAPAGRRTFLTDLGGGLLQVEMVTLQEEDAGEYGCMVDGARGPQILHRVSLNILPPE  
EEEETHKIGSLAENAFSDPAGSANPLEPSQDEKSIPLIWGAVLLVGLLVAAVVLFAVMAKRQ  
ESLLSGPPRQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 161-181

**N-myristylation sites.**

amino acids 17-23, 172-178

**Amidation site.**

amino acids 73-79

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**FIGURE 93**

GGCGCGCTTGCCTGGGCTCTCCGGAAAGGAGACGTGGCGCGGTGGGCCGGTGATACCCGGGCG  
CTTTATAGTCCCCTCCTCCCTCCACCTCCTCCTCCTCCTCCTGGGGCAGAG  
GAGGTTGTGGCGGTGGCTGGAGAAAGCGGGCGGAGGAATGGAGGAAGGAGGGCGGGCGTAC  
GGAGTCTGGTCCC GGCGGGCCGGTGTACTGGTCCTCTGCGGCCCTGGAGGCCTCCGGCG  
GCGGCCGAGCCCTCCTCAACTCAGCGATGACATCCCTTCCGAGTCACACTGCCCGCACCG  
AGTTCTCTGCCCCACAACGGAGTTTATATAAAGAAGATAATTATGTCATCATGACAAC TG  
CACATAAAGAAAAATATAATGCAACTTCCCCTTGTGACAAGTGGGGATGAGGAAGAAGAAA  
AGGATTATAAAGGCCCTAACCCAAGAGAGCTTTGGAGCCACTATTTAAACAAAGCAGTGT  
CCTACAGAATTGAGTCTTATTGGACTTACGAAGTATGTCATGGAAAACACATTGGCAGTACC  
ATGAAGAGAAAGAAACTGGTCAGAAAATAAATATTACAGAGTACTACCTGGGAATATGTTGG  
CCAAGAACCTCTATTGAAAAGAACGAGAACGAGAAGAAAAGGAAAATCAAATGAGATT  
CCACTAAAATATCGAAGGTCAGATGACACCATACTATCCTGTTGGAAATGGAAATGGTACAC  
CTTGTAGTTGAAACAGAACCGGCCAGATCAAGTACTGTGATGTCATATGTCATCCTGAAT  
CTAACGATGAAATTCTTCAGTAGCTGAAGTTACAACCTGTGAATATGAAGTTGTCAATT  
CACCACTCTGTGCAGTCATCCTAAATATAGGTTAGAGCATCTCTGTGAATGACATATTT  
GTCAATCACTGCCAGGATCTCCATTAAAGCCCCCTACCCCTGAGGCAGCTGGAGCAGCAGGAAG  
AAATACTAAGGGTGCCTTTAGGAGAAATAAAGAGGGTTCGGTTGGTGGAAATATGAATTCT  
GCTATGGCAAACATGTACATCAATACCATGAGGACAAGGGATAGTGGAAAACCTCTGTGGTTG  
TCGGGACATGGAACCAAGAACGACATTGAATGGCTAAGAAGAAATACTGCTAGAGCTTATC  
ATCTTCAAGACGATGGTACCCAGACAGTCAGGATGGTGCACATTATGGAAATGGAGATA  
TTTGTGATATAACTGACAACCAAGACAGGTGACTGTAAAACCTAAAGTCAAAGAATCAGATT  
CACCTCATGCTGTTACTGTATATGCTAGAGCCTCACTCCTGTCAATATATTCTGGGGTTG  
AATCTCAGTGTAAATCTTAGATACAGCAGATGAAATGGACTTCTCTCCCCA  
ACTAAAGGATATAAGTTAGGGAAAGAAAAGATCATTGAAAGTCATGATAATTCTGCCC  
ACTGTGTCATTATAGAGTTCTCAGCCATTGGACCTCTCTAAAGGATGGTATAAAATGACT  
CTCAACCACCTTGTAATACATATGTGTATATAAGAGGTTATTGATAAAACTCTGAGGCAGAC  
ATTGTCTCGCTTTTTCACTTTGTGTCTTATAAAACTGACTGTTCTTGCTTGG  
TACTGTGATTCCAAAATACTCATCCAAGCAAGTTAGAGTCCAGCCTAATCAAATGTCA  
ATTGTGTTACCTATTGAAAGTTTTAAATAATAGATTATTATGTAATTATAGTATATGTAA  
GTAGCTAATGAAGTAAAGATCATGAAGAAAGAAATTGATAGGTGAAATGAGAGACCATGTAA  
AATATGTAAATTCTAGTACCTGAAATCCTTCAACAGATTAACTATAGCAACTGCTCTGC  
AAGTAGTTAAACTAGAAACTGGGCACATGGTAGAGGTCACATGGGAGTTGTCTCACCTTG  
TTAATCTCAAGAAACTCTTATTATAATAGGTGCTCTCTCAGAACCTTATCTATTACT  
TTTTCTTCTTATGAGTATGTTACTCTCAGAGTATCTGTGATGTAGACAGTTGGTGTG  
TTCTGAGACTCAGAATGGTTACTCTAACAAAACACTGTGCTGTATCCCTGTACTTGCT  
ACTGTAATATGGATTCACCTCTGAACAGTTACAGCACAATATTATTTAAAGTGAATAAAA  
ATGTCCACAAGCAAAAA

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**FIGURE 94**

MEEGGGGVRSVPGLVLCGLLEASGGGRALPQLSDIPFRVNWPGEFLPTGVLYKE  
DNYVIMTTAHKEKYKCILPLVTSGDEEEKDYKGPNPRELLEPLFKQSSCSYRIESWTYEVC  
HGKHIRQYHEEKETGQKINIHEYYLGNMLAKNLLFEKEREAEKEKSNEIPTKNIEGQMTPYY  
PVGMGNTPCSLKQRPRSSSTVMYICHPESKHEILSVAEVTTCEYEVVILTPLLCSPKYRFR  
ASPVNDIFCQSLPGSPFKPLTLRQLEQQEEILRVPFRRNKEGVGWWKYEFICYGKHVHQYHEDK  
DSGKTSVVVGWTWNQEEHIEWAKKNTARAYHLQDDGTQTVRMVSHFYGNGDICDITDKPRQVTV  
KLKCKESDSPHAVTVYMLEPHSCQYILGVESPVICKILDADENGLLSPN

**Important features of the protein:****Signal peptide:**

amino acids 1-30

**Glycosaminoglycan attachment site.**

amino acids 28-32

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 337-341

**N-myristoylation sites.**amino acids 6-12, 23-29, 29-35, 49-55, 141-147, 152-158, 192-198,  
196-202**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 54-60

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**FIGURE 95**

TTCCGTTCTGGAGGAGTGAGGGCAACGGTCGGAGAAAAAGGAAAAAAGAAGGGCTCAGC  
GCCTCCCCGCCGGCGTGGACAGAGGGCACAGTTCCGCAGGCGGTGAGGTCGCTGAGGG  
CCCGCCGGAGTGTTTCTTGTGAGCACGGTCAACCCCAGGTTACAGTCCCTGAGTCA  
TCTCATCAATGCCTCCATACACCAAAAAACACTTCTGTTCTCAGTGGAGTGTCAAGTTTC  
TCAAACCAGCATCGAGATGTAGTCCCTGAGCATGAGGTCCAGCAGTGAGCCTTCACTTAA  
CTTAAGGGACCTGGATTATCTGAACATAAAATTGGACAGATTGATCAGCTGGTAGAAAATCT  
ACTTCCTGGATTTGTAAGGCAAAACATTCTCCATTGGCATACATCCCAGTCTGC  
ACAATCCTCTTGAAAATAATGGTAACCTAGATATAATTAGTACATTACGTTCCCTTG  
CTTGTATCGACATCATTCAAGAGCTTCAAAGCATTTGTCAGATCTCAGTACTGGCCAGT  
TTTCATACAGTCTCGGGTTTAAACTTGAATCAAGGACACGACGTCTCCAGTCTACCTC  
CGAGAGATTAGCTGAAACACAGAATATAGGCCATCATTGTGAAGGGTTTTGCGGGA  
CAGAGGATCAGATGTTGAGAGTTGGACAAACTCATGAAAACAAAAATACCTGAAGCTCA  
CCAAGATGCATTAAAATGGTTTGCAGGAAAGCTGAAAGCTCAAGCACTCACACAAAA  
AACCAATGATTCCCTAAGGCAGACCCGTCTGATTCTCTCGTCTGCTATTGGCATTAA  
TGGACTTCTAAAAAACCCATTTTATCTGTCCGCTTCCGGACAACACAGGGCTGATTCTGC  
AGTAGATCCTGTCAGATGAAAATGTCACCTTGAACATGTTAAAGGGTGGAGGAAGCTAA  
ACAAGAATTACAGGAAGTGTGAATTCTGAAAATCCACAAAAATTACTATTCTGGAGG  
TAAACTCCAAAAGGAATTCTTTAGTTGGACCCCCAGGGACTGAAAGACACTTCTGCCG  
AGCTGTGGCGGGAGAAGCTGATGTTCTTTTATTATGCTCTGGATCCGAATTGATGAGAT  
GTTTGTGGTGTGGAGGCCAGCGTACAGAAATCTTTAGGGAAGCAAAGGCGAATGCTCC  
TTGTGTATATTATTGATGAATTAGATTCTGTTGGTGGAAAGAGAATTGAATCTCCAATGCA  
TCCATATTCAAGGCAGACCATAATCAACTTCTGCTGAATGGATGGTTAAACCAATGA  
AGGAGTTATCATAATAGGAGCCACAAACTTCCCAGGGCATTAGATAATGCCTTAACGTCC  
TGGCGTTTGACATGCAAGTTACAGTCCAAGGCCAGATGTTAAAGGTCGAACAGAAATT  
GAAATGGTATCTCAATAAAATAAGTTGATCAATTCCGTTGATCCAGAAATTATAGCTGAGG  
TACTGTTGGCTTCCGGAGCAGAGTTGGAGAATCTGTGAACCAGGCTGCATTAAAGCAGC  
TGTTGATGGAAAAGAAATGTTACCATGAGGAGCTGGAGTTTCAAAGACAAAAATTCTAAT  
GGGGCTGAAAGAAGTGTGAAATTGATAACAAAAACAAACCATCACAGCATATCATGA  
ATCTGGTCATGCCATTATTGCATATTACACAAAAGATGCAATGCCTATCAACAAAGCTACAAT  
CATGCCACGGGGCCAACACTTGGACATGTGTCCTGTTACCTGAGAATGACAGATGGAATGA  
AACTAGAGCCCAGCTGCTGCACAAATGGATGTTAGTATGGGAGGAAGTGGCAGAGGAGCT  
TATATTGGAACCGACCATATTACACAGGTGCTTCAGTGATTTGATAATGCCACTAAAAT  
AGCAAAGCGGATGGTTACAAATTGGAATGAGTGAAAAGCTGGAGTTATGACCTACAGTGA  
TACAGGGAAACTAAGTCCAGAAACCCATCTGCATCGAACAGAAATAAGAATCCTCTAAG  
GGACTCATATGAACGAGCAAAACATATCTGAAAACATCATGCAAAGGAGCATAAGAATCTGC  
AGAAGCTTATTGACCTATGAGACTTGGATGCCAAAGAGATTCAAATTGTTCTGAGGGAA  
AAAGTTGGAAGTGTGAGTGATAACTCTTGTGATGAGTGCCTGCTGGTTTATTGCAAGAATA  
TAAGTAGCATTGCAGTAGTCACTTTACAACGCTTCCCTCATCTGATGTGGTGTAAATT  
GAAGGGTGTGAAATGCTTGTCAATCATTTGTACATTATCCAGTTGGGTTATTCTCATT  
TGACACCTATTGCAAATTAGCATCCCATGGCAAATATATTGAAAAAAATAAGAACTATCAG  
GATTGAAAACAAAAAA

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**FIGURE 96**

MFSLSSTVQPQVTVPPLSHLINAHTPKNTSVSLGVSVSQNQHRDVVPEHEAPSSEPSLNLRD  
LGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFFENKYGNLDIFSTLRSSCLYR  
HHSRALQSICSDLQYWPPVFIQSRGFKTLKSRTRLQSTSERLAETQNIAPSFKGFLLRDRGS  
DVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALTQKTNDLRRTRLILFVLLLFGIYGLL  
KNPFLSVRFRTTGLDSAVDPVQMKNVTFEHVKGVEEAKQELQEVEFLKNPQKFTILGGKLP  
KGILLVGPPGTGKTLARAVAGEADVPFYASGSEFDEMFGVKPNEGVIIGATNFPEALDNALIRPGRF  
FIDEELDSVGGKRIESPMHPYSRQTINQLLAEMDGFKPNEGVIIGATNFPEALDNALIRPGRF  
DMQVTVPRPDVKGRTEILKWYLNKIKFDQSVDPPIIARGTVGFSGAELENLVNQAALKAAVDG  
KEMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAIIAYYTKDAMPINKATIMPR  
GPTLGHVSLLPENDRNNETRAQLLAQMDVSMGGRVAEELIFGTDHITTGASSDFDNATKIAKR  
MVTKEGMSEKLGVMTYSDTGKLSPETQSAIEQEIRILLRDSYERAKHILKTHAKEHKNLAEAL  
LTYETLDAKEIQIVLEGKKLEVR

**Important features of the protein:****Transmembrane domain:**

amino acids 238-259

**N-glycosylation sites.**amino acids 28-32, 90-94, 230-234, 278-282, 535-539, 584-588,  
623-627**N-myristoylation sites.**

amino acids 35-41, 266-272, 286-292, 325-331, 357-363, 599-605

**Amidation site.**

amino acids 387-393, 709-713

**ATP/GTP-binding site motif A (P-loop).**

amino acids 322-330

**AAA-protein family proteins**

amino acids 315-336, 343-386, 405-451

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**FIGURE 97**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCGATTTCTCCCCAGTTCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTGACATTTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGCACTAACGGCGGAGGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCACGGGAG  
GCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCTTCAGCCTTCTCTGCTGCGTTTATCTCCTATGGACTCCTCCACTGGACTGAAG  
ACACTCAATTGGGAAGCTGTGTGATGCCACAAACCTTCAGGAAATACGAAATGGATTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAGATGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTGCAAGACACAAAGCCTGCAATCGATGCTGCCCTGCCATTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGAAGATCAGC  
AGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACGCCAGATTCTGAGTCACTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTCTGCAATGGATGGAG  
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCAAACACCACATCTTTACTGTACTAGTCTTGCT  
GGTCACAGTGTATCTTATGCATTACTTGCTTCCTGCATGATTGTCTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTGTAATATCTTCTGCTATTGGATATATT  
TATTAGTTAATATTTTATTTGCTATTAATGTATTATTTTACTTGGACATG  
AAACTTAAAAAAATTCACAGATTATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT  
ACAGTAAAAAAAAACCTTGTAAATTCTAGAAGAGTGGCTAGGGGGTTATTCAATTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATTGCACATCTACCTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTCTACAAATAAGTTCTTGCATACCAAAAAAAAAAAAAAA

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**FIGURE 98**

MKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNGFSEIRGSVQAKDGNIDIR  
ILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDH YTLRKISSLANSFLTIKKDLRLC  
HAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEETE

**Signal sequence:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 107-110, 140-143

**N-myristoylation site.**

amino acids 51-56

**Interleukin 10:**

amino acids 9-176

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## FIGURE 99

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**FIGURE 100**

MRLLPEWFLLLFGPWLLRAVSAQIPESGRPQYLGLRPAAGAGAGAPGQQQLPEPRSSDGLGVGR  
AWSWAWPTNHTGALARAGAAGALPAQRTKRKPSIKAARAKKIFGWGDFYFRVHTLKFSLVTG  
KIVDHVNGTFSVYFRHNSSLGNLVSIVPPSKRVEFGGVWLPGPVPHPLQSTLAEGVLPGL  
GPPLGMAAAAGPGLGGSLGGALAGPLGGALGVPGAKESRAFNCHVEYEKTNRARKHRPCLYD  
PSQVCFTETQSQAACWLCAKPKVICIFVSFLSF DYKLVQKVCPDYNFQSEHPYFG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 273-288

**N-glycosylation sites.**

amino acids 72-76, 133-137, 143-147, 149-153

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 35-41, 58-64, 60-66, 81-87, 84-90, 184-190, 194-200,  
203-209, 205-211, 206-212, 209-215, 217-223, 221-227, 224-230

**Cytochrome b/b6 Qo site signature.**

amino acids 5-11

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**FIGURE 101**

AATGCCCAATGCGCACCCACAGCTCGCCTCTGCAAGTGTCTTCTGGTGTCCCCGATG  
GCGTCCGGCCTCAGCCCTTCCTCCCCATCAGGGGCAGTGCCCACGTCTTGAGCTGCAGC  
GAGGGACGGATGGCGAACCCCTCCAGTCCCCTCAGAGGCGACTGCAACTGCCCGGCCGTGC  
CTGGACTCCCTACAGTGGCCCTACTCTCGTGA  
CTCCCTCGGCCCTGGAAATAGGACTGTGG  
ACCTCTTCCCAGTCTTACCGATCTGTGTGACTTGACTCCTGGAGCCTGCGATATAAATT  
GCTGCTGCGACAGGGACTGCTATCTTCTCCATCCGAGGACAGTTTCTCCTGCCTCCAG  
GCAGCGTAAGGTCTTCAAGCTGGTTGTAGACA  
ACTCTGTTATCTTCAGGAGTAATTCCC  
CGTTTCTTCAAGAGTTTCAAGGATTCTAATGGAATCAGGCAGTTTGTGTCCATGTGAACA  
ACTCAA  
ACTTAAACTATTCCAGAAGCTCAAAAGGTCAATGCAACCAACTTCCAGGCCCTGG  
CTGCAGAGTTGGAGGCGAATCATTCACTTCAACATTCAA  
ACTCAATCACCACCATCTTTT  
ACAGGGCTGGGACCCATTCTACTTACTTCCCAAGTGGCTGTAA  
TAAGCTGCTGAGAC  
AACCTGCAGGAGTTGGAGCTGGGGACTCTGTGCTGAAAGCAATCCTGCAGGTTCTAGAGA  
GTAAAAGTACA  
ACTTGCACTCGTTTCAAGAACCTGGCTAGTAGCTGTACCTTGGATTCA  
CCCTCAATGCTGCCTTTACTATAACTCACAGTCTAAAGGTTCCAAGAACGATGACTGATC  
CACAGAATATGGAGTTCCAGGTTCTGTAATA  
ACTTACCTCACAGGCTAATGCTCCTGTGAGAC  
CTGGAACACTTGTCAAGATGTAGTTCTCAGGTAC  
CTGAGATAGAGACCAATGGGACTT  
TTGGAATCCAGAAAAGTTCTGTCAGTTGGGACAA  
ACCTGACTGTTGAGCCAGGCCGCTT  
CCTTACAGCAACACTTCATCCTCGCTTCAGGGCTTTCAACAGAGCACAGCTGCTCTCA  
CCAGTCTAGAAGTGGGAATCCTGGCTATATAGTTGGGAAGCCACTCTGGCTCTGACTGATG  
ATATAAGTTACTCAATGACCCCTTTACAGAGCCAGGGTAATGGAAGTTGCTGTAAAAGAC  
ATGAAGTGCAGTTGGAGTGAATGCA  
ATATCTGGATGCAAGCTCAGGTGAAGAACGGCAGACT  
GCAGCCACTTGCA  
GCAGGAGATTATCAGACTCTTCA  
TGGACTCTGCTGAGCTGCTGAGGCTATGTTGAGCCAGGAGTATGTTG  
CCATCTTGGTAATGCTGACCCAGGGCAGAAAGGAGGGTGGACCAGGATCCTCAACAGGC  
ACTGCAGCATTTCAGTATAAACTGTA  
CTCCTGCTCTCATACCAGTTCCCTGGAGATCCAGG  
TATTGTGGCATATGTAGGTCTCCTG  
CCAACCCGCAAGCTCATG  
TACAGGTTGAGATCTGACTGAGGTTG  
TATACCA  
CTGAGTGCAGTCTATA  
CAGGATTCTCAGCAAGTTACAGAAGTATCTTGACA  
ACTCTTG  
TGAAC  
TTTGTGGACATTACCCAGAAGCCACAGCCTCCAAGGGCCAACCC  
AAAGGGACTGGA  
AATGGCCATTGACTTCTTCCCTTCAAAGTGGCATT  
CAGCAGAGGAGTATTCTCTCA  
AAAAAT  
GCTCAGTCTCTCCATCCTTACCTGCTGCTCTTACTACTTGAGTTCTCA  
ACCTGAGACTA  
**TGTGA**  
AGAAAAGAAAATAATCAGATT  
TCAGTTCCCTATGAGAA  
ACTCTGAGGAGCATT  
AGGATAATAGATGACCT  
AACTGAAGGAATCCTGTATATGAAAGGAGTT  
ATTTAGAAAAGCAATA  
AAAATATTTTATT  
ATCNTAAAAAAA

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**FIGURE 102**

MRTPQLALLQVFFLVFPDGVRPQPSSPSGAVPTSLELQRGTGGTLQSPSEATATRPAVPGL  
PTVVPTLVTAPSAPGNRTVDLFPVLPICVCDLTPGACDINCCCDRDCYLLHPRTVFSFCLPGSV  
RSSSWVCVDNSVIFRSNSPFPSSRVFMDSGIRQFCVHNNSNLNYFQKLQKVNATNFQALAAE  
FGGESFTSTFQTQSPPSFYRAGDPILTYFPKWSVISLLRQPAGVGAGGLCAESNPAGFLESKS  
TTCTTRFFKNLASSCTLDSALNAASYYNFTVLKVPRSMTDQPQNMEFQVPVILTSQANAPLLAGN  
TCQNVSQVTYEIETNGTFGIQKVSLSLGQTNLTVEPGASLQQHFILRFRAFQQSTAASLTSP  
RSGNPGYIVGKPLLALTDDISYSMTLLQSQGNGSCSVKRHEVQFGVNAISGCKLRLKKADC  
LQQEIYQTLHGRPRPEYVAIFGNADPAQKGGWTRILNRHCSISAINCTSCCLIPVSLEIQVLW  
AYVGLLSNPQAHVSGVRFLYQCQSIQDSQQVTEVSLTLVNFVDITQKPQPPRGQPKMDWKWP  
FDFFPFKVAFSRGVFSQKCSVSPILCLLLGVLNLETM

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 484-505, 581-600

**N-glycosylation sites.**amino acids 78-82, 165-169, 179-185, 279-285, 331-337, 347-351,  
410-414, 487-491**N-myristoylation sites.**

amino acids 30-36, 41-47, 124-130, 232-238, 236-242, 409-415

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 420-431

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**FIGURE 103**

CCTAATTCTCAAGGTGATGCTATTTAGGAAGTCATAACTCATGTGAGTGGAGCCATGTGGAT  
TAAGAAGTGATAGGAGAGCTGCTGTCTGCTCTCCACTGTGTGAGGATAACACAGGA  
AGACAGCCATCTGGTGGAGGAAGAGAGGGCCCTGCCAGATACCGGACCTGCTGACACCTTGAT  
CTTGGACTTCCCCTCTCCAGGAAGGCCTGACCTCAGTTGCTCCAGGGTAAAGAATTGGCA  
GTGCCACACCCACGCTGTTGATAACATTCTCACCATACCAGTGAGGGTGAATGTGTACA  
CGCCCAGCTCCTGCCCTGTTACTCTCCACAGTATGCGAAGAATATCCCTGACTTCTAGCCCTG  
TGCGCCTCTTTGTTCTGCTGTTGCTACTAATAGCCTGGAGATCATGGTTGGTGGTCACT  
CTCTTGCTTCAACTCACTATAAAATCATTGTCAGACCTGGACAGCCCTGGTGTGAAGCGC  
AGGTCTTCTGAATAAAATCTTCAGTACAACAGTGACAACAAACATGGTCAAACCTC  
TGGGCCTCTGGGAAGAAGGTATATGCCACCAGCACTGGGGAGAATTGACCCAAACGCTGG  
GAGAAGTGGGGCAGACCTCAGGATGCTCCTTGACATCAAACCCAGATAAAGACCAAGTG  
ATCCTCCACTCTGCAAGTCGAGATGTTGTCACGTGAAGCAGAACGGTGCACTGGTGCAT  
CCTGGCAGTTGCCACCAATGGAGAGAAATCCCTCTTGACGCAATGAACATGACCTGGA  
CAGTAATTAAATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAA  
AGTATTCAGGAAGCTCTCAAAGGGAGACTGCGATCACTGGCTCAGGGATTCTTAGGGACT  
GGGAGGCAATGCCAGAACCGACAGGCAGAAGATCCACTAGAGGTGATACCACGGCGCAG  
AGTTGTTCACCTGTTGCTCGATCGCTGACAGCCTGGCTCCACTGCTGTGTTCCCTGA  
GTCAAGTGGAGGGGGAGCCTGCAATGAGCGGAGATCGCCCTCTGCATTCCAGTCTGGCAAC  
AGAGCAAGACTCCGTCTAAAAAAAAAATTTTCACTACATATTTTAAAGATAGG  
GCTGGGCACAGCAGCTCACATCTATAATCCAACACTTTGGGAGGCCTAGGCAGGAGGATCAC  
TTGAGCCCAGGAATCTGAAGCTGCAGTGAGCCTTGCTCGTGAGATTGGAACCTATGACCT  
ACCACCAAGCCCACCTGGTCTAACACCCCCCTCTATGTGTGAGAGGGAGAGAAGAAAAGTG  
AGGGAGAAAAGAGAGATAAGCAAAGAACAGAGAGGAAAATGGAAATAAGAGGAATTGGGG  
GAATTAAACAGAGGGGAGGGCATGGATCCCCGGAGTTAGAAGAGTAGCAGCTGTGGATTAC  
TACGCAGTGGAGGAAGAAGAGTTGTTGAAATTATGAGAGGTAGTATAATCATTGTGAGG  
CAGTTTCTGCATTCAACCATTCTCACAGACTAAGTTACTCATAAGCAAACGTGCAATTACA  
TTACACTGAAATTCTCCCTAACATCATTTGCAATTGAAATAAGTACGGTTTCAAACAAAC  
CTGATATAGCAGAACTGACTGTATAAATTATGTGAGCACAGTGCAAGTAATTCTTGTGTT  
TGTGTTGTTTGTGAGACAGAGTCTCACTCTATCTCCAGGCTGGAGTGTAGTGGTGCATCC  
CGGCTCACTGCAACCTCGATCTCCAGGCTCAAGCGATTCCCTGCCCTGAGCCTCTGAGTAG  
CTGGGATTACAGGCATGAGCCACCACGCCGGCTAATTTGTATTTAGTAGAGACGGGTT  
TTCACCCCTGTTGCCAGGCTGGTCTGAAACTACGGACCTCAGGTGATCTGCCCTCAGCCT  
CTCAAAGTGCTGGATTATAGCATGAGCCACTGAGCCCAGACACAAGTAGTTCTTCTGATAA  
ACACTTTAACACTGAATGCA

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**FIGURE 104**

MRRISLTSSPVRLLFLLLLIALEIMVGGHSLCFNFTIKSLSRPQWPCEAQVFLNKNLFLQ  
YNSDNNMVKPLGLGKKVYATSTWGELETQTLGEVGRDLRMLLCIKPQIKTSDPSTLQVEMFC  
QREAERCTGASWQFATNGEKSLLFDAMNMTWTVINHEASKIKETWKKDRGLEKYFRKLSKGDC  
DHWLREFLGHWEAMPEPTGRRST

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 11-30 (possible type II protein)

**N-glycosylation site.**

amino acids 36-39, 154-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-5, 182-185, 209-212

**Casein kinase II phosphorylation site.**

amino acids 86-89, 93-96, 142-145, 185-188

**N-myristoylation site.**

amino acids 46-51

**Amidation site.**

amino acids 77-80, 207-210

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**FIGURE 105**

TTTCCGAGTGACCTCTTGATGCTGGCTTCTCTCACCGTCCCCGTGGAGCCATGA  
TGCTGCTGGAATCTCCTATAGATCCACAGCCTCTCAGCTCAAAGAACCCCCGCTTGTGCTTG  
GTGTTCTGCATCAAATACGAAGCTGCGACAGGCAGAAAGGCTGTTGAAAATCAACTTGTG  
GACCGGAGTCATAGCACATATTGGGGATGTGATGTTACTGGGACAGCAGATGGCCGGTCA  
TAAAACTTGAAAATGGTGAAATAGAGACCATTGCCGGTTGGTCCGGCCCTGCAAAACCC  
GAGATGATGAGCCTGTGTGGAGACCCCTGGTATCCGTGCAGGGCCAATGGACTCTCT  
TTGTGGCCGATGCATAAAGGGACTATTGAAGTAAATCCCTGAAACGTGAAGTGAAACTGC  
TGCTGTCCTCCGAGACACCCATTGAGGGAAAGAACATGTCCTTGTGAATGATCTTACAGTCA  
CTCAGGATGGGAGGAAGATTATTCACCGATTCTAGCAGCAAATGGCAAAGACGAGACTACC  
TGCTTCTGGTATGGAGGGCACAGATGACGGGCCTGCTGGAGTATGATACTGTGACCAGGG  
AAAGTAAAAGTTTATTGGACCAGCTGCCGGTCCGAATGGAGTCCAGCTGTCTCCTGCAGAAG  
ACTTTGTCCTGGTGGCAGAAACAACCATTGCCAGGATACGAAGAGTCTACGTTCTGGCCTGA  
TGAAGGGCAGGGCTGATCTGTTGTGGAGAACATGCCCTGGATTCCAGACAACATCCGGCCA  
GCAGCTCTGGGGGTACTGGTGGCATGTCGACCATCCGCCCTAACCTGGTTTCCATGC  
TGGATTCTTATCTGAGAGACCCCTGGATTAAAAGGATGATTTTAAGCTCTTAGTCAAGAGA  
CGGTGATGAAGTTGTGCCCGGTACAGCCTCGTCAGACTCAGCGACAGCGTGCCTTCC  
GGAGAACCTGCATGATCCCAGGGCTGGTGGCCACCTACATCAGCGAGGTGCACGAACACG  
ATGGGCACCTGTACCTGGCTCTTCAGGTCCCCCTCCCTGCAGACTCAGCCTCCAGGCTG  
TTTAGCCCTCCAGATAGCTGCCACGCCAGGCCAGGAGTCTCACACTCAGGCACCAG  
GCCCTGGTCCAGGAGGAGCTGTGGACACAGTCGTGGTCAAGTGTCCACATGCACCTGTTAGTC  
CCTGAGAGGTGGTGGGAATGGCTGCTTCATTCTCGAGGATGCCGGGCCCCACCTGGCTTG  
TCTTCTGTTAGAGGGAAAGTGTAAACATATCTGCCATGAGGAACATAAAATTGTAAGCCA  
TTTCTCTAAACAAAACAAACTTCTAAGTACAATCATTCTCTAGGATTTGGGAAGCTCCT  
TGCACCTGGAACAGGGCTCAGGTGGTGGAGCAGTAAGGCACTACCCAGAGAGCTTGCTGCTG  
CGGCCCTGCTGCCCTCAAAGTCTTACTATATATAACGTGCGGTACACCTTCT  
TCGTTGTGGTGGGATGGAAGAGCAGAGGGAGCATGCCAGGGTGTGAGGCCAGCGGTGA  
GAGCCGTGTTAGCCAAGACATGGAACAGTGTGTTCAAGGGTTATGTGGGGCTGGCTCTCCA  
TAGTGTGTATGAAAAGCTTGTGACTCTAGCGGCTCAGAGAGGACTTGTGGTTCTTCT  
GTGAATATCTCCGTGCTGACCATGCTGGAATTGGATGATTCTGCAATTGGACCTACTGCAG  
GGGTCCGTTAGTAACGTCTGTGATCTTGTGACCTCTAGACCCCCAAGTTGCTGTATATT  
CACAAGTATGTCTACACACTGG

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**FIGURE 106**

MLAVSLTVPLLGAMMLLESPIDPQPLSFKEPPLLLGVLPNTKLQAERLFENQLVGPEIAH  
IGDVMFTGTADGRVVKLENIEITIARFGSGPCKTRDEPVCGRPLGIRAGPNGLFVADAYK  
GLFEVNPWKREVKLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQRRDYLLLVMEG  
TDDGRLLEYDTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETTMARIIRRYYVSGLMKGGA  
FVENMPGFPDNIRPSSGGYWVGMSTIRPNPGFSMLDFLSERPWIKRMIFKLFSQETVMKFVP  
RYSLVLELSDSGAFRRSLHDPDGLVATYISEVHEHDGHLYLGSFRSPFLCRLSLQAV

**Important features of the protein:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 1-21 (possible type II)

**N-glycosylation sites.**

amino acids 116-119, 152-155

**Casein kinase II phosphorylation sites.**

amino acids 19-22, 27-30, 98-101, 146-149, 221-224, 286-289, 332-335

**N-myristoylation sites.**

amino acids 71-76, 92-97, 189-194, 244-249, 338-343

**Amidation site.**

amino acids 164-167

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**FIGURE 107**

AACGAAGCGTGC CGC TTTGGTAACCGGCTAGAAATCCCGCAC GCG CGC CTGCC CCTCTCCC  
CAGGCCTGAGCTGCC CCCCCACTGCC TTTCTTCTTCC CGAGTCAGAACGCTCGAGGG  
CCCAGAGAGGCGGTGGGGTGGCGACCCTACGCCAGCTCCGGGCGGGAGAAAGCCACCCCT  
CCC CGC CCCAGGAAACCGCCGGCTCGGCCTGCCAGAGCC**A**TGGAAATTCTCCTGGCTGG  
AGACGCGCTGGCGCGGCCCTTTACCTGGCGTTCTGCGCTTGCGCTGGCCCTGGGGCTGCTGC  
AGGCCATTAAGCTGTACCTGCGGAGGCAGCGGCTGCTGCGGGACCTGCGCCCTTCCCAGCGC  
CCCCCACCCACTGGTCCCTGGGCACCAGAAGTTATTCAAGGATGATAACATGGAGAAGCTTG  
AGGAAATTATTGAAAAATACCCCTCGCCTCCCTTCTGGATTGGCCCTTCAGGCATT  
TCTGTATCTATGACCCAGACTATGCAAAGACACTTCTGAGCAGAACAGATCCAAGTCCCAGT  
ACCTGCAGAAATTCTCACCTCCACTCTGGAAAAGGACTAGCGGCTCTAGACGGACCCAGT  
GGTCCAGCATCGCCTACTAACCTGGATTCCATTAAACATCCTGAAAGCATAACATTG  
AGGTGATGGCTATTCTGTGAAAATGATGCTGGATAAGTGGAGAAGATTGCAGCACTCAGG  
ACACAAGCGTGGAGGTCTATGAGCACATCAACTCGATGTCTGGATATAATCATGAAATGCG  
CTTCAGCAAGGAGACCAACTGCCAGACAAACAGCACCCATGATCCTTATGCAAAAGCCATAT  
TTGAACTCAGCAAAATCATTTACCGCTTGTACAGTTGTATCACAGTGACATAATT  
TCAAACTCAGCCTCAGGGCTACCGCTTCCAGAAGTTAACCGAGTGTGAATCAGTACACAG  
ATACAATAATCCAGGAAAGAAAAGAAATCCCTCCAGGCTGGGTAAGCAGGATAACACTCCGA  
AGAGGAAGTACCAAGGATTCTGGATATTGTCCTTCTGCCAAGGATGAAAGTGGTAGCAGCT  
TCTCAGATATTGATGTACACTCTGAAAGTGGACATTCCTGGCAGGACATGACACCTTGG  
CAGCAAGCATTCCGGATCCTTACTGCCCTGGCTCTGAACCCCTGAGCATCAAGAGAGATGCC  
GGGAGGGAGGTCAAGGGCATCTGGGGATGGGTCTCTATCACCTGGGACAGCTGGGTGAGA  
TGTGTACACCACAATGTGCATCAAGGAGACGTGCCGATTGATTCTGCAGTCCGTCCATT  
CCAGAGATCTCAGCAAGCCACTTACCTCCAGATGGATGCACATTGCCGCAGGGATCACCG  
TGGTTCTTAGTATTGGGGTCTTCACCACAAACCTGCTGTCTGGAAAAACCCAAAGGTCTTG  
ACCCCTTGAGGTCTCTCAGGAGAATTCTGATCAGAGACACCCCTATGCCACTTACCAATTCT  
CAGCTGGATCAAGGAAC TGCAATTGGCAGGAGTTGCCATGATTGAGTTAAAGGTAAACCATTG  
CCTTGATTCTGCTCCACTCAGAGTGACTCCAGACCCACCAGGCCTCTTACCTTCCCCAAC  
ATTTTATCCTCAAGCCAAAGATGGATGATTGACCTGAAGAAACTCTCTGAATGT**TAGA**  
TCTCAGGGTACAATGATTAACAGTACTTGTGTTTCGAAGTTAAATTACAGCTAATGATCCA  
AGCAGATAGAAAGGGATCAATGTATGGTGGAGGATTGGAGGTTGGTGGGATAGGGGTCTCTG  
TGAAGAGATCCAAAATCATTCAGGTACACAGTGTGTCAGCTAGATCTGTTCTATATAACT  
TTGGGAGATTTCAGATCTTCTGTTAAACTTCACTACTATTAAATGCTGTATACACCAATA  
GACTTTCATATATTCTGTTGTTAAATAGTTTCAGAATTATGCAAGTAATAAGTGC  
TGTATGCTCACTGTCAAAATCCCAACACTAGAAAATCATGTAGAATAAAAATTAAATCT  
CACTTCACCTAGCCGACATTCCATGCCCTGACCAATCCTACTGCTTTCTAAACAGAATA  
ATTTGGTGTGCATTCTTCAGACTTTCTTACATTATGAGAAATGTAGCAATGTA  
TTGTATAGATGTGATCATTCTTACATTGTTATTGATTTTCACTTAATAAAAATTCACCT  
TATTCTTAAAA

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**FIGURE 108**

MEFSWLETWRWARPFYLAFFCLALGLLQAIKLYLRRQRLLRDLRFPAPPTHWFLGHQKFIQD  
DNMEKLEEIIEKYPRAFPFWIGPFQAFFCIYDPDYAKTLLSRTDPKSQYLQKFSPPLLGKGLA  
ALDGPKWFQHRLLTGFFFNILKAYIEVMAHSVMMMLDKWEKICSTQDTSVEVYEHINMSL  
DIIMKCAFSKETNCQTNSTHDPYAKAIFELSKIIFHRLYSLLYHSDDIFKLSPQGYRFQKLSR  
VLNQYTDIIQERKKSLQAGVKQDNTPKRKYQDFLDIVSAKDESGSSFSIDVHSEVSTFLL  
AGHDTLAASISWILYCLANPEHQERCREEVRGILGDGSSITWDQLGEMSYTTMCIKETCRLI  
PAVPSISRDLSKPLTFPDGCTLPGAGITVVLSIWGLHHNPWKNPKVFDPLRFSQENSDQRHP  
YAYLPFSAGSRNCIGQEFAFIELKVTLIALILLHFRVTPDPTRPLTFPNHFILKPKNGMYLHLK  
KLSEC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 310-330, 397-413, 459-473

**N-glycosylation site.**

amino acids 206-210

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 265-269, 504-520

**N-myristoylation sites.**

amino acids 25-31, 298-304, 353-359, 450-456, 456-462

**Cytochrome P450 cysteine heme-iron ligand signature:**

amino acids 447-457

**Cytochrome P450 cysteine heme-iron ligand proteins.**

amino acids 444-475

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**FIGURE 109**

GGCGTTCCGGGCCTCAACTTGGCGTCGTGAGATTCTTGTGAGGCGTCTGCCTGGAAGCCGGC  
AGCAATTTGCTCTTAAAGAGAAAAAGAAGGCTAGGGACTCAGATTCCCTGGATTCTGAGAT  
CCAGACCAGCTCCTCCCAGACCTCTCCAGAAGAAGCCATGGGAACCCTCGTATCCAGCATT  
GCTGATCCTCCTGGTCTAGGAGCCTCCCTGACCTCAGGCTAGAGCTGTATTGTCAAAA  
GGGTCTGTCCATGACTGTGGAAGCAGATCCAGCCAATATGTTAACGGACCACAGAGGAAGT  
GGAGACTTGTGACAAAGGGGCACTTGCCAGGAAACCATACTAATAATTAAAGCAGGGACTGA  
GACAGCCATTTGCCACGAAGGGCTGCATCCCGAAGGGGAGGAGGCCATAACAATTGTCCA  
GCACTCTCACCTCCCGCCTGATCGTACGCTCCTACAGTAACACTGTGAGGATTCTCTG  
TAATGACAAAGACAGCCTGTCTCAGTTGGGAGTCAGTGAGACCACAGCTTCACTGTGTC  
AACAAACCTCCATTGTCCAACCTGTGTGGCTTGGGACCTGTTAGTGCTCCTCTTCC  
CTGTCCCAATGGTACAACTCGATGCTATCAAGGAAAATGAGATCACTGGAGGTGGCATTGA  
GTCGCTGTGGAGGTCAAAGGCTGTACAGCCATGATTGGCTGCAGGCTGATGTCTGGAATCTT  
AGCAGTAGGACCCATGTTGTGAGGGAAGCGTGCACATCAGCTGCTCACTAACCTCGAAA  
GACTGAAAATGGGCCACCTGTCTCCCATTCTGTTGGGGTTACAGCTACTGCTGCCATT  
GCTGCTGCCATCATTATTCACTTTCCTAAGAAGGCACCTCTGGCCTGGTCTGAGGACAT  
CTTTTTGACTGGGAGCCTTACTGTTGAGGTTCAACAAGCTGAGGAGTAGATGGGAATTT  
GAGGGAGAATACAGAGATACTATGAACGTATTGACATTAAATACAATTCTGCTATAATT  
TTTGTATGCAGTAGGCGTTACTAATAAACATTCTGCTGTGA

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**FIGURE 110**

MGTPRIQHLLILLVLGASLLTSGLELYCQKGLSMTVEADPANMFNWTTEEVETCDKGALCQET  
ILIIKAGTETAILATKGCIPEGEEAITIVQHSSPPGLIVTSYSNYCEDSFCNDKDSLSQLFWEF  
SETTASTVSTTLHCPTCVALGTCFSAPSLPCPNGTTRCYQGKLEITGGGIESSVEVKGCTAMI  
GCRLMSGILAVGPMFVREACPHQLLTQPRKTENGATCLPIPVWGLQLLPLLLPSFIHFS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 184-201

**N-glycosylation sites.**

amino acids 45-49, 159-163

**N-myristoylation sites.**

amino acids 31-37, 70-76, 99-105, 147-153, 160-166, 174-180,  
175-181

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**FIGURE 111**

CGAGAAGAGGACAGAGGAGACTGAGCAAAGGGGGTGGGCTCCAGGCACCCCTAGCCAATTCTGCCCTCCAT  
CCCAAGGGGCAGAGAAATTGTCTTCTTGACTCTACGAGGAAAAAAAAAAAAAAACCATTAA  
AGGGAAAGATAAACGGAGACGGAGGAAGGTGGCAGCCAGATTACTTAGAGAGGCACAGAGGAGAGAGATCGGGG  
TGAGTCGGCATGGGACTCCCAGGGCCCAGCACCCGCCTCCCCAGCTGCTTCTAATTCTGCTGAGCTGT  
CCCTGGATCCAGGGCTGCCCTGAAGGAGGAGGAGATTGCCAGAGCCTGGAAGTGGAGACCCCCACGGTGGCC  
TCTGAGGCCCTGGCTGAACTGCTCATGGGCCCTGCTGAGGAGGGGCCAGAGATGGCTACCTGCCAGGATCT  
GATCCGGACCCCCACGCTAGCCACCCCTCCGGCCAGACTCTCGCAGTGCCCTCCCTGCCACGGGCACTGAG  
CCGGGGACAGGGCCTGACAACAGCGTCACCCCTAAGGGGTCAAGGGGCCAGGGCCACTGCCAGAAGT  
CTGACCCGCCCAAGGAACCACAGCCCCACCCCCACCCAGGCCGCTCCCTGGGCCCTGAG  
GGAGGAGAGGAGGAGACGACCACTCATCACCAAGACAACGTTACCAACTACGGTGACCAAGCCAGTTCTG  
TGTAAATAACAACATCTCGAGGGCGAAGGGTATGTGGAGTCTCCAGATCTGGGAGGCCCTGAGCCACCCCTG  
GGGCTCTGGACTGCACCTACAGCATCCATGTCTACCCCTGGCTACGGCATTGAGATCCAGGTGAGACCGTGAAC  
CTGTCACAGGAAGAGGAGCTCTGGCTGGTGGGGATCCCAAGGCCAGGCTGGCCCCCGACTCCTGCCAAC  
TCATCCATGCTTGGAGAAGGACAAGTCTCGGAGGCCAACCAACCGCTGCTTCTGCACTTCAAGAGCCACGG  
GTCCCAAGGGCGGTGGCTTCAGGATCCACTATCAGGCCAACCTCTGAGCTGCTGGCTTCCCTCCCCGGCCGGCC  
CATGGGACGTGAGTGTGACGGACCTGCACCCCTGGGCACTGCCACCTTACTGTGATTGGGCTACCAAGCTG  
CAGGGAGAGGAGACCCCTATCTGCCCTAATGGCACCCGGCATCTGGAACGGTGAACCCCCAGCTGCATGGCA  
TCCCTGGTGGCACCATCCAAATGCCACCCCTGGGCCATCGTGTCCCCAGGCCAGGGGAGCCGTAGGGCCC  
AACCTCACCTGGCGTGGCTCATTAAGGCACTGAGGAGGCCAACCCAGGCTGCTTGAAGGGTCTCGCTG  
GATGAGGACAATGACGGCTGATGGTGGCTCAGGGCCAGCCCCCTATCCCCCGTATCTGATCTATGATTGGACATG  
GACGATGTCCCCGAGGGGCTCATCAGTACGCCAGTCCCTACGCTGCTGGAGCTGCTGTGAGACACCTGCC  
AATCCCTGCTTAAGCCTTCATTGAGGCTTGGAGGAGATCGCTGCTGGCCCTCCAGGATATGCCCTG  
AATGTCACTACCACGGACCCCTGAGTATGCCACGGGCACTGGCAACCTTCTCGTGCCTCCAGGATATGCCCTG  
GAGCCCCCTGGCCCCCAATGCCATGAATGTGTGGATCCCACAGAACCCCCACTGGAACGACACAGAGCCGGCC  
TGCAAAGCCATGTGTGGAGGAGCTGCGAACCGAGCTGGCGTGGCTCTCTCCGACTGCCAGAGCT  
AGCCCCGGGCAAGACTGCCTGGGGCGTGCACGTCCAGGAAGAGAACGCACTTGTGCTCAAGTTGAGATATTG  
AATGTGCGGAAGGGACATGCTGACGCTGTTGACGGGACGGTCCAGCGCCAGTCTGGCCCAGCTGCGG  
GGACCTCAGCCGCCGCCGCCCTCTCTCCCTGGGCCAGGCTCAACTGCAGTTCAAGGCCAGGGCACC  
CCAATCCAGGCCCTGGCCAGGGCTCTGTATTGCACTTCAAAGAGGCTCCGAGGAACGACACGTGCCAGCTG  
CCACCTCCGGAGTGGGGCTGGAGAACGGCATCCCACGGGACCTGATCCGGGCCAGGTGCTCACCTACCAAGTGC  
GAGCTGGCTACGAGCTGCTAGGCTCCGACATTCTCACTTGCAGTGGGACCTGCTTGGAGGCCGCC  
GCCGCAAAAGATCATGACTTGTGCTGACCCCTGGCGAGATTGCCAACGGCACCGCAGGCC  
TTCCCCCTGGCTCCACGTCAGTACCGCTGCCAGGGTACAGCCTCGAGGGGAGCCATGCTCACCTGC  
TACAGCCGGGACACAGGCACACCCAAGTGGAGCGATAGGGTCCCCAATGCGCCTTGAAGTACGAGCGTGCCTG  
AACCCGGGGTTCCCGAGAAATGGCTACCGAGCGCTGACAAGCACCACCTACAGGGCGAGCTCTGCC  
TTCTGCTATGAGGGCTTGTGAGCTTACGGCGAGGTACCCATCACCTGTGCCCCGGCACCCCTCCAGTGGACC  
AGCCAGCCCCACTCTGCAAAGTGAACCCAGACACAGATCATCACCGCAGGGAGGGGGAAACCTGGCCCTG  
GCCATCTGCTGCCCTAGGCTGGCAITGTCTCGGAGTGGCTTACATCTACTACACCAAGCTTCAAGGA  
AAGTCCCTTTCGGCTTCTCGGCTCCACTCTACAGCCCCATACCGTGGAGCTCGGACTTCAGCAACCCGCTG  
TATGAAGCTGGGATAACGCGGGAGTATGAAGTTCCATCTGAACCCAGACTACAGCTGCAGGACCCAGGACGC  
CCCTCCCTCCATCTGGCAGAGGGAAATACGGGACCCGGTCTGCTGCCCTCTGGCTGCCCTCCCTGGCTG  
TGAAATAGTCTCCCTATCCCACGAGGGGGCTTGATGCCCTGGAGATCCTACAGTAAATAAACAGCATCCTG  
CCGCCAAAAAA

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**FIGURE 112**

MGT PRAQH PPPP QPLL FLILL SCP WIQGL PLKEEE ILPE PGSETPTVASEA LAELLHG ALLRRG  
PEM GYLPGS DPDPTI LATPPAG QTLAVPSL PRATEPGT GPLTT AVTPNGVR GAGPTA ELLTPP  
PGTT APPPPSPAS PGPL GPEGGE ETTTI I TTTTVTTV TS PVLCNNN ISEGE GGYVES PDL  
GSPV SRTL GLLD CTYSI HVYP GYIE IQVQT LNL SQQE LLVLAGGGSP GLAP RLLA NSMLG  
EGQV LRSPTN RLLL HFQS PRVPR GGGF RIHY QAYLLSCGFPPR PAHD VSVT DLHPGGTATFH  
CDSG YQLQ GEETLIC LNGTRPSWNGETPSCMAS CGGTIH NATLGRIVSPEPGGAVGP NLT CRW  
VIEAAEGRRLHLHF ERVSL DEDND RLMVRSGGSP LSPVIYDSMD DVPERGLI SDAQSLYVEL  
LSETPANPLLLSLR FEAF EEDRC FAPFLAHGNVTTDPEYRPGALATFSCLPGYALEPPGPPN  
AIECVDPTEPHWN DTEPACKAMCGGEL SEPA GVVLSPDW PQSYSPGQDCVWGVHVQEEKRILL  
QVEILNVREGDM LTLFDGDGPSARVLAQLRGQP RRRLSSGPDL TLQFQAPPGPPNPGLGQG  
FVLHFKEVPRNDTCPELPPP EwgW RTASHGDLIRGTVL TYQCEPGYELLGSDILT CQWDLSWS  
AAPPACQKIMTCADPGEIANGHRTASDAGFPVGSHVOYRCLPGYSLEGAAMLT CYSRDTGTPK  
WSDRVPKCALKYEPCLNP GPV PENGYQTLYKHHYQAGESLRFFCYEGFELIGEV TITCVP GHPS  
QWTSQPLCKVTQTTDPSRQLEG GN LALAILLPLGLVIVLGSGVYIYYTKLQGKSLFGFSGSH  
SYSPITVESDFSNPLYEAGDTREYEVS I

**Important features of the protein:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 842-864

**N-glycosylation sites.**

amino acids 176-180, 222-226, 247-251, 332-336, 355-359, 373-377,  
473-477, 517-521, 641-645

**Tyrosine kinase phosphorylation site.**

amino acids 61-69

**N-myristoylation sites.**

amino acids 2-8, 84-90, 111-117, 114-120, 190-196, 198-204,  
235-241, 309-315, 333-339, 351-357, 472-478, 484-490, 528-534,  
626-632, 665-671, 775-781, 842-848

**Amidation site.**

amino acids 384-388

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**CUB domain proteins profile.**

amino acids 202-218, 376-392, 553-569

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**FIGURE 113**

GGCGCGGGCGGAGCTGCCGCCGCGCGTCCGCACTCCTCGGCCCTCGGCCTCGATGGGACGG  
GGCGCGCGGGAGCAGGAGGCGGCCGTGGGGTGCCTGGGCCGCGGGAGCCTACTGTGGGGCTCGGCATG  
GCGGGCGCAGGACCTGAGCTTCCTCAGGGAGCGGGAGCAGCTGCTGGCCGCGATGGGACGGAGTGGGG  
CCGTCCGGCGCGGCCGAGCGCTGAGCGGGAGCAGCTGACCTCAGGCCCTCGCGAAGCGCCGGCA  
GCTCGGGAACATGGCCCTGGAGCGGCTCTCGTGGCTCAAAGTGTAAATAACAGTACTGGTAGTGGAAAGG  
GATTGCGGTGGCCCAAAAACCAAGATGGACAAAATATTGAATCAAGCATATTCTGCAACCCAGTGTGGCAT  
TTGGGTCGAACCAGCAATGGAGGTCAATTGCTTCGCAAAATTATCCTGACTCATATCCACCAAAACAAGGAGTG  
TATCTACATTTGGAAGCTGCTCACGTAAAGAATAGAGTTGACCTTGATGAACATTATATAGAACCATC  
ATTGAGTGTGGTTGATCACTGGAAGTTCGAGATGGCATTGGTTCTCTCCTTATAGATCGTTACTG  
TGGCGTAAAAGCCCTCATTAAATTAGATCAACAGGGAGATTGATGTTAGTTAGTCTGATGAAGAGCT  
TGAAGGACTGGGATTTGAGCAAAATATTCAATTGATTCAGACTCCAGACTTACTACCTAGGAGGTATTTAAA  
TCCCATTCAGATTGTCAGTTCGAGCTCTGGAGCTGATGGAATAGTGCCTCTAGTCAGGTAGAACAGAGGA  
GAAAACAAAACAGGCCAGCGCTTGATTGACATCTGGACCAATTAAAGCCACTCAGAACAGTAAAGATTTATGAG  
GTTCTAGATTATCAAATGGAGCACTCAAATGAATGCAAGAGAAACTCGTTGCACTATGATGAAAGCAGTTC  
TATTGAAAACCTGAAGGCCAGTTGAGCACTGTGGCAATGATGTAATGCTAAACAGGAATTGGAGTGT  
TCGAATGTTGAGATGAAGGTAGTCGGTTAGCAGGTTGCAATGCTTTACTCCTTGTGGAGCCTCCCTG  
CACAAGCAGCACTTCTTTGCATAGCAACATGTGCATCAATAATTCTTAGTCGTAATGGTGTCAAATTG  
TGCATACCCCTGGGATGAAAATCATTGTAAGAAAAGAAAAAGCAGGAGTATTGAAACAAATCAACTAAGACTCA  
TGGAAACATTATTGGCATTACTTCAGGGATTGCTTGGCTTCTCATTATTCTATTACTACAGTGAAGAACAA  
GCCTCGAAAAAGGTATGGCTTCGAAACCGCTTTAATAAAACGGGTTCCAAGAAGTGTGATCCTCCTCA  
TTATGAACTGTTTCACTAAGGGACAAGAGATTCTGAGACCTGGCAGACTTGTGAGAACATTGACAACTA  
CCAGAAGATGCGGGCTCCACCGCTCCGCTGCATCCACGACCACACTGTGGTCGAGGCCAGCGT  
CAAACAAAGCAGGACCAACCTCAAGTCCATGGAACATTCTTCCGAAATGACTTGCACAAACACAGCCAATGAA  
AACATTAAATAGCACCTCAAGAAAAGTAGTTACACTTCAAACAGGGACATGAGTGCCTGAGCAGGCCCTGGA  
AGACCGAGTAATGGAGGAGATTCCCTGTGAAATTATGTCAGGGGGAGAAGATTCTGCAACAGCATCCATATC  
CATTGACTCTATCTCTGCTAATGGTGTGAAATTCTTAGGGTGTGACTACGTCAGCCTCCAGGGCACCAT  
ACTGTTCCAGCAGCCAAACCTTCTCCCACATCACAACATCGAAGACCTTGATTACGTTAACCTATTGATGG  
TGATGTTTATTCTCTCAGGAGTCTATATATGTTAAACCAATCAAGGAACCTTACTCTATTCACTGGAACAAAT  
AATCATCTTATTGCTGGTGTATTAGGAAGCACTGCCAGTTAAAGGCAATTAGAAGAGGTGGATGGATGG  
AGCCAGGCTCAGGCTGCCCTCGTTAGCAACAAGAAGACTGCTCTGACTGATAACAGCTCTGCAATATT  
TGATGCCACAATAAACTTGATTTTTTACATTCTTTTATTCTCTCTAAATTAAATTGTTTATAA  
GCCTATGTTTACCATTTCTACATAAGTACAAGTGGTAATGACCCACATCTCAGTATAGGCATT  
TGTTCTGAGTGTCAAAACAGCTAGTTACTGTGCCAAATTAGACCCAGTGTCTTACCCATCTGTTCT  
TCTGGCTAATCTGTACTTCTGCCCTTAAATTACTGGCCCTTATTCTTATTCTGTGAGAAATAATAGAT  
GATATGATTATTACCTTCAATTATATTCTCAGTTACTAGAAAATTCTCAATCTGGGATATATGTAC  
CATTGTCAGCTATGACTAAAATTGAAAAAGATAAAAATTCTAGCAAGCCTTGAAGTTACCAAGTATAGTC  
ACATTCACTGACAGCCCATTCCAGTAAAGAATCATTCACTTGGAGAGGCCCTATAATTACATT  
TTTGCAATGTTCTTCGCTAGATTGTTACATAGCTCCATTCTGTTGGTTGCTTACAGCATATGGTAACCA  
AGGTTAGATGCCAGTTAAACCTTGAAGAAATTGGATGAGCCTGAGATTGCTCTTAACCTGGGACATGACATT  
TTCTAGCTCTATCAAGAATAACAACTCCACATTGTTAAACTGCACTTTGACTTTTTATGGTATAAAA  
CAATAATTATAACAAAGCTATTGTTAGCTTGTGAAATTGACCTTGTGAAATGCTCTTGTAC  
AAATCAAGATGAAAGACCTACAGGACAGATTCTTCACTGTTGACATCAGTGGCTTGTATGCAAATATGCTGT  
GTTGGACCTGGACGCTATAACTTATTGTAAGACCTTGAAATGTCACATAAGCTCTTCTTGTAC  
TGTATTAGTTGTGATAAAATTCTACTGTGTGATATTATGCTCTAAATCACTACACAATCCATATTAAAA  
TATACATTGTACCTGAAAAAAA

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**FIGURE 114**

MALERLCSVLKVLITLVVEGIAVAQKTQDGQNIGIKHIPATQCGIWVRTSNGGHFASPNYP  
DSYPPNKECIYILEAAPRQRIELTFDEHYIIEPSFECRFDHLEVRDGPFGFSPLIDRYCGVKS  
PPLIRSTGRFMWIKFSSDEELEGLGFRAKYSFIPDPDFTYLGGILNPPIPDCQFELSGADGIVR  
SSQVEQEEKTKPGQAVDCIWTIKATPKAKIYLRFLDYQMEHSNECKRNFAVYDGSSSIENLK  
AKFCSTVANDVMLKTGIGVIRMWAEGSRLSRFRMLFTSFVEPPCTSSTFFCHSNMCINNSLV  
CNGVQNCAYPWDENHCKEKKKAGVFEQITKTHGTIIGITSGIVLVLLIISILVQVKQPRKKVM  
ACKTAFNKTGFQEVDPPPHYELFLRDKEISADLSEELDNYQKMRRSSTASRCIHDDHCG  
SQASSVKQSRTNLSSMELPFRNDFAQPQPMKTFNSTFKSSYTFKQGHECPEQALEDRVMEEI  
PCEIYVRGREDSAQASISIDF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 348-369

**N-glycosylation sites.**

amino acids 311-315, 385-389, 453-457, 475-479

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 426-430, 479-483

**N-myristoylation sites.**

amino acids 22-28, 32-38, 54-60, 186-192, 279-285, 318-324,  
348-354, 352-358, 441-447

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**FIGURE 115**

GGTCTCTGTCCTGGCTGGCTCTGCGCTCTGGCTGAGCC**ATGTT**CCTCTCCTGCCCTC  
CTCACTGAGCTTGGAAAGACTGCAAGCCCACGAAGGTTCTGAAGGAATATTCTGCATGTCACA  
GTTCCACGGAAGATTAAGTCAAATGACAGTGAAGTTCAGAGAGGAAGATGATTACATCATT  
ACAATTGATGGACAACCTTACACTACATCTCGAAAACAATCATTCTTACCCCAGAACACTTT  
TTGGTTATACTATAATGAAACTGGATCTTGCATTCTGTCTCCATATTATGATGCAT  
TGCCATTACCAAGGATATGCTGCCAATTCCAATTCACTTGACACTCAGTATATGTTCT  
GGTCTCAGGGGATTCTCCAGTTGAAAATATCAGTTATGGAATTGAAACCAGTAGAACATTTCA  
GCAAGATTGAGCATATAATTATCAAATGAAAAATAATGATCCAAATGTATCCATTAGCA  
GTAATTACAGTCATATTGGCAGAAAAGACCAGCCCTACAAAGTCTTAAACTCACAGATA  
AAAAATCTTCAAAACTATTACCCCAATATCTGAAATATACATTATAGTGGAAAAGCTTG  
ATGTTACCCAGTTCAAATTGACTGTTACTGCTTCTTGGATTGTGGTCAAATGAAAAC  
CAGATTCCACCAGTGGGATGCTGATGATATTACAAAGATTGGCATGGAAACGGGAC  
TATCTCATCCTACGGCCCCATGACATAGCATACTTACTTGTTCAGGAAACATCCTAAATAT  
GTGGGAGCAACATTCTGGCACCGTATGCAATAAAAGCTATGATGCAGGTATTGCTATGTAT  
CCAGATGCAATAGTTGGAGGGATTTCGGTTATTAGCTCAACTGCTTGGCCTTAATGTA  
GGATTAAACATATGATGACATCACTCAGTCTGAGAGCTACATGCATCATGAATCAT  
GAAGCAGTGAGTGCCAGTGGTAGAAAGATTAGCAACTGCAGCATGCACGACTATAGATAT  
TTTGTTCAAAATTGAGCTAAATGCCCTCAGAAGCTTCAAATTGCAACCATTACATCAA  
AATCAACCAGTGTGGTAATGGGATTGGAAATCCAATGAAGAACATGTGACTGTGGTAATAAA  
AATGAATGTCAAATTAAAGAAGTGTGATTATAACACATGTAACAGGCTCAGTAAAAA  
TGTGGTTCTGGACCATGTTGACATCAAAGTGTGAGTTGTCATAGCAGGCACTCCATGTAGA  
AAGAGTATTGATCCAGAGTGTGATTTCAGAGTACTGCAATGGAACCTCTAGTAATTGTT  
CCTGACACTTATGCACTGAATGCCGTTGTGCAAGTGGAACTGCCTATTGCTATAACGGA  
CAATGTCAAACTACTGATAACCAGTGTGCAAGATATTGGAAAAGGTGCTCAAGGTGCTCCA  
TTTGCCTTTAAAGAAGTTAATTCTGTCATGAAAGATCTGAAAAGTGTGGTTAAAAT  
TCACAACCATTACCTTGTGAACGGAAGGATGTTCTGTGGAAAATTAGCTGTGTTAGCCA  
CATAAAAATGCTAATAAAAGTGAACGCTCAATCTACAGTTATTCAATATTCAAGACCATGTA  
TGTGTATCTATAGCCACTGGTCTCCATGAGATCAGATGGAACAGACAATGCCATTGTT  
GATGGCACCATGTTGTCAGAAATGTAAGTGTGAAATAAAACCTGCAGAAAAGTTCATTAA  
ATGGGATATAACTGTAATGCCACCACAAATGCAAGGGAAAGGGATATGTAATAATTGTT  
AATTGTCATGCTTCCCTGGACATAGACCTCCAGATTGTAATTCCAGTTGGTTCCCCAGGG  
GGTAGTATTGATGGAATTTCAGAAATCTGGTGAATTACTGAAAAGGCTACAAT  
ACACACTGGAACAACTGGTTATTCTGAGTTCTGCATTCTGCCGTTTCATAGTTTC  
ACCACTGTGATCTTAAAGAAATGAAATAAGTAAATCATGTAACAGAGAGAACATGCA  
AATCGTAATTCCCGTTGATCAGAAAGCGATGACGTGGACATTAAATTGACAGAACCTT  
CCATAGCAAATAACCTAAAGGAACGAAATGTGCTTATTATAACCTACGTTATCCCCAATGC  
ATTGTAATGTCAAACTTGGAAAATAAGCCTGCGTGCCCTCCC

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**FIGURE 116**

MFLLLALLTELGRLQAHEGSEGIFLHVTVPRKIKSNDSEVSERKMIYIITIDGQPYTLHLGKQ  
SFLPQNFLVYTNETGSLHSVSPYFMMHCHYQGYAAEFPNSFTLSICSGLRGFLQFENISYG  
IEPVESSARFEHIYQMKNNDPNVSILAVNYSHIWQKDQPYKVPLNSQIKNLSKLLPQYLEIY  
IIVEKALMFTQFKLTVILSSLELWSNENQISTSGDADDILQRFLAWKRDYLILRPHDIAYLLV  
YRKHPKYVGATFPGTVCNKSYDAGIAMYPDAIGLEGFSVIIAQLLGLNVGLTYDDITQCFCLR  
ATCIMNHEAVSASGRKIFSNCMSMDYRYFVSKFETKCLQKLSNLQPLHQNPVCNGFILESNE  
ECDCGNKNECQFKKCCDYNTCKLKGSKCGSGPCCTSKELSIAGTPCRKSIDPECDFTEYCN  
GTSSNCVPDTYALNGRLCKLGTAYCYNGQCQTTDNQCAKIFGKGAQGAPFACFKEVNSLHERS  
ENCDFKNSQPLPCERKDVLCGKLACVQPHKNANKSDAQSTVYSYIQDHVCVSIATGSSMRSDG  
TDNAYVADGTMCGPEMYCVNKTCKVHLMGYNCAATTCKKGKGICNNFGNCQCFPGHRPPDCK  
FQFGSPGGSIDDGNFQKSGDFYTEKGYNTHWNWFILSFCIFLPFFIVFTTVIFKRNEISKSC  
NRENAEYNRNSSVVSESDDVGH

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 665-684

**N-glycosylation sites.**amino acids 36-39, 76-79, 122-125, 149-152, 156-159, 177-180,  
270-273, 335-338, 441-444, 537-540, 587-590, 601-604, 703-706**Casein kinase II phosphorylation sites.**amino acids 74-77, 208-211, 221-224, 304-307, 337-340, 346-349,  
376-380, 415-418, 499-502, 639-642, 708-711**Tyrosine kinase phosphorylation site.**

amino acids 243-249

**N-myristoylation sites.**amino acids 53-58, 79-84, 266-271, 298-303, 372-377, 403-408,  
408-413, 442-447, 462-467, 469-474, 488-493, 567-572, 610-615,  
616-621, 634-639**Amidation site.**

amino acids 328-331

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**FIGURE 117**

CCACCGTCCGGACCGTGGGCTCAGTGGCGTCGCAGAAGGCTAAGGGAGTGTGGCG  
GGCGCTCCGGAGCCAACATGCCTCGTATGCGCAGCTGGCATGGCCCCGGCAGCG  
GAAGAGCACCTACTGTGCCACCAGTGGCCAGCACTGTGAAGCCCTAACCGGTCTGTCAAAGT  
TGTAAACCTGGATCCAGCAGCAGAACACTTCAACTACTCCGTATGGCTGACATCCGGGAAC  
GATCGAGGTGGATGATGTAATGGAGGATGATTCTCTGCGATTGGTCCAACGGAGGATTGGT  
ATTTGCATGGAGTACTTGCAATAATTGACTGGCTGGAGAACGTCTGGCCATGTAGA  
GGACGACTATATCCTTTGATTGTCAGGTCAAGATTGAGTTGTACACTCACCTGCCTGTGAT  
GAAACATCTGGTCCAGCAGCTCGAGCAGTGGGAGTCCGAGTCTGTGGAGTTTCTTGTGA  
TTCTCAGTTCATGGTGGAGTCATTCAAGTTATTCTGGCATCTTGGCAGCCCTGAGTGCAT  
GATCTCTCTAGAAATTCCGCAAGTCAACATCATGACAAAAATGGATCTGCTGAGTAAAAAAGC  
AAAAAAGGAAATTGAGAAATTAGATCCAGACATGTATTCTTTATTAGAAGATTCTACAAG  
TGACTTAAGAAGCAAAAATTCAAGAAACTGACTAAAGCTATATGTGGACTGATTGATGACTA  
CAGCATGGTCGATTTTACCTACGATCAGTCAGATGAAGAAAGCATGAACATTGTATTGCA  
GCATATTGATTTGCCATTCAATATGGAGAAGACCTAGAATTAAAGAACCAAAGGAACGTGA  
AGATGAGTCTCCTCTATGTTGACGAATATTCAAGAATGCCAGGATGAAT**TGA**AGAGTTA  
CTAAAAGTAACCCTAAAGAGCTTGTGGCAAACCAGCAGAACATTCTCTTCAAAAGGAT  
GCAATAGTAGAAAGCTACTTATTAAATGAAAAAAAGTAAAACCTCGTTCTTATCAGCCTCA  
TGCCTGAATCAAATTAAATTCTGAAACTGCTGCTGTTAAAGTGGATCTTTAGTAT  
TATAACAGCATCACTTAGATTTGTAAGTCAAAATTGAAATGAATGCACATAGATTATATA  
TAAATTAGCACCTGAGCTAACGTTAAGGCCGGTCTAAACTTATTTCACCTTTGTATTATTT  
TTGAGATGCAGGAATTACTGTAACAAAATATGTATGTCCGAAGGGAAAAAGCTGCAAGGATAT  
ATATAAGACCACTGCTTATCTGTATCTCCCATTTCCTATATTGAAAATGTATATTATTTAT  
ATAACTAAAAAGTAAAATAACTATGTTTGAGAT

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**FIGURE 118**

MPRYAQLVMGPAGSGKSTYCATMVQHCEALNRSVQVVNLDPAAEHFNYSVMADIRELIEVDDV  
MEDDSLRFGPNGGLVFCMEYFANNFDWLENCLGHVEDDYILFDCPGQIELYTHLPVMKHLVQQ  
LEQWEFRVCGVFLVDSQFMVESFKFISGILAALSAMISLEIPQVNIMTKMDLLSKAKKEIEK  
FLDPDMYSLLEDSTSDLRSKKFKKLTKAICGLIDDYSMVRFLPYDQSDEESMNIVLQHIDFAI  
QYGEDLEFKEPKEREDESSMFDEYFQECQDE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 151-170

**N-glycosylation sites.**

amino acids 31-35, 47-51

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 212-216

**Tyrosine kinase phosphorylation site.**

amino acids 189-197

**N-myristoylation sites.**

amino acids 13-19, 76-82, 154-160

**ATP/GTP-binding site motif A (P-loop).**

amino acids 10-18

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**FIGURE 119**

GGGCGCTGGGAGACACCGGACGCCGCTGGCTGCCTGGCTCAGGCCCGCTGGGCC  
GACCCGCTCGGTACCGCCGGCTGGCGCAGCTGCCGGCTGCCGCCAGGGCCATGCC  
AGGCCAACGAGGAGGCCACGCCATCCCCTAGCCCAGGTGGCCAGGTCTGCCACCG  
CGGGCCCTGGCC**ATG**GAGCCCCCTATTCTGCTGACGGCGCACTACGATGAGTTCCAAGA  
GGTCAAGTACGTGAGCCGCTGCCGGCGGGGGCGCGCGCGGGCTCCCTGCCCGGGCTT  
CCCCTGGCGCTGCCGTCAGCGTACCGGGGCCGGTCCGGCTGCCGCTGGAACCGCG  
CGAGGTGTGCCCTGCTGTCGGGCTGGTGTTCGCCGCCCTCTGCCATTCTGGCGCTAT  
GCTGCCCTCAAGTACCTGGGCCGGTCGCCGGCGCGCTGTCCCAGGGCTGCC  
TGAGCGAAGGCCCTGCCGCGCCGCTGCCCTGGCGCAACCTGGACGCCAGCATCGA  
CCATGCCAGGACTTCTACTCGTTCGCTGCCGCGGGTGGCTGCCGCCACGCCATCCCCGA  
CGACAAGCTCACCTATGCCACCATGCCGCCATGCCGAGCAAACGAGGAGGCCAACGGCG  
CCTGCTGGCGCCGGGGGGTGGGCTGCCGCCGGCGCGGCCAGCGCAAGGTGCCGCCTTCTT  
CCGCTCGTGCCTCGACATGCCGAGATCGAGCGACTGGGCCCGCACCCATGCTAGAGGTCT  
CGAGGACTGCCGGGCTGGGACCTGGCGCGCGAGGAGCGTCCGGGTCGCCGCCGATG  
GGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAGGCCGCCGCTTCTCGCT  
CACGGTCAGCTGGACGACAGGAACCTCGCGCTACGTACGCCATTGACCAGGATGGCT  
CACCTGCCAGAGAGGACCTGTACCTCGCTCAGGATGAGGACAGTGAGAACATCTGGCAGC  
ATACAGGGTGTTCATGGAGCGAGTGCCTCAGCTCTGGGTGAGACGCTGTGGAACAGAACGGC  
CCAAGAGATCTGCAAGTGGAGCAGCAGCTGCCAACATCACTGTGTCAGAGTATGACGACCT  
ACGGCGAGATGTCAGCTCATGTACAACAAAGGTGACGCTGGGCAGCTGCCAGAACAGATCCCC  
CCACTTGCCTGGAAAGTGGCTGCTAGACCAGATCTCCAGGAGGACTCTCAGAGGAAGAGGA  
GGTGGTGTGCTGGCGACAGACTACATGCCAGGTGTCGAGCTCATCCGCTCCACACCCCA  
CCGGTCTGACAACACTACCTGGTGTGGCGCGTGGTGGCTGAGTGAACACCTGTCCCC  
GCCATTCCGTGAGGCACTGCACGAGCTGGCACAGGAGATGGAGGGCAGCGACAAGCCACAGGA  
GCTGGCCGGGCTGCTGGTGGCCAGCCAATGCCACTTGGCATGGCGCTGGCGCCCTT  
TGTACATGAGCACTTCTCAGCCGCCAGCAAGCCAAGGTGAGCTAGTGGAAAGACATCAA  
GTACATCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCAGACAGGCTGCTGC  
TCGGGCCAGCTCCAGTACATGATGGTGTGGCTACCCGGACTTCTGTTGAAACACCGA  
TGCTGTGGACAAGGAGTATGAGTTGGTCCATGAGAACAGCTACTTCAAGAACATCTGAA  
CAGCATCCCCCTCAGCATCCAGCTCTCAGTTAAGAACATGGCAGGAGGTGGACAAGTCCAC  
GTGGCTGCTCCCCCACAGCGCTCAATGCCACTATCTACCCAAACAAGAACAGATGGT  
CCCCCGGGCATCCTGCAGCCCACCTGTACGACCCCTGACTTCCACAGTCTCTCAACTACGG  
GGCATCGCACCATATTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGCCAGTA  
TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCTCCTACAGGCCCTCTGCAAA  
GGCTGAGTGCATCGTCCGCTCTATGACAACACTCACTGTACAAACCAGCGGGTGAACGGAA  
ACACACGCTGGGAGAACATCGCAGATATGGCGCTCCTCAAGCTGGCTACCGCCTATCA  
GAAGTGGGTGCGGGAGCACGGCCAGAGCACCCACTTCCCGGCTCAAGTACACACATGACCA  
GCTCTCTCATGCCCTTGCCAGAACCTGGTGCATCAAGCGCGGTGCACTGCTACCT  
GCAGGTGCTGACTGACAAGCATGCCCTGAGCACTACAGGGTGTGGCAGTGTGCTCCAGTT  
TGAGGAGTTGGCGGGCTTCCACTGTCCCAAGGACTACCCATGAACCTGCCACAAGTG  
TTCCGTGTGG**TGA**GCTGGCTGCCGCCCTGCACGCCACTGCCGCCAGGAATCACCTCC  
TGCTGGCTACCGGGGAGGCATGCCGCCGGTGGCAGGCCAGGGCTCTGGCACCAACCTGCCCTTCC  
AGCCCTCCAGGACCCGGTCCCCCTGCTGCCCTCACTTCAGGAGGGCCTGGAGCAGGGTGA  
GGCTGGACTTGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTTAAGGGGG  
CCAGACCCTCTGCCAGGCTGGATTGTACGGGCCACCTCGCTGTGTTCTGCTGCAAAGTC  
TGGTCAATAAATCACTGCACTGTTAAAAAAA

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**FIGURE 120**

MEPPYSLTAHYDEFQEVKVSRGAGGARGASLPPGFPLGAARSVTGARSGLPRWNRREVCLL  
SGLVFAAGLCAILAAMLALKYLGPVAAGGGACPEGCPERKAFARAARFLAANLDASIDPCQDF  
YSFACGGWLRRHAIPDDKLTYGTIAAIGEQNEERLRLLPGGPGGAAQRKVRAFFRSCLD  
MREIERLGPRPMLEVIEDCGGWDLGGAERPGVAARWDLNRLLYKAQGVYSAALFSLTVSLD  
DRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAYRVFMERVLSSLGADAVEQKAQEILQ  
VEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLQIFQEDFSEEEVVLLA  
TDYMQQVSQLIRSTPHRVLHNLYLVWRVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVC  
LGQANRHFGMALGFVHEHFSAAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAARAKLQ  
YMMVMVGYPDFLLKPDADVKEYEFEVHEKTYFKNILNSIPFSIQLSVKKIRQEVDKSTWLPP  
QALNAYYLPNKNQMVFPAQILQPTLYDPDFPQSINYGIGITIIGHELTHGYDDWGGQYDRSGN  
LLHWWTTEASYSRFLRKAECEIVRLYDNFTVYNQRVNGKHTLGENIADMGVLKAYHAYQKWVRE  
HGPEHPLPRLKYTHDQLFFIAFAQNWCICKRRSQSIYLQVLTDKHAPEHYRVLGSVSQFEEFGR  
AFHCPKDSPMNPAHKCSVW

**Important features of the protein:****Transmembrane domain:**

amino acids 64-88

**N-glycosylation sites.**

amino acids 255-259, 322-326, 656-660

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 722-726

**N-myristoylation site.**amino acids 24-30, 26-32, 27-33, 40-46, 47-53, 65-71, 148-154,  
169-175, 170-176, 237-243, 450-456, 604-610, 607-613**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 85-96

**Prenyl group binding site.**

amino acids 772-777

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 609-619

**Neutral zinc metallopeptidases, zinc-binding region proteins.**

amino acids 609-619

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**FIGURE 121**

CGGACTGCCGGACCGCGC**ATGG**AGTCGACCGGCAGCGTCGGGAGGCCCGGGCGGACCC  
GGGTGCTGGTGGTGGCGCGCATCGCGGGCTGGCGCGCAGAGGCTCTGCAGGCCACT  
CCGCCTTCCCACCTGCCGGTCTGGAGGCCACGCCCGCCGGGCCATCCGCTCG  
AGCGCTGCTTCGGTGGCGTGGAGGTGGCGCGACTGGATCCATGGGCCCTCCGGGTA  
ACCCCGTCTTCCAGCTGGCTGCTGAGTACGGCTGCTGGGGAGAAGGAGCTGTCCCAGGAGA  
ACCAGCTGGTGGAGACCGGGGTACGTGGCCTGCCCTCCGTGAGCTACGCCAGCTCCGGG  
CCAGCGTGAGCCTCCAGCTGGTGGCGAGATGGCGACTCTGTTCTACGGCTGATAGACCAGA  
CCCGGAGATTCTGCACGCTGCAGAGACCCGGTCCCCAGCGTCGGGAGTACCTCAAGAAGG  
AGATTGCCAGCACGTGGCCGGCTGGACAGAGGATGAGGAGACCAGGAAGCTGAAGCTGGCG  
TCCTGAACTCCTCTTCAACCTGGAATGCTGTGAGCGGCACCCACAGCATGGACCTGGTGG  
CCCTGGCACCTTGGGGAGTATACCGTGCTGCCGGGCTGGACTGCACCTTCTAAGGGCT  
ATCAAGGACTCACAAACTGCATGATGCCGCCCTGCCGGAGGACACTGTAGTTTGAGAAC  
CTGTGAAGACCATCCACTGGAACGGGTCTTCCAGGAGGCAGCCTTCCGGGAGACCTTC  
CAGTGTGGTAGAGTGTGAGGATGGAGACCGGTTCCCGCGCACCATGTCATGTCACCGTGC  
CCTTAGGTTCTTAGGAAACATTGGACACCTTCTTGACCCCTCCCTGCCGGCTGAGAAGG  
CAGAACATCAGGAAGATAGGTTGGACCAACAACAAAATCTCCTGGAGTTGAGGAGC  
CCTCTGGAGCCAGACTGCCAGCTGATCCAGCTGGTGTGGAGGACACGTGCCCTGGAGG  
ATGCTGCCCTGAGCTACAGGACGCCCTGGTCCGGAGCTCATTGGCTTGTGGCTGCCTG  
CCTTGCCTGTCCACGTTCTGTGGTTCATGCCGACTTGAGTCTGAGTTCATGGAGA  
CTCTGCGATGAAGAAGTACTTCTGTGTCACCCAGTGCTCCGGAGAGTGACAGGAAACC  
CACGGCTCCCCCGCCCAAGAGCGCTCTGCCGTCTGGCACAGCGCCCCGTACACTAGGG  
GGCCTACAGCTACGTGGCCGTGGCAGTACTGGGGCGACCTGGACCTGCTGGCTCAGCCCC  
TCCCTGCAGACGGCGCCGGCCAGCTCCAGATCCTGTTGCCGGGAAGCCACACATCGCA  
CGTTTACTCCACGACGCACGGGCTCTGCTGCGGATGGAGGGAGGCCACCGCTCCTCA  
GTCTGTGGGCCCGCAGGTGCAGCAGCCCAGGCCAGGCT**TAG**CTGGCCAGCCTACTCTG  
TTCCACCCGTGTGGGGTAGGCTGGGACCGTCATTCTCTGACAGATTCAGTCTGGCTTG  
AAATTGGGGATTTAATGAGGGCTCTGGTTGGTAACCAGGGCACCTCTCAGTTCT  
TGTGTCTGTTATTGGAGTCTGGCCAGGGTTGACTTGAGCTGAGACACCAGATGCTCACGGAGA  
TGCTGGACACATAAGCAAGTTACAGCCACAAAAAA

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**FIGURE 122**

MESTGSVGEAPGGPRVLVVGGGIAGLGAQRLCGHSAPPHLRVLEATARAGGRIRSERCFGGV  
VEVGAHWIHGPSRGNPVFQLAAEYGLLGEKELSQEQLVETGGHVGLPSVSYASSGASVSQLQ  
VAEMATLFYGLIDQTREFLHAAETPVPSVGEYLKKEIGQHVAGWTEDEETRKLKLAVLNSFFN  
LECCVSGTHSMDLVALAPFGEYTVPGLDCTFSKGYQGLTNCMMAALPEDTVVFEKPVKTIHW  
NGSFQEAAFPGETFPVSVECEDGDRFPAAHHIVTVPLGFLREHLDTFFDPPLPAEKAEAIRKI  
GFGTNNKIFLEFEFPFWEPDCQLIQLVWEDTSPLEDAAPELQDAWFRKLIGFVVLPAFASVHV  
LCGFIAGLESEFMETLSDEEVLLCLTQVLRRVTGNPRLPAPKSVLRSRWHSAPYTRGSYSYVA  
VGSTGGDLDLLAQPLPADGAGAQLQILFAGEATHRTFYSTTHGALLSGWREADRLLSLWAPQV  
QQPRPRL

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 364-385

**N-glycosylation site.**

amino acids 253-257

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 408-412

**N-myristoylation sites.**amino acids 20-26, 21-27, 25-31, 105-111, 119-125, 164-170,  
216-222, 227-233, 443-449, 484-490**Aminooxidase Flavin containing amine oxidase:**

amino acids 23-497

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**FIGURE 123**

CGGACGCCTGGGGAAAGATGGATAAATAATTCTGTACACGTGCCCTGGCCTCTGGAGCTCAGCTGCCAGTCCAC  
GTCTAGGAATCTAGCATCTGGGACCAAGACACTTTACAGCAATCATCACCCCTTGAGAGGGAGGTGAGCTCAC  
CAGGACTCATCTGCCATTCAGACCTTTGCTGCTACCTGCCAGGTGGCCCCACTGCTGACGAGAGATGGTGA  
TCTCTCAGTCTCCCGGACTCTTGAAGCAGTATCGCTGACCCAGTCTTGTCTCTCATGCCACCTCC  
CCTTCAGGCCGGGAGCCGAGCTCAGAGCTCAGGCCAGTGGCCCTGAGTATCCCATCTGCCCTCGTCGGGA  
GGAGGTGGAGTTCCCGTGCACCTATGCCACAGCTGGCCAGCAGGAGATGGAGATCCGCTGGTCCGGAGTCA  
GACCTCAATGTGGTACACCTGTACAGGAGCAGCAGGAGCTCTGCCAGCAGTGGCCGTTCCGGAACAG  
GACCAAGTGGTCAAGGAGCAGCATGCCATGGCAGCTGGTCTGCCAGCTTACAGCATATCCCCTGACAA  
GGGCACATATGGCTGCCGCTTCACTCCGACAACCTCTCTGGCGAAGCTCTGGGAACTGGAGTAGCAGGGCT  
GGGCTCAGACCCCTACCTCTCCCTGAGGGCTCAAGGAAGGAGGCACTCAGCTGAGGCTCAGATCCAGTGGCTG  
GTACCCAAGCTAAGGTTCAAGTGGAGAGACCAACAGGGACAGTGCCTGCCCTCAGAGTTGAAGCCATCGTCTG  
GGATGCCAGGACCTGTCAGTCTGGAAACATCTGTGGTCTCCAGCAGCATGTGTCGGTCTC  
CATCCAGAATCTCTCTTGAGCCAGAAGAAAGAGTTGGTGGTCCAGATAGCAGACGTGTCACCCGGAGCCTC  
TGCCTGGAAAGAGCGCTGTCGCGACCCCTGCTGTTGGCTGCCCTGGCCCTGGCCGCTCTCC  
GAAGCAGGGAGAAGCCAGAAAAGCTGAGGAAGCAGGGGAGAAGAGACAAGAGAAAATCAGTGCAGAGCTGA  
AAAGCTTCAGACAGAGCTTGACTGGAGACGGGCTGAAGGCCAGGCTGAGTGGAGAGCAGCCCCAAAATATGCA  
GGATGTGACGCTGACCCGGCTCGCGCACCCCAGCCTGGAGGTGCGAGGATGGCAAGAGCAGTGTCTCC  
CGGGCGCCGCCAGGCCGGCTGCCACCCGAGCGGTTCTGGAGCAGACGTGCGCCTGAGCCTGGAGCG  
GTTCTCCGGCCGCGCCACTAGGGAGGTGACCGTGGCCGCGCAGCCGCTGGTCCCTGGCGCCTGCGTGGC  
CGCGGTGCCGCCGGGCGCTGCGCCCTGAGGCCCTGCGGGCTACTGGGCTGCTGGGCTGTGGAACCGGCTG  
CGAGTACTTCGTCCTGGCCCGCACCGCTCGCGCTCACCTCGCGTGGCCCTGGCGCTGGCGTCTCC  
GGACTACGAGGCCGGAGAGCTGTCCTCTCAACGTGTCGACGGCTCCACATCTCACCTCCACGACACCT  
CTCGGGCGCCTCTGTGCGTACTTCAGGCCAGGGCCACGACGGCGCGAACATCCGGATCCCCTGACCATCTG  
CCCCTGCCGGTAGAGGGAGGGCTCCCCGAAGAGAACAGTGCACACCTGGCTACAGCCCTATGAGCCCG  
GGACCCCGCCCTGGACTGGTGGTCAAGGCCCTCGTGGCGCGGACTGGCCGGGGCCCTGGATCC  
GCCAGCGCTTGCTCTCCCTCGCTGAAGGGAGCAGGTGCAACAGCAAATGTCAGCGAGGGGACAAAGA  
GAGGGACCTTGCCTACCGTAGATGTGATGTGAGTGGATTTCTCAAGGAAGGAGACAAGTCAAAGCTCG  
TTTGTGGATTGTGGACTGAGCCAGGACTACAAATATCCACGTCGCTCAGAGCTGGGTGCTCACGGTGGC  
GGTGGCAAGAAGCCAGCATGGAGAAAGAAGGGAGAAAATTTGGTGACTIONGCCTAGAGGATCAGTTAATTG  
TATAGTTTATATTTTGTATATGTTGCTAGCTCTAAAGGTGAGATGCAATAACACTCGTAAGCAACGA  
GTTCACCTAAGTAAGGCTCAGATCTCTAGTTAAAACCATTCCCATAAAATGAAGTGGAGGAACAGTGTCT  
TCTGAGCCGGGCAAAATTCAAGGTGAGCCTGGAGCATTGTGTGGTGAAGAAAATAAGGCTAAAAGT  
GACGGCAACCGGCAAAAGGGTAGGGAGCCAGGCCAGGGCCTCACTGACCAATTGTGGACAATTGAACAT  
CAGGATGAATAATGACAGGAGAGATTATAACACACTGAAATAAAACATAATCCATGAGTTCATGCTGATACTCAA  
ATTTCTTTAAAAGGAGAAACAGGAAGGTTCTTGGAGGTGAATCTAAATTATGGTGAAGGTCTGGAGA  
ACAGGCTGTTCCAGTCTCAAAGCAGTAACTTATACACTACTATAAGTTGAAGGGGAAGGTTACCTTAC  
AATGGAGACATCTACAGATCATCCAAGTGAATTAAACATCATCAATGATGGGACCAAGGACATTATTAGT  
TTGACAACGGGAAAGTGTCTCACCCCTACCCCAAGACATTCTCTGTCGGCAGGCTGGAGTGC  
GCCTCAACCTCTGGGCCAAGTGAATCCTCCACCTCAGCACACAACACCATGCCAATTAAAGTGCCTATAG  
AGACGGGGCTCACTTGTACCCAGGCTGGTCTCAAACCTCTGCCCTCAAGCAATCCTCCACCTGGCCTCC  
CAAATGCTGGTCTACAGGCTGAGCCGCTGTGCCTGGCTTATTTCAGAGTGAAGACATTGTACTGTGGCTA  
TGTAGGAGAACATTGTTCTAGCAAACATACTGAAGTTTAGATATAATTACACAGTGTCTGCCACTGA  
ATTCAGTGAACAGTGGAAAAAATAAAACATATGAATATAAGGAAAGAGACAAGTCAAATGTAGTAAA  
ATGACAACACTTGGTGACTIONGTTGACAGATGTTCATGTTACTATCAATGTCAGGTTGCTGTGGGT  
TTGAAATTTCGAAACTAAGAGTTGGTGGGGGAGAAGGATACACCAAAAACATAAGTGAATTATCTGGATG  
GGAAAATGTTGGTATTGCAATTCTAAAATGTCTTTGTTAATGTCATAATGTATATGATCAG  
TTCTGTAATAAGGGAAACACTTTCA

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**FIGURE 124**

MVDLSVSPDSLKPVS LTSSLVFLMHL LQLPGEPSSEVKVLGPEY PILALVGEEVEFPCHLWP  
QLDAQQMEIRWFRSQTFNVVHLYQEQQELPGRQMPAFRNRTKLVKDDIAYGSVVLQLHSIIPS  
DKGTYGCRFHSDNFSGEALWELEVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDH  
QGQCLPPEFEAIWDAQDLSLETSVVVRAGALSNVSVSIQNLLSQKKELVVQIADVFVPGA  
SAWKSAFVATLP LLVLAALALGVLRKQRRSREKLRKQAEKRQEKLTAEKLQTELDWRAE  
GQA EWRAAQKYAVDVTLD PASAHPSLEV SEDGKS VSSRG APPGPAPGHPQRFSEQTCA LS ER  
FSAGRHYWEHV GRRSRWFLGACLA AVPRAGPARL SPAAGYWL GLWNGCEYFVLAPH RVALT  
LRVPPRRLGVFL DYEAGELSFFNVSDGSHIFTFHDTFS GALCAYFRP RAHDGGEHPDPLTICP  
LPVRGTGVPEENDSDTWLQPYEPADPALDW

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 247-272

**N-glycosylation sites.**

amino acids 102-106, 139-143, 224-228, 464-468, 516-520

**Tyrosine kinase phosphorylation site.**

amino acids 105-114

**N-myristoylation sites.**

amino acids 129-135, 220-226, 399-405, 423-429, 480-486

**Amidation site.**

amino acids 390-394

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**FIGURE 125**

TATAGTCCCAGCTACTCATGGGCTGATGCAGGTTGAGGCAGGAGGTTCATGAGCCCAGGGAGGTTGGAGCTGTAA  
 TGAGCTAGGATTCTGCCTCTGCACTCCTAGCTGGATGACAGAGCAAGACCCCTGTCTCAAAAAAAGAAAAAAA  
 AAAAAGAATGCATGAACCAGACATGACAGTTCTGGCTCAAAGATCTCCAATAAGGAAATGATTTTTTAACC  
 ACCAATGCTGCAGGAAAAAGCAACATATTTAAGTTATCCAATAACACCTATCCAATAATTGTAATCATTATCAT  
 GACATTGAGCTGTTATTTCTTTAGGTGAAACACCCATTCAAAGTCAGTCAATCTCTTCA  
 CCTAAAGAGTTGGGCTGATCATGTCCTAAACCTTGGACAGGAATGATGAAACATTTTGATGAGATATAGG  
 ATGTATGAAACTGTGATGAAGGCCCTGAAGATAGAGGCTCTTATGGTGTGAAACATGTCAGTCTCCCTAT  
 ATTTGAAAGGACCAGTGTACCATGAGTACTGTGAGTGTGAGGAGCTCCAGGAGAAGACTCTTCT  
 TGTCCAACCAAGGAACCACAGATTGCAAAAGATTTCCTCCAGCATCAATCTCCAGCAAATGCTAAAAA  
 GAAGTCCCAGGTTGGGATGAGAGAGGTGCCATTGTCATTACACGATCTCAATAACCATGTTACCGG  
 AGATCTTAGGAAATACACAGACTTCAGATGTTCTGATGAGATTGTTATCATTGACAAGAAAGGTCCTT  
 CTCCAGATTAGAATTATGTTATCTTGAGATTGGCCCTGGAGATCGAAAAGTCATGGAACCCCTAGC  
 CCCATACCTATCATTCATGGTGTGGCTCTGGATTCAAGAGATGTTGTCCTTCAACGTATGACATACCCAC  
 TCCATGTTGAAGCCATGGGGGTTCACAAATGATCTCTCTATTCAAGGGAAATACAGGGCCTCTGGATC  
 AATAAACAGAGAGAGCTTCTCAGAGGTAGAGACAGCCGAGAGGAGGCTCAGTGGTACAGCTGTCAAA  
 GAAAATCTCAGCTACTAGATGCAGGAATTACAGGATATTCTTCTCAAGAGAAAAGGAGCTTGGAAAAA  
 GCCAAGTTGATGGGTTCTTGATTCTTAAGTACAAGTATCAAGTAAATGTTGAGATGGACCGTGGCTGCTTAC  
 AGATATCCATATCTCATGCTGGGAGCAGTCTGGTTAAAGCAGGACTGCCATATTATGACATATTCTACATG  
 GCACTAGAACCTTGAAGCATTATGTCATTAAAGAAATCTGAGTGTATTAGAGAAAGTTAAATGGGCT  
 AAGGAAATGATGAAGAACAGGAAAGATTGCAAAAGAAGGACAGTGTGATGGCTAGGGACCTACTACAGCCACAC  
 AGGCTTACTGCTACTATTACAAAGTACTGCAGAAATATGCGAGGCCAGTCAGCAAACCGAAGTACGTGAT  
 GGAATGGAACCTGTCTCAGCCAGAAGATGCGACAGCCATCTGCCAGTGGCACAGGAAAAGCCTCAAGAGAA  
 GAACTTTGAGTCAGGGCAGAACATCACCTCTGTGTATCCCGTACACTTTAAAGGAAAGATTGAACTAACGCT  
 GAAGGACAGTATAGAAGACTGCACCAAGTGGACTAGTCTCCCGGGCTTATATGAGATGGATATAGCAG  
 TACTGGTGTAGTATCCCTCATCTGAAATGCTTAGGACAGGAGTGTTCAGGCTCAGATTGTTAAGATTGGG  
 AATATTGTCATGTACATAATGAGGTATCTGGGATGAGATCCAAGTCTAAACACAAAATTCAATTATTTAT  
 ATATACCTTGTTCACATACCTGAAGGTAATTATATAATTATTTAATAATTGTGTCATGAAACAAAGTTGT  
 ATACATGAACTGTCAAGAACAGGTGTCACTATCTAGCACCAGTGGTGTGTCAGCACTAAAAAGTT  
 TTGGATTGGGTTATTCAGATTAGTTGATGAGGAAATGTCACCTGAACTGTGTTATTGAAACAGCATACCA  
 AATATCATTGAATATTAAATCTTGTGTAAGGAAACTGCTTATTCAGCATGATGTTCTAAAGAAAAGAAACT  
 TGGGGATCATAGCCGATAGAGAGACTTGCTAAATATAATCAGCCTCTGCAAACACTGTTACATATTGTT  
 TTACATATTGTTATTCTATCCCCGTTCACCTTCTCTTCACTTCAATTATGAAGAGAAAATAT  
 TTGTCAGGGTGTCCCCCGCCCCCGTCACTGCATAATTCTCTTACAAGCTGTTGGCTTCTATTAA  
 TAACAGCTCTTTAGAAGGCTGATAAGGATATTAAAGGAAGAAGAATGACTCTGTTATTAAAGGTGGCAT  
 GGAGACTGTGGAGGAATATTAAAGCAACTCATATCTTAAACTAAATTGGCAAGGCCAGACAA  
 CATTAAGGAGAAATGTACCTTAAGTGTAGTAAATCCAAATCTATCTGAGTTGTAACCCATCAAAGACAATACAG  
 TTATTACATAGATGAAGGTATGCTATAGGCATCATTCTATTATCTTATATTGAATAGGTGAAAGATAACTGTAG  
 TCAGGGAAAGGCATTGTCATTAAAGCTGAAAAGGGGATCTTGAAAACACTGAAAACCTCTACAAACAACT  
 TCAGGAAGCCTGCTATCTGGGATTCACTAATAATAGGCCAAGAACAAAGGCAAGCATTCTCACTCCACC  
 ACTTTCTATTTCAGTGGGTGTCATTGCTACGATGAAGACTTTGGAAATTCTCTTCTTCTAGGACAGGGTCA  
 GGATTAGGACTCATAGCCTGAAGCTCATTACATACTCTGTAAACCATCAGTCAAGGTTGAGTCAACTAAAG  
 TGCATGTTCTAAACAAAGACTATCTCATTCCAAATTAAATATGTAECTCTGGCCGGTGCAGTGGCTCAG  
 CCTGTAATCCCAGCACTTGGCAGGGAGATGGCGATCTTGGAGGTAGGGAGCAGGCCCTGGCA  
 ACATGGTAAACCCCGTCTACTAAAAAATAGCCAGGCTGGGCAATTGCTGAACTTCTGCTTAATCCAGCT  
 ACTCGGGAGGCTGAGGGCAGGAGAATCACTGAACTGGGAGGAGGGTGCAGTGTGAGGATTACCAACTG  
 CACTCCAGCCTGGGTGACAGAGTGAAGACTCCATCTCAAAACTGAAAATAAAAAATATGTAATTCTCTAA  
 CTGAAATATTACTTAATCTGGAAAACAATGTAACATTAAAGGTTACATCTATTCTGCTGAAGAACAA  
 TAAACAGAATTGTTGACTAAGCATAACCAATTTCAGAACAGTCTAATCAATGCCAAGTATCCAAGGCAAACCTC  
 TAATACCCATCCATTGTGCAAACACACAAGCACGCAAGTATTAATAAGAGCAAGCTGTCCTGAGCCCATACCTA  
 ATGAATTGTGCTTAAATATTGTAACATTGTGTTGAGGCTGTCAAACACTGGGATTATGGCAAGAAAGGTTGCC  
 TAACCTACACCTTCTGCCCTCAAATTCCAGGTGCTAAAGGCTAATGCAATTAAACATCTTACATTAA  
 TTTATATTGCTCTGCCAAACAGGCTAATGTTAAAGGCAAGTGGAGACAAACAGGAGGCTAATCTACA  
 TAATTCTCATCTGCCAATTCAAGCGCAGGCTTAAAGAGTTAGTGTAAATGGCTTCTGGTTGAAACAAAAA  
 ATGCATCTATGTGGTGAAGGTTGGGAGGAGTTCACCAATTATGAGGAGAAGATGGAGTGAAGGAATTCTT  
 ACTTTTGCTTATACCTTCTATAATTAGATTTTTACTGTAAGTATGGTCAAATTGCAAAATTAAG  
 AAAAATGCCAACCTAGAAAAGACAATAATGCAACAAAGATAAAACAGGAACAGCAAATATTATATTTC  
 CATTGCTCTTTAAATCTATGTTAGAACCTTATCTGGGACTTATGTATATATACCTTTAAATAAA  
 ATAATTTCTAAATAAAAGTTG

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**FIGURE 126**

MVELFIFLFLGETPFKVVVKSLSPKELVRIHVPKPLDRNDGTFLMRYRMYETVDEGLKIEVL  
YGDEHVAQSPYILKGPVYHEYCECPEDPQAWQKTLSCPTEPQIAKDFASFPSINLQQMLKEV  
PKRGDERGAIHVHTILNNHVYRRSLGKYTDKMFSDIELLSLTKVLLPDILEFYVNLDWPL  
EHRKVNGTPSPIPIISWCGSLDSRDVVLPTYDITHSMLEAMRGVTNDLSSIQGNTGPSWINKT  
ERAFFGRGRDSREERLQLVQLSKENPQLLDAGITGYFFFQEKEKELGAKLMGFDFFKYKYQV  
NVDGTVAAYRPYLMLGDSLVLKDQSPYYEHFYMALEPWKHYPVPIKRNLSDLLEKVKWAKEND  
EEAKKIAKEGQLMARDDLQPHRLYCYYYQVLQKYAERQSSKPEVRDGMELVPQPEDSTAICQC  
HRKKPSREEL

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 250-254, 363-367

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 444-448

**N-myristoylation site.**

amino acids 208-214, 319-325, 388-394

**Endoplasmic reticulum targeting sequence.**

amino acids 448-453

**Mitochondrial energy transfer proteins signature.**

amino acids 25-34

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**FIGURE 127**

AGCCGTCGGAGGGAGCCGGAGCGCTCTCCGAGTTGGTGTAGATTGGTGGTCATCCAACAT  
GCAGAAATGAATGAGCAGTGAAAGCAGCAGAGCCGATGGGTATGAGGATGTAAGTGCCTT  
GAAGGCTTCCACACCCTACTCCAGGAATCATGAATAAACTGGAGGATAAGCAGGACCAGAT  
GATACCATGAAGAGAAGTTACAGGCCCTATTGCCAACGTGTTAAGTTCCCTGCTGATCTTG  
GCACTGACCGAAGCGTGGCATTGCCATCCAGGAACCCTCCAGGAATCTTCAGGTC  
CTCCCTCAGGCACTCCCCGGAACATGGTACAGCAGCCCACAGCTTACCAAGACATACT  
TCTGTGGTGTGCTGACCCCCAATCCCAGTGGACCCCCCTCACAGGCTGCAGCTCCATGGCA  
ACACTGACACCCGTGCAGAGGGGCAACCTCACGCACACCCTCCACATCTCCACCATCGCTGCGACA  
GTAACCGCCCCCTATTCTGAAAGCTCCCTGTCCACAGGGCCGCTCAGCAGCCATGGCAACC  
ACATCCTCCAAGCCAGAGGGCCGCCCTCGAGGGCAGGCTGCCCCCACCATCCTGCTGACAAG  
CCACCGGGGGCACCAGCCGCCACACAGGCCACCCACTACCCACACGCAGGCCCC  
AGGCCACAGGCTTCCCGAAAAGGGGCTGGTAATTCATCACGCCCTGTCCCCCTGCACCT  
GGTGGCCACTCCAGGAGTAAAGAAGGACAGCGAGGACGAATCCAAGCTCCACACCTCTGGGG  
CAGAAGCGGCCCTGGGAAAATCTTCAGATCTACAAGGGCAACTTCACAGGGTCTGGAA  
CCAGAGCCCTTACCCCTCACCCCCAGGACCCACTCTGGGCTACTCCTTTCACCACAGCC  
CAGACAGTGGCTGCACAGTGCACAGCAATACCTCATGGCACCCACCACCTCCCTG  
GGCCTGCAAAGGACAAGCCAGGCCCTCGCAGAGCAGCCAGGGGGTGGTCTACCTTCACC  
AGCCAAGGAGGGACACCAGATGCCACAGCAGCCTCAGGTGCCCTGTCACTCCACAAGCTGCC  
CCAGTGCCTTCTCAGGCCACACAGGTGACCCACAGGATGGCCAGGCCATAGTGA  
TGGCTACTGTTACCCCTGGCACCGACAGCAGACCTCTGTCTACCAGCTCTGGGTCTCAGGCT  
GCCACGGGGCCCACCCAGCTGCCTTCAGATACCAGTGTCTCAGCCCTTCCAGGGGATCCT  
CAGGGAGCATCCACAACCCCACAAGCTCAACCCATCCCTCAGGGTCTCAGAAAGCA  
TCTGGAGCCAAGGAGGAGACTGTGGCACCCCTACCATGACCGACGGGTGCCAGTCC  
TCCACAGTGGTATCCACAGCCACAGGAATTCCCTCAACCGCTGGTCCCCGCCGGACCTGG  
AAGCCTGGGACAGCAGGGAACATCTCCATGTGGCGAGGGGACAAACCGCAGCACAGGCC  
ACCATCTGCCTGAGCAAGATGGATATGCCCTGGGTGATCTGGCCATCAGCGTCCCC  
TCCTGCTCTGCTGCTGACGGTGTGCTGCATGAAGAGGAAGAAGAACGCCAACCGGAG  
AACAAACCTGAGCTACTGGAACACACCATCACCAGTGGACTACTTCACAGGCATGCTGGAG  
CTGCCAGGGAGATCCAGTCCCTGAAACCTCTGAGGACAGCTCAGAGCCCCGCTCCCC  
GCCAATGGCGACTATAGAGACACTGGGATGGTCTTAAACCCCTCTGTCAAGAAACACTG  
TTTGTGGAAACGATCAAGTATCTGAGATCTAACTACAGCAGGCATCAGTGGCTT  
TTTTCTGCTCTAAATTATAAAATACAAATATATATATATAAAATATAACCTTGTCAAC  
TGACTTAATGAGAACATTTCAGTTTCTATGAATTGTCAACATCTTTTACAAGT  
GTGGTTAAAAAAAAAACTTACAGAATGATCTGTGGCTTATAAAATAAAGGTATTCT  
AAGCAAAAAAAAAAAAAAA

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**FIGURE 128**

MKRSLQALYCQLLSFLLILALTEALAFAIQEPESPRESLQVLPSGTPPGTMVTAPHSSTRHTSV  
VMLTPNPDGPPSQAAAPMATTLPRAEGHPPHTISTIAATVTAPYSESSLSTGPAPAAMATTS  
SKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTRRRPRPGSSRKGAGNSSRPVPPAPGG  
HSRSKEGQRGRNPSSTPLGQKRLGKIFQIYKGNFTGSVEPEPSTLTPTPLWGYSSSPQPQT  
VAATTVPNSNTSWAPTTSLGPAKDKPGLRRAAQGGSTFTSQGGTPDATAASGAPVSPQAAPV  
PSQRPHHGDPQDGPSHSDSWLTVPGTSPRPLSTSSGVFTAATGPTPAAFDTVSAPSQGIPQG  
ASTTPQAPTHPSRVSESTISGAKEETVATLTMDRVPSPPLSTVVSTATGNFLNRLVPAGTWKP  
GTAGNISHVAEGDKPQHRATICLSKMDIAWVILAISVPISSCSVLLTVCCMKRKKKTANPENN  
LSYWNNNTITMDYFNRHAVELPREIQSLETSEDQLSEPRSPANGDYRDTGMVLVNPFQCQETLFV  
GNDQVSEI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 469-487

**N-glycosylation sites.**

amino acids 178-182, 223-227, 261-265, 446-450, 504-508, 509-513

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 495-499

**N-myristoylation sites.**

amino acids 44-50, 48-54, 175-181, 222-228, 279-285, 286-292,  
288-294, 296-302, 351-357, 374-380, 427-433, 442-448

**TonB-dependent receptor proteins signature 1.**

amino acids 1-44

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**FIGURE 129**

AGGGGAGGGCGGGCGCCGCTGCACACACGCACACGGAGCTATGGGGTGCCATGTTGCCACCAG  
CTGCCACGTGGCCTGGCTTTGGTCTGATCTCTGGATGCTGGGCCAGGTGAACCGGCTGCC  
CTTCTTCACCAACCACCTCTTGATACATACCTGCTGATCAGCGAGGACACGCCCTGTGGGTTCTGG  
TTCTGTGACCCAGTTGCTGGCCAAGACATGGACAATGACCCCTGGTGTGGCTCCGGCAGGCC  
GGAGGAGGCCTCGCTTTCAGTGGAGCCTGACACTGGCGTGGTGTGGCTCCGGCAGGCC  
ACTGGACAGAGAGACCAAGTCAGAGTTCACCGTGGAGTTCTCTGTGTCAGCGACCACCAAGGGGT  
GATCACACGGAAAGGTGAACATCCAGGTGGGGATGTGAATGACAACGCGCCACATTTCACAA  
TCAGCCCTACAGCGTCCGCATCCCTGAGAATACACCAGTGGGACGCCATCTCATCGTGA  
TGCCACAGACCCCGACTTGGGGCAGGGGCGAGCGTCCCTACTCCTCCAGCCCCCTCCCA  
ATTCTCGCCATTGACAGCGCCCGCGGTATCGTCACAGTGATCCGGGAGCTGGACTACGAGAC  
CACACAGGCCTACCACTACGGTCACGCCAACAGATCAAGACAAGACCAGGCCTGTCCAC  
CCTGGCCAACTTGCCATCATCATCACAGATGCCAGGACATGGACCCCATCTCATCACACCT  
GCCTTACAGCACCAACATCTACGAGCATTCTCCTCCGGGCACGACGGTGCATCATCACCGC  
CATAGACCAGGATAAAGGACGTCCCCGGGCATTGGCTACACCATGTTCAAGGGAAATACCAA  
CAGCATCTTGGCCCTGGACTACATCAGCGGAGTGCTGACCTGAATGGCCTGCTGGACCGGGA  
GAACCCCCCTGTACAGCCATGGCTCATCTGACTGTGAAGGGCACGGAGCTGAACGATGACCG  
CACCCCATCTGACGCTACAGTCACCGACCTCAATATCCTGGTTATTGACATCAATGACAA  
TGCCCCGGAGTTCAACAGCTCCGAGTACAGCGTGGCCATCACTGAGCTGGCACAGGTGGCTT  
TGCCCCCTCCACTCTCATCCAGGTGGTGGACAAGGATGAGAATTGGGCTGAACAGCATGTT  
TGAGGTGACTTGGTGGGAACAACCTCCCACCTCATCATCTCCCCGACCTCCGTCCAGGG  
GAAGGGGACATTCTGATTGGGTGGCCATCCACTGGACTACGAGACCGTGGACCGCTACGA  
CTTTGATCTCTTGCCAATGAGAGTGTGCCTGACCATGTGGCTATGCCAAGGTGAAGATCAC  
TCTCATCAATGAAAATGACAACCGGCCATCTCAGCCAGCCACTGTACAACATCAGCTGTA  
CGAGAACGTACCGTGGGACCTCTGTGCTGACAGTCCTGGTAGTCCCCGCTTCACTGCAGG  
GCCACTGAGCTCTCCAGGGCCACTGTGGTAGGGCACCCAGAGGGATTGTCCAAGGGACCT  
CAGCAATCAGGGAAAGGAGGCACCCCCAAATCCCTGAGCTGTGTTGGTGTATTAAAAAAA  
GTTTTGGACTCTCAGGAAGGGCTCCCTGACCTAGGGTGAATATGGAAAAGGAGC  
CTGAGGGGTGACGAGACTGAGCTGAGGACACTGGTTTCTGCCCTTCCCTGAGAGAGACTCAG  
TGAGGGTGGCTGGAGCCCTGGAAGCCCCCTAAATGGTGGAAAGGTGCCAGCCATCCTG  
AGAAGGGCAACCCCTCTCATGTGAGCACAGGCACCAAGAGGGCAGGGCCTGGAGGGTACC  
GGGGCACCCCCAGCTGCCCATGGCTGGACTTGGCTTGACAAGGGCCCTCCAGTGTCA  
TGTATCTGTCAGTACTCTGGTTGCAAGGGACAGAAACCTTAAGTAGTTCAAGAAAAAGG  
ATTGGCTCATGTAACCTAAAAGTATAAGTGATTTCAGGCCGGCTCGGTGGCTCACGCC  
ATCCAACACCTTGAGAAAGCCGAGGTGGCGGATCACTTGAGGTGGAGTTGAGACCAGCC  
TGGCCAACATGGAAAACCCGTCTACTAAAAAATACAAAATTAGCCGGGTGTGGTGGC  
ACGCCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGC  
AGGTTGCAGTGAGCCGAGATTGTGTCAGTGCCTCCAGCCTGGCGACAGAGCCAGATTCTG  
CTC

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**FIGURE 130**

MGCHVATSCHVAWLVLISGCWGQVNRLPFFTNHFFDTYLLISEDPVGSSVTQLLAQDMND  
PLVFGVSGEEASRFFAVEPDTGVVWLRQPLDRETKSEFTVEFSVSDHQGVITRKVNIQVGDVN  
DNAPTFHNQPYSVRIPENTPVGTPIFIVNATDPDLGAGGSVLYSFQPPSQFFAIDSARGIVTV  
IRELDYETTQAYQLTVNATDQDKTRPLSTLANLAIITDVQDMDPIFINLPYSTNIYEHSPPG  
TTVRIITAIDQDKGRPRGIGYTIVSGNTNSIFALDYISGVTLNGLLDRENPLYSHGFILTVK  
GTELNDDRTPSDATVTTFNILVIDINDNAPEFNSSEYSVAITELAQVGFALPLFIQVVDKDE  
NLGLNSMFEVYLGVNNSHFIISPTSVQGKADIRIRVAIPLDYETVDRYDFDLFANESVPDHV  
GYAKVKITLINENDNRPIFSQPLYNISLYENVTVGTSVLTVLSPRFTAGPLSSPGPTVVRHP  
EGFCPRDLSNQGRRHPQIPELCLLVY

**Important features of the protein:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 355-374

**N-glycosylation sites.**amino acids 155-159, 206-210, 349-353, 393-397, 434-438, 466-470,  
472-476**N-myristoylation sites.**

amino acids 2-8, 49-55, 162-168, 270-276, 278-284, 316-322

**Amidation site.**

amino acids 515-519

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**Leucine zipper pattern.**

amino acids 298-320

**PTS HPR component serine phosphorylation site signature.**

amino acids 377-393

**Cadherins extracellular repeated domain signature.**

amino acids 120-131, 336-347

**Cadherins extracellular**

amino acids 120-144, 336-360

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**FIGURE 131**

GTGGGCCGCCCCCTGCTGCGTCCATGCTGATGTTGCGGTGATCGTGGCCTCCAGCGGGC  
TGCTGCTCATGATCGAGCGGGGCATCTGGCCGAGATGAAGCCCCTGCCCTGCACCCGCCG  
GCCGCAGGGCACAGCCTGGCGGGAAAGCCCCAAGCCTGGGGCCTGTCCTCAGGGCTG  
GGGACGCGGACTTGCAAGTGCAGGACGTCCGGAACAGGACCCCTGCGGGCGGTGTGCGGAC  
AGCCAGGCATGCCCGGGACCCCTGGGACTTGCGGTGGGCAGCGCGCACCCCTGCTGCGCC  
ACATCCTCGTAAGTGCACGTTACCGCTTCCTACTGCTACGTCCCCAAGGTGGCCTGCTCTA  
ACTGGAAGCGGGTGTGAAGGTGCTGGCAGGCGTCCCTGGACAGCGTGGACGTCGCCCTCAAGA  
TGGACCACCGCAGTGACCTGGTGTTCCTGGCCGACCTGCGGCCTGAGGAGATTGCTACCGCC  
TGCAGCACTACTTAAGTTCCTGTTGTGCAGGAGCCCTTGGAACGCCTCCTCTGCCTTAC  
GCAACAAGTTGGCGAGATCCGAGAGTACCAAGAACGCTATGGGCTGAGATAGTGAGGCGGT  
ACAGGGCTGGAGCGGGGCCAGCCCTGCAGGCGACGATGTCACATTCCCCGAGTTCTGAGAT  
ACCTGGTGGATGAGGACCCCTGAGCGCATGAATGAGCATTGGATGCCGTGTACCACTGTGCC  
AGCCTGTGCCGTGCACTATGACTTGTGGCTCCTATGAGAGGCTGGAGGCTGATGCAAATC  
AGGTGCTGGAGTGGGTACGGGACCAACCTCACGTCCGATTCCAGCTGCCAGGCCTGGTACC  
GGCCAGCCAGCCCCGAAAGCCTGCATTACCACTTGTGCAGTGCCTGGGGCCCTGCTGCAGG  
ATGTGCTGCCTAAGTATATCCTGGACTTCTCCCTTTGCCCTACCCACTGCCTAATGTCACCA  
AGGAGGCGTGTCAGTACATGGGTGTGGGCCAGCAGCTGGTGGGACTGGTTCAACG  
CCAGCTTCTGTGCTTCTGCCCTGTCATTGGAGAAACTCTGGCTCTGGGCTTGGGCTTCTC  
AGGATCCTGGATGGCAGAGACTGCCCTCAGAAGTTCTGTCCAGGGTGGCACCCACAGTGA  
CTCAGAGGACAGGGCTAGGCAGGAGACCTGCTGCTCCCTATTGGGGGATCTCTGGGGGCA  
GACACCAGTTGCCAATGAAGAACACATCTGATCTAAAGACTGGCTCCAGACCCGGGCTGC  
CAGGATTATGCAGTCCACTGGTCTACCTTAATTAAACCTGTGCCAAACTCAGAGATGGTAC  
CAGCCAGGGCAAGCATGACCAGAGCCAGGGACCCCTGTGGCTCTGATCCCCATTATCCACC  
CCATGTGCCCTCAGGACTAGAGTGAGCAATCACCTTATAAAATGACTTTGTGCCCTTGCT  
CCAGTCTAAAATTCTACACCTGCCAGTTCTTACATTTCAGGAAAGGAAACGGAA  
GCAGGGTTCTGCCCTGGTAGCTCCAGGACCCAGCTCTGCAGGCACCCAAAGACCCCTGTGCC  
CAGCCTTCTGAGTTCTCGGAACCTCCCTCCATTCTCCCTCCCTCCCCACAAGGCCT  
TTGAGGGTGTGACTGTGGCTGGTATATCTGGCTGCCATTCTGATGCATTATTAAAATT  
TGTACTTTGATAGAACCTTGTAAAGGGCTTGTCTTCTAATAGCTGACTTTAATAAG  
CAGTTTATATAT

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**FIGURE 132**

MLMFAVIVASSGLLMIERGILAEAKPLPLHPPGREGTAWRGKAPKPGGLSLRAGDADLQVRQ  
DVRNRTLRAVCQPGMPRDPWDLPVGQRRTLLRHILVSDRYRFLYCYVPKVACSNWKVMKVL  
AGVLDSDVRLKMDHRSDLVFLADLRPEEIRYRLQHYFKFLFVREPLERLLSAYRNKFGEIRE  
YQQRYGAEIVRRYRAGAGPSPAGDDVTFPEFLRYLVDEDPERMNEHWMPVYHLCQPCAVHYDF  
VGSYERLEADANQVLEWVRAPPVRFPARQAWRPASPELHYHLCASPRALLQDVLPKYILD  
FSLFAYPLPNVTKEACQQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 67-71, 325-329

**Tyrosine kinase phosphorylation sites.**

amino acids 152-159, 183-183

**N-myristoylation sites.**

amino acids 89-95, 128-134

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**FIGURE 133**

CGGCAGTTCTGGCCCTGCAGCTGGAGGTACCCCTGAGTTCTGAGGGCGTAGTGCTGTTCTG  
GTATTCTCATCGCGGTACCTCTACCGGTGTGGACAAGTAAAGTTGAATCAGCTCTCCATG  
GCCTGGCACCAAGTCCCCGCTGAGCCATTTCTTGGCTAAAAGTCCCCGCCAGAGGCC  
AATTCTCGCGCGGGCGGTGGAGATCGCAGGTCAGGCTGCAGATGGGTCAAGGGTTGT  
GGAGAGTGGTCAGAAACCAGCAGCTGCAACAAGAAGGCTACAGTGAGCAAGGCTACCTCACCA  
GAGAGCAGAGCAGGAGAATGGATGCGAGCAACATTCTAACACCAATCATGTAACAAAGTCC  
AAGGAGGCATTGACATATATCATCTTGAAGGCAAGGAAATCGAAAGAACAGGAAGGATTCA  
TTAATTGGAAATGTTGCCCTGAGCTAACGCTTACCATCTTGTCCCTACCTGAATGCAACTG  
ACCTTGCTTGGCTTCATGTGTTGGCAGGACCTGCGAATGATGAACCTCTGGCAAGGGT  
TGTGCAAATCCACTTGGGTCACTGTTCCATATAACAATAAGAACCCACCTTAGGATTTCTT  
TTAGAAAATTGTATATGCACTGGATGAAGGCAGCCTCACCTTAATGCCAACCCAGATGAGG  
GAGTGAACTACTTATGTCAGGGTATCCTGGATGATTGCCAAAGGAAATAGCAAAGTTA  
TCTTCTGTACAAGAACACTAAATTGGAAAAACTGAGAATCTATCTTGATGAAAGGAGAGATG  
TCTTGGATGACCTGTAACATTGATAATTAGAAATCAGTTCTGCCAAATGCACTGAGAG  
AATTTTTCGTATCCATGCCCTGAAAGAGCGTGGAGAGTATCTGAAACTCTTATAACAA  
AGTTCTCACATAGATTCTGTGCTGCAACCTGATTTAATGCGAGAACTTGGCCTTAGTCCTG  
ATGCTGTCTATGTAATGCTACTCTTGATTCTACTTCCATTGACCTCACTAGCCCTCATG  
TGAAGAATAAAATGTCAAAAGGAATTATTGAAATACCCGTCGGCTGCTCAAAATATTA  
GTGAAGATTTGAGGGCATTTATGACAATATCTACCTTATTGCCATGTGGCTGCATAAA  
AAGCACAATTGCTAGGACTTCAGTTTACTCAGACTAAAGCTACCCAGGACTAGCAGAT  
ATGGGGTTACATCAGTGTGGCATTGTAGCCTGAGTATACAATCAAGCTTCAGTGTGCAAC  
CTTTTTCTTGCCATTTCATTTAGTAATTCCCTGGGAACCTAAATAATTTGCAGA  
ATTTTCCTAATTGTTATCACGTTGCACAAAGCAGAGCCACTGTCTAACACAGCTGTT  
AACGAATGATAAAACTGACATTATACTCTAAAGATGGTGTATTGTCATTAGATTTGCCTGA  
AAAACTTATCCATTCCATTCTTATACAAATACCATGTAATGTGTACATATTAACAAAG  
AGATTATAGTCATAATTATTTATTGAAAGATTTAACTAAAGTTTCTCTC

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**FIGURE 134**

MGQGLWRVVRNQQLQQEGYSEQGYLTREQSRRMDASNISNTNHRKQVQGGIDIYHLLKARKSK  
EQEGFINLEMLPPPELSFTILSYLNATDLCLASCVWQDLANDELLWQGLCKSTWGHCSIYNKNP  
PLGFSFRKLYMOLDEGSLTFNANPDEGVNYFMSKGILDDSPKEIAKFIFCTRNLNWKKLRIYL  
DERRDVLDLVTLHNFRNQFLPNALREFFRHIAPEERGEYLETLITKFSHRCACNPDLMR  
LGLSPDAVYVLCYSLILLSIDLTSPHVKNKMSKREFIRNTRRAAQNISEDFVGHLYDNIYLIG  
HVAA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 253-272

**N-glycosylation sites.**

amino acids 37-41, 87-91, 298-302

**N-myristoylation site.**

amino acids 110-116

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**FIGURE 135**

GGCACGAGGGAGCCTCCTTAGGGGTGGAAAGGACTTGCATAGTCGCTGAGGCCACCA  
TCTGCTCTCTTACTGGCCAAGGGCGTAAAAGATACTTCCCATTAGCTAGAGAGCAAACCC  
CAGAAAGCCTATTGGCTGCGCCGTCCGCGGGCTTGGTCCGTTGAAGGCGGGCTGCGGCTG  
CGAGAGGAGGGCGGGCGGGAGGCTAGCTGTTGCTGGTGCTGGAGGCACGTGTGCAGTCC  
CGGAAGCGCGAGGGGAAACTGCTCCGCGCGCCGCGGGAGGAGGAACCGCCCGTCTTA  
GGGTCCGGGCCGGCCGGCCATGGATTCAATGCCCTGAGGCCGCTCCGCTGTCTTGTCTT  
CTTCCCTTGCTGCTGCTGCTGCTGCTGCTGCCGGCCCCGGAGCTGGGCCGAGCCAGGCC  
GGAGCTGAGGAGAACGACTGGGTTGCCTGCCAGCAAATGCGAAGTGTGAAATATGTTGCT  
GTGGAGCTGAAGTCAGCCTTGAGGAAACCGCAAGACCAAGGAGGTGATTGGCACGGCTAT  
GGCATCCTGGACCAGAAGCCTCTGGAGTCAAATACACCAAGTCGGACTTGCGGTTAATCGAA  
GTCACTGAGACCATTGCAAGAGGCTCCTGGATTATAGCCTGCACAAGGAGAGGACCGGCAGC  
AATCGATTGCCAAGGGCATGTCAGAGACCTTGAGACATTACACAACCTGGTACAAAAGGG  
GTCAAGGTGGTGTGGACATCCCCTATGAGCTGTTGAGGAGGTGATCGAGGACTGGTACAGG  
CTCAAGAACAGTGTGATGTGCTGGGAAGAGTTGAGGAGGTGATCGAGGACTGGTACAGG  
AACCACCAAGGAGGAAGACCTGACTGAATTCCCTGCGCCAACCACCGTGTGAAGGGAAAAGAC  
ACCAGTTGCCCTGGCAGAGCAGTGGTCCGGCAAGAAGGGAGACACAGCTGCCCTGGGAGGGAG  
AAGTCCAAGAAGAACGAGCAGCAGGGCCAAGGCAGCAGGCCAGGGAGTAGCAGCAGCAAACAA  
AGGAAGGAGCTGGGTGGCCTTGAGGGAGACCCAGCCCCGAGGAGGATGAGGGCATCCAGAAG  
GCATCCCCTCTCACACACAGCCCCCTGATGAGCTCTGAGGCCACCCAGCATCCTGTCTG  
AGACCCCTGATTGAAAGCTGAGGAGTCAGGGCATGGCTCTGGCAGGCCGGATGGCCCCGC  
AGCCTTCAGCCCCCTCCTGCCCTGGCTGTGCCCTTCTGCCAAGGAAAGACACAAGCCCCAG  
GAAGAACTCAGAGCCGTATGGTAGGCCACGCCGTCTTCCCCTCCCCAAGTGTCTCTC  
CTGACCCAGGGTTCAGGCAGGCCTGTGGTTCAAGGACTGCAAGGACTCCAGTGTGAACTCAG  
GAGGGGCAGGTGTCAGAACACTGGCACCAGGACTGGAGCCCCCTCCGGAGACCAAACCTCACC  
CCCTCAGTCTCCCCAACAGGGTACTAGGACTGCAAGCCCCCTGTAGCTCTCTGCTTACCC  
CTCCTGTGGACACCTTGCACTCTGCCCTGGCCCTCCAGAGGCCAAAGAGTAAAAATGTTCTG  
GTTCTGATTCTGAAAAAAAAAAAAAAATTCTT

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**FIGURE 136**

MDSMPEPASRCLLLLPLLLLLLPAPELGPSQAGAEENDWVRLPSKCEVCKYVAVELKSAF  
EETGKTKEVIGTGYGILDQKASGVKYTKSDLRLIEVTETICKRLLDYSLHKERTGSNRFAKGM  
SETFETLHNLVHKGVKVMDIPYELWNETS AEVADLKKQCDVLVEEFEEVIEDWYRNHQEEDL  
TEFLCANHVLKGKDTSCLAEQWSGKKGDTAALGGKKSSRAKAAGGRSSSKQRKELGGL  
EGDPSPEEDEGIQKASPLTHSPPDEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**N-glycosylation site.**

amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 227-231, 228-232

**Tyrosine kinase phosphorylation site.**

amino acids 142-150

**N-myristoylation sites.**

amino acids 36-42, 74-80, 86-92, 125-131, 222-228, 237-243,  
250-256, 263-269

**Amidation sites.**

amino acids 212-216, 222-226

**ATP/GTP-binding site motif A (P-loop).**

amino acids 62-70

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**FIGURE 137**

CACGCCCTCCCGCTGCCAGCCGGCACGGGATCTTAATCAGTCACTATGAAAACTCATTAGCT  
CCACAGCA**ATGAGT**CTCCACTGCTGAAGCTGGCGCTGTGCTTAGTACCATGGCAATGATCT  
CAAACGGATGTCCAAACTCTCCATCCTGGTGGGACTGAACACCACGAGGCTGTCACTC  
CGGATACTTAACTCAGATTAGTCCTAAAGAAGGGTGGCAGGTGTACAGCTCAGCTCAGGATC  
CTGATGGGCGGTGCATTGCACAGTTGCTCCAGAACAAAACCTGTGTTCCGGGATGCCA  
AAAGCAGGCAACTCGCCAACTACTGGAAAAGGTTCAGAACATGTCCTAGTCTATTGAAGTCT  
TAAACTTGAGAACTCAGAGAGATTCCAATATGTTTAAAATGAAAACCCAAATGAAAGGGC  
TGAAGGCAAATTCCGGCAGATTGAAGATGATCAGAAAGACACTTATGACCAAGCATTTCAGG  
AGTTGAAAGAGAAAATGGACGAGCTCCTGCCTTGATCCCCGTGCTGGAACAGTACAAAACAG  
ATGCTAAGTTAATCACCCAGTTCAAGGAGGAATAAGGAATCTGTCCTGCTGTCCTCACTGGTA  
TTCAGGAGGAATTGGTGCCTATGACTACGAGGAACACACAAAGAGTGCTGAGCTGGAAA  
CAAGACTTCGTGACTGCATGAAAAGCTAACATGTGGCAAACGTGAAAATCACAGGCCAG  
TTACAGTCAGACATCTGGAACCCGATTGGTGTGGATGACAGACCCCTTAGCATCTGAGA  
AAAACAACAGAGTCTGGTACATGGACAGTTACTAACAAATAAAATTGTCGTGAATACAAT  
CAATTGCGACTTTGTCAGTGGGGCTGAATCAAGGACATACAACCTCCTTCAAGTGGCAG  
GAACTAACCATGTTGTCATAATGGCTCACTCTATTAAACAAGTATCAGAGTAATATCATCA  
TCAAATACAGCTTGATATGGGGAGAGTGCTGCCAACGAGCCTGGAGTATGCTGGTTTC  
ATAATGTTACCCCTACACATGGGGTGGATTCTGACATCGACCTAACGGCTGATGAAATCG  
GGCTGTGGGCTGTGTATGCAACTAACAGAACATGCAAGGAAATTGTCATCAGCCAACCTAAC  
AAGATACCTTGAGGTGATGAAGAGCTGGGACTGGCTACCCCAAGAGAACAGTGCAGGGAAAT  
CTTCATGATCTGGGACACTGTATGTCACCAACTCCACTTAACGGAGCCAAGGTGTATT  
ATTCCTATTCCACCAAAACCTCCACATATGAGTACACAGACATTCCCTCCATAACCAAAACT  
TTCACATATCCATGCTTCACTAACATGCAAGAGATCGAGCTCTCATGCTGGAACAATGGCC  
ACCAGGTGCTGTTCAATGTCACCCATTTCATATCATCAAGACAGAGGATGACACA**TAGGCAA**  
ATGTGACATGTTTCAATTGATTTAACAGTGTGATTGTGATAAAACTCTATAAGACCCCTTCC  
GTTTTTTCTTCACTATTATTTTCATCATTTCTCAAAGCAAAGCATTGTTATTGTAAGTT  
GGTGTGTTCAAAACATAGCTGAGCTGTCTAACATTACCATGTTGAAACACATCTTAACCTCT  
AAATTACAAGGCTATCATGTCCTGTCTGAAAGACTAAAAAAGAGTTAAGT  
GGCTAAAGTCATAGTTTGCAAGAGATTATGATCTGCCTTATATTAGAGTCAGAGACTAATG  
GTGGCTTAAATGCAAGAACATGCTTTTAAACTGTCATTGTTACTGTCCTTGCTCCA  
TCTCAGGAAATATTTGGTAGGAATTAGGAGAACAAAAGCACTTTATCCCATTATTCTT  
AAAAAAATGTAAGGATTTCATTTATATTGAAAAAATAATTAAATCATTGCTGTTAACACAA  
TTCTCTGATGCCGTGCTGTACAGTCATTAAATCTTGTCTAACATTATTGGCAGTATG  
TATTCTACCATGTAACCAACCATGTCATTGTATCTCTTCACCTCTGTGAAAGTAATATT  
TTTATAAAANACACTGNAATTAAAAAAACAAAAAAACAAAAAAACAAAAAA

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**FIGURE 138**

MSPPLLKLGAVLSTMAMISNWMSQTLPSLVGLNTTRLSTPDLTQISPKEGWQVYSSAQDPDG  
RCICTVVAPEQNLCSDAKSRQLRQLLEKVQNMSQSIEVNLRTQRDFQYVLKMETQMKGKA  
KFRQIEDDRKTLMTKHFQELKEKMDELLPLIPVLEQYKTDALKITQFKEEIRNLSAVLTGIQE  
EIGAYDYEELHQRVLSLETRLRDCMKKLCGKLMKITGPVTVKTSRGAWMTDPLASEKNN  
RVWYMDSYTNKIVREYKSIADFVSGAESRTYNLPFKWAGTNHVVYNGSLYFNKYQSNIIIKY  
SFDMGRVLAQRSLEYAGFHNVYPYTWWGGFSIDLMADEIGLWAVYATNQNAGNIVISQLNQDT  
LEVMKSWSTGYPKRSAGESFMICGTLYVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI  
SMLDYNARDRALYAWNNGHQVLFNVTLFHIIKTEDDT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 215-219

**Tyrosine kinase phosphorylation site.**

amino acids 106-114

**N-myristoylation sites.**

amino acids 9-15, 31-37, 235-241, 239-245

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**FIGURE 139**

GAACGAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGTGAGCAAAGGCCTCACCAATGGCCG  
AGTCCCCCGGCTGCTCCGTCTGGGCCGCTGCCACTGCCGTATAGCTGCCACTGGA  
GGAAATGCCAGAGAGAGGATGCAAACCAAGCAAGTGCAGTGTATCTGGTTGGCCTGCTCT  
TCCTCACCTCCTCTTCCCTGAGCTGGCTGTACATCGGCTCGCCTCTCAATGACCTGC  
ACAACCTCAATGAATTCTCTTCCCGCTGGGACACTGGATGGACTGGTCCCTGGCATTCC  
TGCTGGTCATCTCTACTGGTCACATATGCATCCTGCTATTGGCCTGGCCCTGCTCCTGC  
GGCTTGAGACAGCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCCCTCATTATGC  
TGCTTGCGGCTGGCCTGTGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC  
GTGTGTCACTGCAGGCCACAGCCCATTCTCATATTGGAGCAGCCGCTGGAATTGCCCTCC  
TGGCCTGGCCTGTGGCTGATACTTCTACCGTATCCACCGAAGAGGTCCAAGATTCTGCTAC  
TGCTCCTATTTTGAGTTGTCCTGGTCATCTACTTGGCCCCCTATGCATCTCCTCACCC  
GCATCATGGAACCCAGAGACTTACCAACCCAAAGCCTGGCTGGTGGACACCGAGGGCCCCA  
TGCTGGCTCCGAGAACACCCGTATGTCCTGGAGACAGCTGAATGCGGAGCTACTGTGT  
TTGAGACTGATGTGATGGTCAGCTCCGATGGGTCCCCTCCTCATGCATGATGAGCACCTCA  
GCAGGACCACGAATGTAGCCTCTGTATTCCAACCCGAATCACAGCCCACAGCAGTGACTTCT  
CCTGGACTGAAGAGACTCAATGCTGGATCCTGGTCCTAGAGAGGGCACCCTCTGGG  
GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACAGCATTAG  
AAGAGCTATTGGAGGAAGCTGCAGCCCTAACCTTCCATCATGTTGACTTGCGCCGACCC  
CACAGAACACACATACTATGACACTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA  
GGGTGCCCAAGCCATGGCTTTGGCTACCAGATGAAGATGGCTAATGTCCAACGACGGG  
CACCTGGAATGCCAGATATGGACGTCAGGGAGGCAACAGAACGGAGAGGGCCCCAGTTTC  
TTAACCTCCCTATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT  
CGGTGAACCTATTGTAGTAACAAGCCCTGGCTTCTCTCTGCTTGGTGTGCAGGGTGG  
ATTGGTCACCACCAACGACTGCCAGCTGCTCAGCAGATGCGTTACCCATCTGGCTTATTA  
CCCCCTCAAACCTACCTAATCATATGGGTCAATTACCAATTGTGTTCCACCATGCTGCTTTGT  
GGACCTCCTCCAAAGGAGATTGTTAAGAAGAGAGGGAAAATGGCTTAGAACAGCAG  
TGCTGCTGACAAGGATCAACAATTGATGGAGTGAATGCCCTGCCCTGCTCCCCACCA  
AGCCAGTCTACATTGCCAAACAGCAAGGGTGGAGAGTGGCTTAAGTGAATGCTTCAGGGG  
TGGTGGGTTGCAAGTGGGGAGCTTGCCAACAGGAGGTTGAACCATGAGGGCCCTG  
CCAGGTGATGGCATTCCCTAACGCTGCTATGGAATCTGCTCCCTTGGGTTTGACCTGAGA  
TGTTGGAGAGAGTGAATGAGAAGTTCTCCTCAAATGAAACTAGAACAGAGGAAGTA  
AAAGGGAGATTGCTCGGA

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**FIGURE 140**

MAESPGCCSVWARCLHCLYSCHWRKCPERMQTSKCDCIWFGLLFTFLLSLSWLYIGLVLLN  
DLHNFNEFLFRRWGHWMWDWSLAFLLVISLLVTYASLLLVLALLRLCRQPLHLHSLHKVLLL  
IMLLVAAGLVGLDIQWQQEWHSLRVSLOQATAPFLHIGAAAGIALLAWPVADTFYRIHRRGPKI  
LLLLLFFGVVLVIYLAPLCISSLPCIMEPRDLPKPGLVGHRGAPMLAVENTLMSLRKTAECGA  
TVFETDVMVSSDGVPFLMHDHLSRTTNVASVFPTTRITAHSSDFSWTELKRLNAGSWFLERRP  
FWGAKPLAGPDQKEAESQTVPALEEELLEAAALNLSIMFDLRRPPQNHTYYDTFVIQTLTVAL  
NARVPQAMVFVLPDEDRANVQRRAPIGMQRQIYGRQGGNRTERPQFLNLPYQDLPPLDIKALHKD  
NVSVNLFVVNKPWLFSSLWCAGVDSVTTNDQCQLLQQMRYPIWLITPQTYLIIWVITNCVSTML  
LLWTFLQRRFVKRGKTGLETAVLLTRINNFMME

**Important features of the protein:****Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506

**N-glycosylation sites.**

amino acids 349-353, 362-366, 415-419, 442-446

**N-myristoylation sites.**

amino acids 163-169, 413-419, 523-529

**Leucine zipper pattern.**

amino acids 93-115, 109-131

**Glutamine amidotransferases class-II active site.**

amino acids 1-13

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**FIGURE 141**

GCCGCCGGCCCGGGCTGGACCCGAGCCAGCAGCCACCGCCGCCGCCAGAAGTTGGGTGAACCGGAGC  
 TGCGGGAGAAACTTTTCTTTTCCCCCTCCCTCCGGAGGAGGAGGAGGAGGAGGGAGGGAGCTGCCG  
 CCGGCCCAAGGCTCGTGGCTCGGGCTGGCGCCGCAGAAGGGGGCGGGGCTCGCCCCCGAGGGGAGG  
 CGCGCCCGGGGCCCCGAGAGGGCGGTAGGACCAGGGCTGCTGGTGCAGGAGGAGGGGGGGGGAGG  
 CGCAGGGAGGGCGCCGCCCGCTCCGGCCGGCTGCAGGAGGAGGGGGGGGGAGGAGGAGGATGTACTT  
 GGTGGCGGGGACAGGGGTTGGCGCTGGGGCACCTCTGGTCTCGCTGGGGCTGCTGCTGCTGGC  
 GCGCTCCGGCACCGGGCGTGGTCTGCTGCTGGCTGACGAGTCCAAGTGCAGGAGGCCAGGAACCTGCCGG  
 GAGCATCGTCAGGGCTCTGGCTGCTACAGTGCAGGCCAGGAACGAGAGCTGCGGGCACCTT  
 CGGGATTACGGAACCTGCAGCCGGGGCTGCGTTGTCATCCGGCCCCGCTCAATGGCACTCCCTCACCGA  
 GTACGAAGCGGGCGTTGCGAAGATGAGAACCTGGACTGATGACCAACTGCTGGTTAAACCATGCAATGAAA  
 CCTTATTGCTGGCTGCAATATAATCAATGGAAATGTGAATGTAACACCAATTGCAACCTGCAGCAATCCCTTG  
 GTTCCAAGTCAGGATATGTGCCCTTCAGCTTAAAGAGAATTAAGAAGAGAACCCAGATTGCTCCAAGGCCG  
 CTGTGAAGTCCAGTTCTCCACGTTGTCAGATTCTGTCATCGAGGTTATGCTCTCCTGGTTATGTGGTTCCGGAGTG  
 CTGTCCTTACCCAGCCGCTGCGTGTGCAACCCGCAAGGCTGCTCCGGAAAGTCTGCCAGCCGGAAACCTGAA  
 CATACTAGTGTCAAAGCCTCAGGAAGCCGGAGAGTGTGACCTCTATGAGTGCACACTGTTCCGGT  
 GGACTGAGGACTGTGGAATGCCCTCTGTCAGCAGACCCGCTGCCCCGGACAGCTATGAAACTCAAGTCAG  
 ACTAACTGAGATGGTTGCTGTAATTGCGCAACAGATGCGAGTGTCTCTGGCTTATGTGGTTCCGGTGTG  
 TGAGGTGGGATCCACTCCCCGATAGTCTCTGCGGCAAGGACACTGGAAAGTGTGTGATGTCTTGATG  
 TGTTAATGATAACAAAGCCAGCCTGCGTATTAACAATGTGAATATATGAGGAGACATGTTGAAATGGACAA  
 CTGTCGTTCTGCGATGCCAACGGGGCGTGCCTACTGCTTCACTGCCCAGTGTGGAGATAAAACTGCGAGAG  
 GTACTACGTGCCGAAGGAGAGTGTGCCCAGTGTGAAGATCCAGTGTATCCTTTAAATAATCCCGCTGGCTG  
 CTATGCCAATGCCATCTGCCACGGAGACCGGGTGGCGGAAGACGACTGCACATTGCCAGTGGCTCAA  
 CGGTGAACGCCACTCGTGTGCGACCGCTGCGGACAGACCTGCACAAACCTGTGAAAGTGTGCTGGGAGTGTG  
 CCCTGTGTGCGAACGAAACCAACCATCATCACAGTGTGACCTGCACATGTGGGGAGTTATCAAACACTGACTCTGAC  
 AGGGAGGACTGCAATTATGGTTCAACAGCGATCACATGGTGTGCGGACCTGTCACTGCATAAACACCGAGGA  
 ACTATGTCAGAACGTAACAAAGGCTGACCTTGAACTGTCCCTCCGGTTCTACTGATGCCAAACCTGTGA  
 GATCTGTGAGTGGCCCAAGGCCAAGAAGTGCAGACCCATAATCTGTGACAAGTATTGTCACCTGGATGT  
 GAAGAATAAGCACGGCTGTGACATCTGCGTGTGAAAGAATGTCCAGAGCTCTCATGCACTAACGATCTGCCCTT  
 GGGTTTCCAGCAGGACAGTCACGGCTGTCTATCTGCAAGTGCAGAGAGGCCCTGCTTCAGCTGGGCCACCCAT  
 CCTGCGGGCACTTGTCTACCGGTTGATGGTCATCATCATAAAATGAGGAGAGCTGGCACGATGGGTGCCGG  
 ATGCTACTGTCTCAATGGACGGAAATGTGTCGCTGTGACCTGCCGGTGCCTGCTGTGCAACCCACCAT  
 TCACCCGGACAGTGTGCCCATGTGCGAGTGTGGTGTGCGAGAGCCAGAGCTCAGTACTCCCTCCAT  
 TTGCCACGCCCTGGAGGAGAACTTTGTGAGGAGAATCTGCGTGTGAGACAGAGGTGTGCCACTTCAGTGGGAAGGCCATGCCGA  
 CCACAGCGGACGGGTGCTGTGAGACAGAGGTGTGCCACCGCTGCTGCCAGAACCCCTCACGCACCCAGGA  
 TTCCCTGTCGCCACAGTGTACAGATCAACCTTCTGGCCCTCTGTGCTGGCAATAACAGCGTACCTAATTACTG  
 CAAAATGATGAAGGGGATATATTCTGCGAGCTGAGTCTGCCCCCTCTGTATCCTGTGAAAGACCTGTCTTGAGAAAAGGCCA  
 TGATGCGTAATTAGCTGTTCTGAGTGTGCGCCCTGTGACCTGAGGAGAGGTTGACCTGGAGGGTCCGGCC  
 GTGTTGCTCTACTCATAGAAGACAAATTCAAAGAAGGTGGTGTGCCACTTCAGTGGGAAGGCCATGCCGA  
 CGAGGAGCGGTGGGACCTTGACAGCTGCACCCACTGCTACTGCCAGGGCCAGACCCCTCTGCTGCGACCGTCAG  
 CTGCCCCCTCTGCCCTGTGTTGAGCCCATCAACGTTGGAGGAAGGAGCTGCTGCCAATGTGTCAGAAATGTATGT  
 CCCAGAACCAACCAATATACCCATTGAGAAGACAAACCATGAGGAGAGGTTGACCTGGAGGGTCCGGCC  
 CACGCCACTGTGAAATGATATGTCACCTCCCTAGAGATATGGGTACCTCCAGTAGATTACAGAGATAACAG  
 GCTGCACCCAAGTGAAGATTCTCACTGGACTCCATTGCCCTCAGITGTGGTTCCATAATTATATGCCCTCTCAT  
 TATAATAGCATTCTATTGCAATCAGAACGAGAAACACTGAGTACCAACTGCTTGCTGGTATGAAACACCAACTAA  
 GCCTTCTCTTAAATAATCAGCTAGTATCTGTTGACTGCAAGAAAGGAACCAAGAGCTCAGGTGGACAGTTCCCA  
 GAGAATGCTAAGAATTGCAAGAACGAGTGCAGGAAAGTCACTGGCTTACAGCATGCAAAACAGAACCATCTACA  
 GGCAGACAATTCTACCAACAGTGTGAAAGGAAACTAGGATGAGGTTCAAAGACGGAAGACGACTAAAT  
 CTGCTCTAAAAAGTAAACTAGAATTGTCAGTGTGACTTGCTTAGTGGATTGATGTGACTTGATGTACAGCGC  
 TAAGACCTTACTGGGATGGGCTCTGCTACAGCAATGTGCGAGAACAGCATTCCACTTCCCTAAAAAA

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**FIGURE 142**

MYLVAGDRGLAGCGHLLVSLLGLLLLLARSGTRALVCLPCDESKCEEPRNCPGSIVQGVCGCC  
YTCASQRNESCGGTFGIYGTCDRGLRCVIRPPLNGDSLTYEAGVCEDENWTTDQLLGFKPCN  
ENLIAGCNIINGKCECNTIRTSNPFEPSPQDMCLSALKRIEEKPDCSKARCEVQFSPRCPE  
DSVLIEGYAPPGECCPLPSRCVCNPAGCLRKVCPGNLNILVSKASGKPGECCLYECKPVFG  
VDCRTVECPPVQQTACPPDSYETQVRLTADGCCTLPTRECLSGLCGFVCEVGSTPRIVSRG  
DGTPGKCCDVFEVNDTKPACVFNNVEYYDGDMFRMDNCFCRCQGGVAICFTAQCGEINCER  
YYVPEGECCPVCEDPVYPFPNNPAGCYANGLILAHGDRWREDDCTFCQCVNGERHCVATVCQQT  
CTNPVKVPGECACPVEEPTIITVDPPACGELSNLTGKDCINGFKRDHNGCRTQCINTEEL  
CSERKQGCTLNCPEGFLTDQNCICECRPRPKCRPIICDKYCPGLLKNKHGCDICRKKC  
PELSCSKICPLGFQQDSHGCLICKCREASASAGPPILSGTCLTVGDHHHKNEESWHDGCRCY  
CLNGREM CALITCPVPACGNPTIHPGQCCPSCADDFFVQKPELSTPSICHAPGGEYFVEGETW  
NIDSCTQCTCHSGRVLCETEVCPLLQCNPSRTQDSCPQCTDQPRPSLSRNNSVPNYCKND  
EGDIFLAAESWKPDVCTSCICIDSVISCFSESCPVSERPVLRGQCCPYCIEDTIPKKVVC  
HFSGKAYADEERWDLDSCTHCYCLQQQTLCASTVSCPPLCVPINVEGSCCPMCPEMYVPEPT  
NIPIEKTNHRGEVDLEVPLWPTPSENDIVHLPRDMGHLQVDYRDNRNLHPSEDSSLDSIASVVV  
PIIICLSIIIAFLFINQKQWIPLLCWYRTPTKPSSLNNQLVSDCKGTRVQVDSSQRMLRI  
AEPDARFSGFYSMQKQNHLQADNFYQTV

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 940-962

**N-glycosylation sites.**

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 992-996

**N-myristoylation site.**amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,  
439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,  
845-851**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 52-63, 844-855

**Cell attachment sequence.**

amino acids 314-317

**Leucine zipper pattern.**

amino acids 3-25

**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 57-69

**VWF domain proteins.**

amino acids 448-456, 382-390

**C-terminal cystine knot proteins**

amino acids 60-86

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**FIGURE 143**

GACGTCTGGCCGGCTCCGGCAAGGGCAGCGGAGGAGCGGCCAGAGCGCGCAGCTAGGGCA  
CTGGC GAAACCCGGGACAGTCCCTCTCGTGC GGCGCAGAGCAGTCCATCCCCGG  
GGTCCC GGCGCGGCTGACTGCCGGCTGGTCCCTGCCGCAGTAGCTCCCCGAGCCGGGCTG  
CACCGGAGGCGCGAGATGGTCGCGCGTCGGCCTCTGCTGCCGCCTGCAGCTGCTACT  
GTGGGGCCACCTGGACGCCAGCCCGGGAGCGCGGAGGCCAGGAGCTGCCAAGGAGGCGGA  
GGCATT CCTAGAGAAGTACGGATA CCTCAATGAACAGGTCCCCAAAGCTCCACCTCCACTCG  
ATT CAGCGATGCCATCAGAGCGTTCA GTGGGTG TCCAGCTACCTGTCAGCGGCGTGG  
CCGCGCCACCCTGCGCCAGATGACTCGTCCCCGCTGCCGGGTTACAGATAACAAACAGTTATGC  
GGCCTGGGCTGAGAGGATCAGTGACTTGTGCTAGACACCGGACAAAATGAGGCGTAAGAA  
ACGCTTGCAAAGCAAGGTAACAAATGGTACAAGCAGCACCTCTCCTACCGCCTGGTGAAC TG  
GCCTGAGCATCTGCCGGAGCCGGAGTTCGGGGCCGTGCGGCCGCTCCAGTTGTGGAG  
CAACGTCTCAGCGCTGGAGTTCTGGGAGGCCAGCCACAGGCCGCTGACATCCGGCTCAC  
CTTCTCCAAGGGGACCACAACGATGGCTGGCAATGCC TTGATGCC CAGGGGGGCC  
GGCGCACGCCTCCTGCCCGCCGCCGGCAAGCGCACTCGACCAAGATGAGCGCTGGCC  
GAGCCGCCGCCGGCGAACCTGTTCGTGGCTGCCGACAGAGATCGGTACACGCTTGG  
CCTCACCACTGCCCGCCGCCGCTCATGCCCTACTACAAGAGGCTGGCC  
CGCGCTGCTCAGCTGGGACGACGTGCTGCCGTGAGAGCCTGTATGGGAAGGCC  
CTCAGTGGCGTCCAGCTCCAGGAAAGCTGTTACTGACTTGA  
GAGACCTGGACTCCTACAG  
CCCCCAAGGAAGGCCCTGAAACGCAGGGCCCTAAATACTGCCACTCTCCTCGATGCCAT  
CACTGTAGACAGGCAACAGCAACTGTACATTAAAGGGAGCCATTCTGGGAGGTGGCAGC  
TGATGGCAACGTCTCAGGCCGCTCCACTGCAGGAAAGATGGTGGCTGCC  
GAGGGCTGCCAGTGTATTGAATGATGGAGATTCTACTTCTCAAAGGGGTC  
GAGGGTCCGGGCCCCAAGCCAGTGTGGGTCTCCACAGCTGTGCC  
CCGCCATCCTGACGCCGCCCTCTCTCCCTCTGCCGCCCTCATCCTCTCAAGGGTGC  
CCGCTACTACGTGCTGCCCGAGGGGACTGCAAGTGGAGCC  
GGACTGGGGAGGCATCCCTGAGGAGGTAGCGGCCCTGCC  
CTTCTCCGAGATGACCGCTACTGGCGCTCGACCAGGCC  
CCGCTGGGCCACCGAGCTGCCCTGGATGGCTGTC  
CTGAAGGCACCTC  
CCCCGGGAGA  
TCCATCTGGAAGTCTGCTGCC  
AAAAAAAAAAAA  
AAAAA

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**FIGURE 144**

MVARVGLLRLAQLLLWGHLDQPAERGGQELRKEAEAFLEKYGYLNEQVPKAPTSTRFSDAI  
RAFQWVSQLPVSGVLDATLRQMTRPRCGVTDTNSYAAWAERISDLFARHRTKMRRKKRFAKQ  
GNKWKYKQHLSYRLVNWPEHLPEPAVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD  
HNDGLGNAFDGPGGALAHAFPLPRGEAHFDQDERWSLSRRGRNLFVVLAHEIGHTLGLTHSP  
APRALMAPYYKRLGRDALLSWDDVIALQSLYGKPLGGSVAQLPGKLFTDFETWDSYSPQGRR  
PETQGPKYCHSSFDAITVDRQQQLYIFKGSHFWEVAADGNVSEPRPLQERWGLPPNIEAAAV  
SLNDGDFYFFKGGRCWRFRGPKPWGLPQLCAGGLPRHPDAALFFPPLRRLILFKGARYYVL  
ARGGLQVEPYYPYPRSLQDWGGIPEEVSGALPRPDGSIIFFRDDRYWRLDQAKLQATTSGRWATE  
LPWMGCWHANSGSALF

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 164-168, 355-359

**N-myristoylation sites.**amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,  
509-515**Amidation site.**

amino acids 312-316

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 237-247

**Matrixins cysteine switch**

amino acids 231-262, 271-284

**Hemopexin domain protein**

amino acids 66-108, 231-262

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**FIGURE 145**

GCCGGCTAGGGCGCCGGAGCCGACCGCAGCGGGGCTCCGAGAGGCCGCACCTGGGACTGGCGCGCG  
CCGCCGCTGCGAGCGCACTGAGCGTGCACATTCCGAGGCACAGCGCCGGAGCAGCGCTCAGAGA  
CCCAGGAGCCAGAGGGCGCCGGAGCCCTCGTCAGAGCCGGCCAGGCACCCACCGCGCTCCGAGTGCAGG  
CGGCCCTCCGCGCACCGTGGCTCCGTCGCCCCACGGAAAGGCACGGGCTGGCGTGCAGGGCGCCGGGAGGAC  
GGCAGGAGGAGGGCGCCGGAGACGGCCGGGAGACTGGGGCAGGGAGACAGCCCTGGGGAGAGGC  
GCCGAACCAGGCCGGAGC**ATGGGGGGCCAGGGAGCTCGGGCGCCTGGCTGTCTGGACTGTCTG**  
CTGGGACCGAGGTGAGCCAAGCAGGCACTGATTCTGGCAGGGAGCTCCCTGACTCCTTCCCGTCAAGGCC  
AGCAGAGCCGCTGCCCTACTCTTGCAAGGACGCCAGGACGCTACATTGTGAAGAACAGCTGTGGAGCTCCG  
CTGCCGCGCTTCCCGCCACACAGATCTACTTCAGTCAACGGCAGTGGGTCAAGGCCAGAACGACCGTCAC  
ACAGGAAGGCTGGATGAGGCCACGGCCTGCGGGTGCAGATCGAGGTGTGCGGCAGCAGGTGGA  
GGAGCTCTTGGCTGGAGGATTACTGGTGCAGTGCCTGGCAGGCTCCGAGGCCACCAAGAGTCGCCG  
AGCCTACGCTCCGATCGCCTACTCTGCCAAGAACTTCGATCAGGAGCCCTCTGGCAAGGAGGTGCCCCTGACCA  
TGAGGTTCTCTGAGTGCAGGCGCCGGAGGGGGTGCCTGTGGCCAGGGTGGAAATGGCTAAGAATGAGGATGT  
CATCGACCCCAACCCAGAACACAATTCTCTGCTCACCATCGGACACACTCATCATCGCCAGGGCCCTGTC  
GGACACTGCCAACTATACTCGTGGCCAAGAACACATCGTGGCCAAACGCCGAGCACACTGCCACCGTCATCGT  
CTACGTGAATGGGGCTGGTCCAGCTGGCAGACTGGTCAACCGTGTGGCCAGGCTGGCAGAA  
GCGCACCCGGACCTGACCAACCCCGCTCAACGGAGGGGCCCTCTGCGAGGGCCAGGCAATTCAAAGAC  
CGCTGACCCACCATGCCAGTCAGTGGGGCTGGACGGAGTGGAGCAAGTGGTCAAGCCTGAGCACTGAGTG  
TGCCCACTGGCTAGCCCGAGTGCATGGGCCACCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTGCT  
CGACTTAAGAACACTGCACAGATGGCTGTGCATGCAAATAAGAAAACACTCTAAGCGACCCACGCCACCTGCT  
GGAGGCTCAGGGGATGGCGCTGTGGCTATGGGGGCTCTGGTGGCCATCTCGTGGCTGGCAATCCTCATGGC  
GGTGGGGTGGTGTACCGCCGCAACTGCCGTACTGACAGACATCACTGACTCATCTGCTGCCCTGAC  
TGGTGGTTTCCACCCCGTCAACTTTAAGACGGCAAGGCCAGAACCCGAGCTCTACACCCCTCTGTGCCCTCC  
TGACCTGACAGCCAGGCCGGCATCTACCGGGACCCGTGTATGCCCTGAGGACTCCACCGAACAAATCCCCAT  
GACCAACTCTCTGCTGGACCCCTTACCCAGCCTTAAGGTCAAGGTCTACAGCTCCAGCACCGGGCTCTGG  
GCCAGGCTGGCAGATGGGCTGACCTGCTGGGGGCTCTGCCCTGGCACATACCCTAGCGATTTCGCCGGGA  
ACCCACTCTGCACTGCCAGCGCCAGCCTCGGTCCCAGCAGCTTGGGCTGCCGGAGACCCAGGGAG  
CAGCGTCAAGGCCACCTTGGCTGGCTGGAGGCTCAGCATCCCCGGCACAGGGGTCAGCTTGTGGTGC  
CAATGGAGCCATTCCCCAGGGCAAGTTCTACGAGATGTACTCATCAACAAGGCAGAAAGTACCCCTCCGCT  
TTCAGAAGGGACCCAGACAGTATTGAGCCCCCTGGTGAACCTGTGGACCCACAGGCCCTCTGTGTGCCGCCCC  
CATCCCTACCATGCCCACTGTGCCGAAGTCACTGCCCCGTACTGGGATCTTCAGCTCAAGACCCAGGCCACCA  
GGGCCACTGGAGGAGGTGGTGAACCTGGATGAGGAGACCCCTGAACACACCCCTGTAUTGCCAGCTGGAGCCAG  
GGCCTGTCACATCTGCTGGACAGCTGGCACCTACGTGTTACGGCGAGTCTATTCCCGCTCAGCAGTCAA  
GGCGCTCCAGCTGGCGCTCTGCCCTGGCCCTCTGCACCTCCCTGGAGTACAGCCTCCGGGCTACTGCTGGA  
GGACAGCCTGTAGCAAGGAGGTGCTGGAGCTGGAGCCACTCTGGGGGATACTGGTGGAGGAGCCGAA  
ACCGCTAATGTTCAAGGACAGTACCATCAACACCTGCCCTCCCTCATGACCTCCCCCATGCCATTGGAGGAG  
CAAGCTGCTGGCAAATACCAAGGAGATCCCCCTCATCACATTGGAGTGGCAGGCCAGAAGGCCCTCACTGCA  
TTTCACCCCTGGAGAGGCACAGCTGGCTCCACAGAGCTCACCTGCAAGATCTGCGTGCAGCAAGTGGAAAGGGGA  
GGGCCAGATATTCCAGCTGCATACCACTCTGGCAGAGACACCTGCTGGCTCCCTGGACACTCTCTGCTCTGCC  
TGGCAGCACTGTCAACCAACCGCTGGGACCTTATGCCCTCAAGATCCCACGTGCACTGCCATCCGCCAGAAGATATGCAA  
CAGCTAGATGCCCAACTCAAGGGCAATGACTGGGGATGTTAGCAGCAAGAGCTCTATGGACCGGTACCT  
GAATTACTTGGCCACAAAGGGAGGCCACAGCTGGCTCCACAGAGCTCACCTGCAAGATCTGCGTGCAGGAGGAGATGG  
GGACCTCAACAGCCTGGCGAGTGGCTTGGAGGAGATGGCAAGAGTGGAGATGCTGGCTGGCTGGCCACCGACGG  
GGACTGCT**TGAGCCTCTGGAGCAGCGGGCTGGCAGGGACTGGCAGGGCAGGTGCAAGGGAGGCCCTGGGAGCC**  
TCCTGATGGGGATGTTGGCTCTGCTTCCCTCCAGTTCACAGCCAGAGTTGCTCTCCCTCTCCCTTCC  
CCCCCAGACCATGACCAGCCTAGAAAATCCATGTAUTCTGTTAGAGGGCCAGAGTCCCTCTCC  
GCTCTCTCTCTGGCCTGAGATCTGTCAGGAACCAAGATGGGCTGAAGGCTCTGGAGGCAGTTGGTGG  
GGCGGGCAGGCAGGAGGCCCTCCACCCCCCCCACCCCTCAGCCCGCAACTCTGGGGTCCGTGGGTTTAG  
TTCCGTTCTCGTTCTCCCTCCAGTATTGATTTCTCTCCCTAAGCCCCCTCTGCTTCCACGCCCTT  
TCCTCTTGAGAGCTAAGTACAATTGAGACAAACTGCTTCTCTCCAGTCCAAAAGCAAAAAGGAAAGGAAAGAA  
AGAAAGCTTCAAGACCGCTAGTAAGGCTAAAGAAGAAAAACACCAAAACCAAGGGAAAAGAAAAACCCAG  
TTCTTAGGAAACGCAAACGATTATTATCCAGATTATTGGATAAGCTTTAAAAA

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**FIGURE 146**

MGARGARGALLALLCWDPRLSQAGTDGSEVLPDSFPSAPAEPPLPYFLQEPMQDAYIVKNK  
 PVELRCRAFPATQIYFKCNGEWSQNDHVTQEGLDEATGLRVREVQIEVSRRQQVEELFGLEDY  
 WCQCVAWSSAGTTKSRRAYVRIAYLRLKNFDQEPLGKEVPLDHEVLLQCRPPEGVPVAEVWLK  
 NEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRSTTATVIVYVNGGWSSW  
 AEWSPCSNRGCRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTICPVDGAWEWSKWSACS  
 TECAHWRSRECMAPPQNNGRDCSGTLLDSKNCTDGLCMQNKKTLSDPNSHLEASGDAALYA  
 GLVVIAIFVVVAILMAVGVVYRRNCRDFTDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV  
 PPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLPSLKVKVYSSSTTGSGPGLADGADLLG  
 VLPPGTYPSPDFARDTHFLHLRSASLGSQQLLGLPRDPGSSVSGTFGCLGGRLSIPGTGVSLV  
 PNGAI PQGKFYEMYLLINKAESTLPLSEGTTQVLSPSVTGCPTGLLCRPVILTMMPHCAEVS  
 RDWIFQLKTQAHQGHWEVVTLDEETLNTPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVK  
 RLQLAVFAPALCTSLEYSLRVYCLEDTPVALKEVLELERTLGGYLVEEPKPLMFKDSDYHNRL  
 SLHDLPHAHWRSKLLAKYQEIPFYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEG  
 QIFQLHTTLAETPAGSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRM  
 LAQKLSMDRYLNYFATKASPTGVILDWEALQQDDGDLNSLASALEEMGKSEMLVAVATDGDC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 374-395

**N-glycosylation sites.**

amino acids 222-225, 347-350

**Glycosaminoglycan attachment site.**

amino acids 492-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 233-236, 234-237

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

**Tyrosine kinase phosphorylation sites.**

amino acids 216-223, 773-780

**N-myristoylation sites.**

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 541-551

**ATP/GTP-binding site motif A (P-loop).**

amino acids 926-933

**Growth factor and cytokines receptors family signature 2.**

amino acids 306-312

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**FIGURE 147**

GAGAGGGACAGAGGCTGGAGAAGGATGTATGGCTGCCCTGGGCTTGTCTGTCCTCCCTGAGCCTGAGCCCCCTT  
ACCTCCTGACCCCATGAAGCACACACTGGCTCTGCTGGCTCCCCCTGCTGGGCTGGGCTGGGCTGGCCCTGA  
GTCAGCTGGCTGCAGGGGCCACAGACTGCAAGTTCTTGGCCGGCAGAGCACCTGACATTCAACCCAGCAGCCA  
GGGCCCCGGTGGCTGGCCCTCGAGTTCGTGCGCCAGGACTCCTGGACTCCCTATGGCACCGTGCGCCGCTTCC  
TCTCGTGCTGCAGCTCAATCTTCCCTCAGAGTTGTAAGGCCCTACTGAAATGAGCTGCCCTCGTGAAGG  
TGAATGAGGTGGTGGCTGGTACGGGCGGGCTACGGTGTGATGCGCTGTGATCGCGGCCCTAACCTGCTGCTGGTGC  
CCACTGCGGGCTTGTCTCTGCTGCCCTGCAACCGCGCTGCGGGGACAGTGAAGACAGAGCACAAGG  
CGCTGCCCTGTGAGCGCGGCCCTCATGGTCTTCTGCTGCTGACCAACCTCTGCTGCTGATTTGGTGTGGTCT  
GTGCTTGTCAACCAACCAGCGCACGCACTGAACAGATGGGCCAGCATCGAGGCCATGCTGAGACCCCTGCTCA  
GCCTCTGGGCTGGCTCTGATGTCACCGAGAGCTGCAAGGCGTGGCACAGCAATTCTCCCTGCCCCAGGAGC  
AAAGTCTCAGAGGAGCTGGATGGTGTGAGCATTGGGAGCAGTCTCGTGCAGGACTCCACACTCAGCTCAGGAGCTCCGTGT  
ACCCCTTGTGGCGCCGTGGCAGTTGGGCCAGGTCTGCAAGGCTCTCGTGCACCACCTGCAAACCTTGAATG  
CTACACTGCTAGACTGCAAGGCCGGCAGCAGGACCTGAGGACAGCCATCGGGGAAACCCGGGACCCCTCCCTTG  
AGCTGCTGCAGGGGCCAGGTCCAGGGAGATTGTGCAAGGGGCTGAGCTGGGGCCACCTGGAGCTGGTGC  
CTGACTTCAGGAGGGCTGGCTCTGAGGACATGTCCTGCAACAGCTAAAGGTGCTCCCGAGGCCAACTTCTCCA  
GCATGGTCAGGAGGGAAACAGCACCTTCAACGCCCTTCAGGCCCTGGCTGCCATGCAAGACATCCAGCTGGTGC  
AAAGCTGAAGAAGGCACTGGCCAGCAGCCGGAAAGGGGTGAGGACACTGGCTGAAGGGTTCGGGGCTGGAGG  
CAGCTCCCGCTGGGCCAGGCACTGCAAGGAGGTGGAGGAGAGCAGCCGCCCTACCTGCAAGGAGGTGCAGAGAT  
ACGAGACCTACAGGTGGATCGTGGCTGCGTGCTGCTCCGTGGTCTATTGTCGGTCTGCAACCTGCTGG  
GCCTCAATCTGGCATCTGGGCTGTCTGCCAGGGACCCAGCCACCGAAGCCAAGGGCGAGGCTGGAG  
CCCGCTTCTCATGGCAGGTGGGGCTCAGCTTCTTGTGCAACCCCTCATCTCTGGTGTGCTGGC  
TCCCTGGTGGTGGCAACCGTGCAGACGCTGGTGTGCGGGAGCTGGAGAACCGCAGCTTGTGAGTTGCAAGACA  
CCCCAGGGAACTGGCCCGTCATGAACCTGTCGAACCTCTTGGCCTGAGGAAGAACATCAGCATCCACCAAG  
CCTATCAGCAGTCAAGGAAGGGCAGCGCTCTGGACAGTCTGCACTCAACGACTCTACGCCCTGGAGGAGC  
ACCTGGATATCAACCGATATAACCAACAAGCTACGGCAGGAGTTGCAAGGCCTGAAAGTAGACACACAGGACTGG  
ACCTGCTGAGCTAGCCGCCGGGACCTGGAGGCCCTGCAAGGAGCTGGGCTTCAGCGCATCCACTACCCCG  
ACTTCTCTGTTCAAGATCCAGAGGCCGTGGTGAAGGACAGCATGGAGCAGCTGGGCCAGGAGCTGCAAGGACTGG  
CCCCAGGCCAAGACAATTCTGTCGGGGCAGCGCTGCAAGGGGCAAGGACTCAAGAACCTTCAACCCAGG  
AGAAGGCTGTCAGGAGGCCCTGGGCAAGGCTTGTGCAAGGACTCAACCTCAGGCTCAGGGCTGGAGTCTGCCCCGA  
ATCTCAGCTGGAGACCTCAGATGTCCTAGGCAATGTCACCTACGTAAGGAGAGCTGCCCTGGCAGGCA  
GGATCTGAGGAATGTGAGTGTGAGTTCTGGCCGGGAGATGGGCTACTTCTCCAGTACCTGCTGGCTGGTGA  
GAGAGGAGGTGACTCAGCGCATGCCACCTGCCAGGCCCTCTCCGGAGGCCCTGGACAACAGCCGTGTGATCTGT  
GTGACATGATGGCTGCCCTGGAATGCCCTCTGGTCTGCCATGGTCACCTTCTTCTGATCCCCAGCA  
TCATCTTGGCTCAAGACCTCAAATACTCCGTCTATCGGAAACGCCCTAGCTCCACAGCTCTGAGGAGA  
CTCAGCTTCCACATCCCCGGTTACCTCCCTGAAGCTGTAAGGCTTGTGGGTGAGGTGACCCCTGAGGCTG  
CTCTGCTCTCTTGTGATTTAGCTGGCCACAGGACTCTGGTAGCTTGTGCTGGCCCTGCTCTTCTGCTCACGAC  
GGCTGGACTCTCCCTGGCTTACCTGGCCACCTTGGCTGCTCTTCTGCTCTTCTGCTCACGAC  
CCCCATATTACGCTCAGAACATCACATGGACTTCTGCACTGCAAGGCCAGCAAGTCCCTACAGGTGTCACC  
CGTTACCCCATGCTGGCTGCACTGCAAGGAAGAGCCTGTTCTCACCTGCTGGAGGCTGGACCCCTGGGGTGG  
GACAGAGGCCCTGCCAACCCACTCCCCCTCCCGTGTCTCCCCCTGCCAACGCCCTCCCCCTGCCAACGCTCC  
CCCCCTCTGAGGCCCTGCCAACCCACTGCCCTGAGGCCCTGAGGCCCTGAGGCCCTGGCCCCACTTCCCTT  
ATGCCCTCTGGCCCTTGCTTCTCCCTAGTCCCCTCTCACCATATCTCACTGCTACCTTGTGCTGGG  
GAGACCAACCTGCCAACCCACTCAGGTAACGCCACTAATCAGGCCAGGGGCCACCATGCCCTAGGTCTGG  
CTGGCTGCAAGGCCCTGCCCTGAGGCCCTCAAGGCCCTGGGGCTTGGGCCCTGCAAGATCTCATC  
CAGGATTATTGTTGTCAGTGGGGTGGAGGGAGGCCCTGCTGAGGCGAGCCTCCCTGCTGCAACCAAGTTAG  
AAATGGGGTACCAAGCACTTAGCTCTGAGTGTGGCTCCAGGAAGGGACCTGGGACCTGGGCCACAGT  
GGGGCTTGGCTTACCTCTGAGGAAGCATTCCACAGGCCCAACCCAACTTCTAGGAGTGTGATCTGG  
GGCCAGAACAGGATTTGACCGGCCCTTATCTGCGCATGTGGCTTAGGGTCACTCCCAGCCATCCCTG  
TCAGCCCTGAGTGTGGACACTGCGTTCCAGAAATGAGGAAGAGGAGAGAAGAGATGGACAGACCTCAGATCC  
ATTTAAAGTGTCTCACTTCAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 148**

MKHTLALLAPLLGLGLALSQAAAGATDCKFLGPAEHTFTPAARARWLAPRVRAPGLL  
DSLYGTVRRFLSVVQLNPPSELVKALLNELASVKNEVVRYEAGYVVCAVIAGLYLLL  
PTAGLCFCCCRCRRCGGRVKTEHKALACERAALMVFLLLTLLLIGVVCAFVTNQRT  
EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAQQFSLPQEQQVSEELDGVGVSIGSAIHT  
LRSSVYPLLAAGVSGLGVQLQSVHHLQTLNATVVELQAGQQDLEPAIREHRDRLLLELLQ  
ARCQGDCAGALSWARTLELGADFSQVPSVDHVLHQLKGVPLEANFSSMVQEENSTFNALPA  
LAAMQTSSVVQELKKAVAQQPEGVRTLAEGFPGLEAASRWAQALQEVEESSRPYLQEVQR  
YETYRWIVGCVLCSVLFVVLNCNLLGLNLGIWGLSARDPSHPEAKGEAGARTLMAGVGL  
SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLGLRKN  
ISIHQAYQQCKEGAALWTVLQLNDSYDLEEHLDINQYTNKLRQELQSLKVDTQSLDLLSS  
AARRDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE  
EAQGLRNLHQEKVVPQQSLVAKLNLSVRALESSAPNLQLETSDVLANVTYLKGELPAWAA  
RILRNVSECFLAREMGYFSQYVAWREEVTQRIATCQPLSGALDNSRVILCDMMADPWNA  
FWFCLAWCTFFLIPSIIFAVKTSKYFRPIRKRLSSTSSEETQLFHIPRVTSKL

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

**N-glycosylation sites:**amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,  
684-688, 707-711, 725-729**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 811-815

**Tyrosine kinase phosphorylation site.**

amino acids 95-103

**N-myristoylation sites.**amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,  
228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,  
477-483, 500-506, 536-542, 644-650, 761-767**Phospholipase A2 histidine active site.**

aminop acids 129-137

**4Fe-4S ferredoxins, iron-sulfur binding region signature.**

amino acids 126-138

**Mitochondrial energy transfer proteins signature.**

amino acids 80-89

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**FIGURE 149**

CACAGCTCCCTCCCAGGACGTGAAAATCTGCCTCTCACCATGAGGCTTCTAGTCCTTCCA  
GCCTGCTCTGTATCCTGCTTCTGCTTCTCCATCTTCTCCACAGAAGGAAAGAGGCCGTCCTG  
CCAAGGCCTGGTCAGGCAGGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA  
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC  
TTTGGGTGGTGCCTGGGCACTCCCACAGGTGTAGCACTCCAAAGCAAGACTCCAGACAGCG  
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCTTCAGCCTTCAC  
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTGGCTGCAAGGACCTGGAAAGTCCAG  
AACTCCACGTCTTGTCTCAATTGTGCCATCAACTTCAGAGCTATCATGAGCCAACCTCACC  
CCACAGGGCCTCAGTCGCCACCATGTGGCCTCTCCAGTGCAAACCACCGAGCATTCCACCAT  
GACCGGTACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAGGGTGGCAAGCACC  
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTCAGGTCCATTAGCCTCCTGGCA  
TTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTAGCCTCCTGACATGAGTCTGC  
TGGAAAGAGCATCCAAACAAACAAGTAATAAATAAATAAAACTCA

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**FIGURE 150**

MRLLVLSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVPSPNSTNLKGHHVRLCKPC  
KLEPEPRLWVVPGALPQV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 48-52

**Amidation sites.**

amino acids 23-27, 33-37

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**FIGURE 151**

CACCGGAGGGCACGCAGCTGACGGAGCTGCCTCGCTCGCTTGCCTCGGCCCTCCA  
CTGGAGCTGTTCGCCCTCCGGCTCCCACCGCAGCCCACCCGGCAGAGGAGTCGCTACCAGC  
GCCAGTGCCTCTGTCAGTCCGCAAACCTCTTGCCTCGCCGCCGGCTGGGCACCAAATAC  
CAGGCTACCATGGTCTACAAGACTCTTCGCTCTTGATCTTAAC TGCAAGGATGGAGGGTA  
CAGAGTCTGCCATCACAGCTCCTTGTCTGTTCTCTCCGACAAACATTGTACCGACC  
ACCATCTGGACTAGCTCTCCACAAAACACTGATGCAGACACTGCCCTCCCCATCCAACGGCACT  
CACAACAACCTGGTCTCCAGTTACAGCATCAGCCCCAACATCTGCTTCTTAAGAACATT  
TCCATAGAGTCAGAGAAGAGGGAGTCACCAAGCCCAGGGTGAATTGGGAAGGCACAAACACA  
GACCCCTCACCTTCTGGGTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACCACGTTGGAG  
GAACACAGCTCGGGCACTCTGAAGCAGGCGTGGCAGCTACACTGTCGAGTCCGCTGCTGAG  
CCTCCCACACTCATCTCCCTCAAGCTCCAGCCTCATCACCCCTATCAACCTCACCA  
CCTGAGGTCTTCTGCCCTCGTTACTACCAACCATACTGTCAGCAGCACCCACCC  
ACTGGAGCTCAAAC TGCAACCAGAGTCCCCGACAGAGGAGTCCAGCTGACCACACACCCACT  
TCACATGCCACAGCTGAGCCAGTGCCCCAGGAGAAAACACCCCCAACAACTGTGTCAGGCAA  
GTGATGTGTGAGCTCATAGACATGGAGACCACCACCTTCCAGGGTATGAGTCAGGAA  
GTAGAACATGCATTAAGTCAGGCAGCATGCCATTACCGTGAAGTCATTGCCGTGGTG  
CTGCTGGTGTGGAGTTGAGCTGCAGCCTACCTAAAAATCAGGCATTCCCTATGGAAGACTTTG  
GACGACCATGACTACGGGTCTGGGAAACTACAACAACCCTGTACGATGACTCCTAACAA  
TGGAATATGCCCTGGGATGAGGATTAAC TGTTTATTATAAGTGTATCCAGTAGAATT  
AATAAGTACCTGATGCGCATTGAACGACAATCTTAAGCCCTGTTTGTGGTATGGTTTTT  
TGTTTCCCTCCCTCCTCTGGCTGCTACAACCTCCCTTCTGGTACAAGAAGAACATTCT  
TTAAAGGTGAGTGGAGGCTGATTGAGCTGAGCTGAAGTGGGCCAGCCTGCAACCAGGCCAGA  
CCACCATGGTGAAGGCTTCTCCCCACTGCAGGACCCACTTGAGAAGGATCGAGGAGGAGG  
ATTTGGGTTGTTGTTAGGGTTACTTCAGGGGAACATTCTATTGTGTTATTCTAAAC  
TTCTATTAGGAAATTACATTAAGTATTAAATGAGGGGAAAGGAAATGAGCTCACGAGGATT  
CACCTGCACTGGAGAGAGCAGGGTTCTCAGATTCTTTAATCTTATTTCTGGTTG  
TTCTGACAGGATGCTGCCGCTGGCTCACGAGCTGGAAAGCAGCTTCTAGCTGCCATT  
TAATGAAAGATGAAAATAGGAAGTGCCCTGGAGGGGCCAGCAGGTACGGGCAGAACATTCT  
CAGGTTGCTGTGGGATCTCAGTGTGCCCTACCTGTTCTCCCTCCAGGGCACCTGTCTG  
AAAGGATGTCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCACAAGTGTACGAGGATT  
GCATTCCAAGAAAAAGGCTATGAGATGAGCTGAGTTAGAGAGAAAGGGAGAGGCATGTA  
CGGTGTGGGAAAGTGGAAAGAGAAGCTGGCGGGGAGAAGGGAGGCTAACCTGCACTGAGTACTT  
CATTAGGACAAGTGAGAATCAGCTATTGATAATGCCAGAGATATCCACAGCTGGAGGCC  
CAGAGACTGTTGCTTATACCCACACAGCAACTGGTCCACTGCTTACTGTCGTTGGATAA  
TGGCTGAAAATGTTAAAAC

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**FIGURE 152**

MVYKTLFALCILTAGWRVQSLPLTSAPLSVSLPTNIVPPTIWTSSPQNTDADTASPSNGTHNN  
SVPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTPSPSGFSSTSQQVHLTTLEEHS  
SGTPEAGVAATLSQAAEPPTLISPQAPASSPSSLSTSPPEVFSASVTTNHSSVTSTQPTGA  
PTAPESPTEESSSDHTPTSHATAEPVPQEKTPTTVSGKVMCELIDMETTTFPRVIMQEVEH  
ALSSGSIAAITVTVIAVVLLVFGVAAYLKIRHSSYGRLLDDHDYGSWGNYNPLYDDS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 258-278

**N-glycosylation sites.**

amino acids 58-61, 62-65, 80-83, 176-179

**Casein kinase II phosphorylation sites.**

amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-  
144, 164-167, 191-194, 195-198, 200-203

**Tyrosine kinase phosphorylation site.**

amino acids 289-296

**N-myristoylation sites.**

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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**FIGURE 153**

ACGTCACTGTCTTGAAGCAGCAGTAGCCTGGAAAGTGAGGCAGGAGGAATTGAGAGGCAGGAA  
GGGNNGCTGGAGACACAGCTGAGCCTGGAAATGAGAGTGAGCATGCCGTGGTCATCATGACTC  
CTCTGCGGCGTGGTCACCATGTTGGTTACTGTGTTGGGCTTTATTGACGGGTCTCCGTCTA  
GGCCTGACCTTGGGTGCCGGAGCCCTGCTGGCTCTGAGCCTATCTACCAACCACCTTCAGCC  
TGGGTGCCAGCTGGGGGCTGGTGGGCTGGCGCTGCTGGGAGCCCTGCTCACACTTCGGTGG  
CCACGTCCATTACAGTTCTGGGCACAACCCTGCTGGGTCTGCAGTGCTTGCCCTGTGTT  
GACTACTTCCTGGAGGGGCTGGCACTGGGAGTTGGCTGGCCAACGCCCTGCAGACACTTCCA  
GCCTTGCCTTCTCTGCTTGATTAGCTGGTCTTACTGGGATCTGCCAGCCTTGGGGCC  
CTTGGAGCCCTGGCCAGTGGAAAGCTCGTGCCTGAGGAACATGGAGGCCACGCTAATGGGTCT  
GTTCCCTGGTTTCCCAGATGCATAAAGGAAGACATATCCCTCCCTGGCAGCAAGGCTACAAT  
GGGAGGGAGGGAGAACATGGAGCATGTGAATAAAATGGCATTAAATACTGAAAAAAA  
AAA

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**FIGURE 154**

MLVHCVGLLLTGLLLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV  
LGTTLLGSAVLVACVDYFLEGLALGSWLQRLQTLPALPSLC

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 38-55, 60-78

**N-myristoylation sites.**

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 67-78

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**FIGURE 155**

TGCAATTAAAGGAGTCGGTCTCTAACTGTTGATCTGTTTTCCCTCTGAGCAATGGGAGC  
TTACCATTTATCCTGAGACTGGCCATTACATCCTGACATTCCTGTACCTGCTGA  
TTCTGGGCTTGTGGAGCTGGATATGCAAAAATGGTCCCCTACTTCTTGGTGAGGTTCACTG  
TGATATAACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTTCAGTAACCTGCAGGAGTTG  
CGGGCCCTCCGGAAACTCTCCCTGCTGGAAGTGGCTGTGGCACGGGGCCA  
ACTTCAAGT  
TCTACCCACCTGGTGCAGGGTGACCTGTATTGACCCAA  
CCCCA  
ACTTTGAGAAGTTTGA  
TCAAGAGCATTGCA  
GAGAACCGACACCTGCAGTTGAGCGCTTGAGCTGCCGGGAGA  
ACATGCACCAGGTGGCTGATGGCTCTGTGGATGTGGTGGCTGCACCC  
CTGGTGTGCTCTG  
TGAAGAACCA  
GGAGCGGATTCTCCCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGCTTCT  
ATTCATGGAGCATGTGGCAGCTGAGTGTGCACTTGA  
ATTACTCTGGCAACAAGT  
CCTGG  
ATCCTGCCTGGCACCTCTGTTGATGGGTGCAACCTGACCA  
GAGAGAGAGCTGG  
AACGGGCCAGCTCTCAAGCTGAAGCTGCAGCACATCCAGGCC  
ACTGTCCTGGAGTTGG  
TGCGCCCTCATATCTATGGATATGCTGTGAAATAGTGTGAGCTGGCAGTTAAGAGCTGA  
ATGG  
CTCAAAGAATTAAAGCTTCAGTTTACATTAAAATGCTAAGTGGAGAAGAGAA  
ACCTTT  
TTTGCCCCGGTTTTGGTTGTTGGTTTTTTGGCAGGAGAATCTC  
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTG  
ACTCTAGCCTGGTG  
ACAAGAGCAAGACTCCGTCT  
AAAAAAAAAAAAAAA  
AGAAGTAGAGAGACAGGGAGAC  
GGGGTCTCACTGTGTTGCC  
TAGGCCGGTCTTGA  
ACTCCTGGCTCAAGTGATTCTCCACCT  
GACCTCCTAAATTGTTGGGATTACAGGTGTGAGACAGTG  
CACCTGGCC  
GAAATAGCTCAAGTT  
TCTGAAAAACAAATCTGAATCTATTGTTATTCTTAGCGTC  
ACTGGTCTGGCTTCA  
GAGAATT  
ACATACAAGGTTGCCACACCTAGTTCTGCC  
CAGCTTATGTCTTTATTCCAGTATTCCACCA  
AAGTTGTTCTGCATTCCAGTTCTCAAGCTTAAGATAAA  
AGATTGTACTTGACAGTTAG  
TATATCCATAAAACTATTGAGGTGGTAAGGTTCTGGGTT  
CATTTCCTTA  
AACTTTGCT  
GAATATTGTAGATTGAGGCAATGAAAAAGTCTACTAA  
ATTAGGAAA  
ACCTTG  
AATAATTAGG  
TATCCTAGGTAAAGAGGCC  
CTAAACATCAAGCAATCTGTGAGTCTGTAAAGAA  
ATAAATATT  
TTGGATTATTCTTATCTAATTCCACCC  
CTGTTGGAAGATGATTCTTGTCTTGCAACTAT  
GGAAGCTGTGAAA  
ATCATCACAGTGCCTCTGAAAGCGAGTGTAGGTTAGGGTTAGAGGGTTA  
ATATTTCCTGCA  
ATGGTTAGGA  
ATT  
TAATAAA  
ATGTAGTATATTCTGAGATGATT  
TAAAGTACTATT  
TAAATCAA  
ATCAA  
ACCA  
ATAA  
ATT  
CACATTG  
GTGTTAGGA  
ACAAAAA

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**FIGURE 156**

MELTIIFILRLAIYILTFPLYLLNFLGLWSWICKKKWFYFLVRFTVIYNEQMASKKRELFNSNLQ  
EFAGPSGKLSLLEVCGGTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVA  
GENMHQVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEHVAECSTWNYFWQQ  
VLDPAWHLFDGCNLTRSWKALERASFSKLKLQHIQAPLSWELVRPHIYGYAVK

**Signal peptide:**

amino acids 1-29

**N-glycosylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 78-84, 80-86, 91-97, 201-207

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**FIGURE 157**

CCGCTGAGATGTACGAACCTCCGGTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT  
GCCACGACCAGGGCCTCTCCCTGGCGTTGGTCACCTCTGCTTCATTCTCCACCGCGCCTATGG  
TCCCTCTGGAGCCAGCGTGGCGGGCTGGCGGCTCCGGGTGGTAGAGAGAGCGGTCCGGGAA  
**CGATGA**AGGCCTCGCAGTGCTGCTGTCTCAGCCACCTTGGCTTCCGTCCCTCCTGC  
TGGTGTGCCTGAACTAAGCGGGCCCTGGCAGTCCTGCTGCAGGCAGCCGAGGCCGCCAG  
GTCTTGGCCTCCTGACCCCTAGACCACGGACATTACCGCCGCTGCCACCGGGCCCTACCCCTG  
CCCAGCAGCCGGGCCGTGGCTGGCTGAAGCTGCGGGCCGCGGGCTCCGAGGGAGGCAATG  
GCAGCAACCTGTGGCGGGCTTGAGACGGACATCACGGAGGGAGGCCGGGAAGGCTCGG  
TGGGTGGCGGCCCTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA  
CCGTGTTGATGGTGGTGAGCGGCGGGTGTGGTACTTCGTGGTCAGGACGGTCAGGATGA  
GAAGAAGAAACCGAAAGACTAGGAGATATGGAGTTGGACACTAACATAGAAAATATGGAAT  
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTGATGCCAATCATCCTC  
**GAAGATAAGA**ATGTGCCTTGTGAAAGAACCTTATCTTCTACAATGAAGAGTGAATTTC  
TATGTTAAGGAATAAGAACGCACTATATCAATGTTGGGGGGTATTTAAGTTACATATATTT  
TAACAACCTTAATTGCTGTTGCAATAAACCGTATCCTTATTATATCTTATATGTAT  
AGAAGTACTCTATTAATGGCTCAGAGATGTTGGGATAAAAGTATACTGTAATAATTATCTG  
TTGAAAATTACTATAAACGGTGTGTTCTGGCGGTTTGTGTTCTGCTTACCATATGATT  
GTAAATTGTTATGTATTAATCAGTTAATGCTAATTATTTGCTGATGTCATATGTTAAAG  
AGCTATAAATTCCAACAACCAACTGGTGTGAAAATAATTAAAATTCTTACTGAAAGG  
TATTTCCCATTTGTGGGGAAAAGAACGCAAATTATTACTTGTGTTGGGGTTTAAAAT  
ATTAAGAAATGTCTAAGTTATTGTTGCAAAACAATAAATGATTAAATTCTTAAAAA  
AAAAA

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**FIGURE 158**

MKASQCCCCLSHLLASVLLLLLPELSGPLAVLLQAAEAAPGLGPPDPRPRTLPPLPPGPTPA  
QQPGRGLAEAAGPRGSEGGNGSNPVAGLETDDHGGKAGEGSVGGGLAVSPNPGDKPMTQRALT  
VLMVVSGAVLVYFVVRTVRMRRRNKTRRYGVLDTNIENMELTPLEQDDEDDNTLF DANHPRR

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 124-140

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,  
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**FIGURE 159**

GCTGCAGGCAGGCGACGGCTACACC**A**TGGGCCGGCTGCTGCGGGCCGCCGGCTGCCGCCGCTG  
CTTTCGCCGCTGCTGCTTCTGCTGGTTGGGGAGCGCTTCTGGGTGCCTGTGTTGGCTGGTCT  
GATGAGCCTGGCCCAGAGGGCCTCACCTCACCTCCACTGGCTAGACCTCCTGCTGCCACTGGC  
TTGGAGCCACTGGACTCAGAGGAGCCTAGTGAGACCATTGGGCTGGAGCTGGCTGGAGCC  
TCTGGCTCAGGCTCCCCAGCGAAGAGAAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC  
TTCTGGGAAGAGGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGACCCACTGCAGATTAT  
GTTTTCTGACTTAACTGAGAAGGCAGGTTCCATTGAAGACACTAGCCAGGCTCAAGAGCTG  
CCAAACCTCCCTCTCCCTGCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCCTCCC  
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA  
GAGGAGGAGGAAGAGGGAGGAGCTGCCACTGCTGAATGGATCCAAGAAGAAGCCAAGCCTCAG  
GTCCGTGACTTTCTCTCACCAAGCAGCAGCCAGACCCCCAGGGGCCACCAAAAGCAGGCATGAA  
GACTCCGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCAGCATGGGCCCAGCTGCTG  
CTGCCTTCAGTCACCCCAACTACAGTGACTCCGGGGACCAGGACTCCACCAGCCAAGAGGCA  
GAGGCCACAGTGCTGCCAGCTGCAGGGCTGGGTAGAGTTCGAGGCTCCTCAGGAAGCAAGC  
GAGGAAGCCACTGCAGGAGCAGCTGGTTGTCTGCCAGCAGCAGGAGGTGCCGGCTTGCCT  
TCATTCCTCAAACCACAGCTCCAGTGGGGCCAGCACCCAGATGAAGATCCCTGGCTCT  
AGAACCTCAGCCCTTCCCCACTGGCCCTGGAGACATGGAACTGACACCTTCCCTGCTACC  
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGAGCTGAAGCTCAATCCAGG  
ATACCCCTGGGATTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGAAAAACTAC  
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACGGGGCCACAG  
CTCCTGGCCCTGGTGGAAAGAGGTGCTGCCCGCCATGGCAGTGGCACCAGTGGGCTGGCAC  
ATCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTCTCATGACACTGGTGGCGAGCAG  
GGGGTGGTGCCACTCAAGATGTCTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAGGAG  
ATTGGCATCCAGAACTATTCCACAACCAGCAGCTGCCAGGCGGGCCAGCAGGTGCCAGC  
GACTACGGCACGCTCTCGTGGTCTGGTCAATTGGGCCATCTGCATCATCATATTGCG  
CTTGGCCTGCTCTACAACCTGCTGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTCGCACGGC  
GAGGAGCTGCCCTCGTGGAGAACGGCTGCCAGCACACCCACGCTGGACGTGGCCAGCGAC  
AGCCAGTCGGAGATGCAGGAGAACGACCCAGCCTGAACGGCGGGGGCCCTCAACGGCCCG  
GGGAGCTGGGGGGCGCTCATGGGGGCAAGCGGACCCAGGACTCGGACGTGTTGAGGAG  
GACACGCACCT**TG**AAGCGCAGCCAGGGCGCAGGCCAGTGGCCGCCAGGACCAAGCGAGGTG  
GACCCCGAAACGGACGGCCGGAGCCGCACCAAGCCCCGCCCTACCCGGGCCCGGGCG  
CCTGGCCCTCGGCAGGGCTCTTCCGCTTCCCGACTTCACACGGCGGCTTCGGACCAAC  
TCCCTCACTCCCAGGGCAGGGCAGGCCCTAAAGCCGCCCTGGCCCCGCTTCCCGCCCTG  
AACCCCGCCCCGCGGGCGGGCGCTTCTGCGCCCCGGACTCAATTAAACCGCC  
GGAGACCACGCCGGCCAGCAAA

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**FIGURE 160**

MGRLLRAARLPPLSPLLVLGGAGFLGACVAGSDEPGPEGLTSTSLLDPLLPTGLEPLDSEE  
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPTADYVFVFDLTEK  
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMPPREEEEEEEEREKEEVEKQEEEEEEEL  
LPVNNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSSLPSVTPTT  
VTPGDQDSTSQEAEATVLPAAAGLVFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTTAP  
SGAEHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQQLLEGQAAEAQSRIPWDSTQV  
ICKDWSNLAGKNYIILNMTEIDCEVFRQHGPQLLALVEVLPRHGSQHHGAWHISLSKPSE  
KEQHLLMTLVGEQGVVPTQDVLSMLGDIRRSLEEIGIQNYSTTSSCQARASQVRSDYGTLFVV  
LVVIGAICIIIIALGLLYNCWQRRLPKLKHVSHGEELRFVENGCHDNPTLDVASDSQSEMQEKG  
HPSLNGGGALNGPGSWGALMGGKRDPEDSDVFEEDTHL

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 499-521

**N-glycosylation sites.**

amino acids 106-110, 193-197, 395-399, 480-484

**Glycosaminoglycan attachment site.**

amino acids 77-81

**N-myristylation sites.**amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,  
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590**Amidation site.**

amino acids 588-592

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**FIGURE 161**

CCAGGGCGGAGCGCAGCTCGCCGGCTTGGCGCCTGGGCCGCGCTCCCCACCGTCGTT  
TCCCCACCGAGGCCGAGCGTCCCGAGTCATGCCGGCTGAACTGCGGGTCTCTATCGCA  
CTGCTAGGGTTCTGCTGCTGGTGCGGCCCTGCCGCGGGGAGAAGCTTTGAGATT  
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCGACTCTGCTGGCA  
AAACCCCTGTTACATCGTCATTCTAAAAGACATATAACCATGTTGCCATCAAGTCTGGAGAA  
AGAATAGTCTTACCTTAGCTGCCAGAGTCTGAGAATCACTTGTCAAGAGATCCAGAAA  
AATATTGACTGTATGTCAGGCCATGTCCTTGGGAGGTTAGCTTCAGCCCTCGACATCG  
TTGTTGCCTACCCCTAACAGAACATTCTCATCTGGATGTCAAAGCTCATAAAGAGCATCGTTA  
GAGCTGCAGTTTCCATCCCTGCCCTGAGGCAGATCGTCCGGTGAGAGCTGCCAGACGGA  
GTCACTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGAACCTCTGCAGC  
AATGGCACTGTGTCGGATCAAGATGCAAGAAGGAGTGAAGGAGTGAACCTCCATGG  
TTCCACCCCAGAAATGTCGGCTTCAGCATTGCAAACCGCTCATCTATAAACGTCTGTGC  
ATCATCGAGTCTGTGTTGGGTGAAGGCTCAGCAACCTGATGTCAGGAACTACCCAGAA  
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTGTCGTTCTGCACACCTGCGGCCAGC  
GTCTCCTCCTCAACTTCAACCTCTCCAAGTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC  
ATCCCCGGCTCCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGAACATG  
GCGGGGAACCTCAACCTCTCTGCAAGGCTGTGACCAAGATGCCAAAGTCCAGGGATCCTC  
CGGCTGCAGTTCCAAGTTGGTCCAACATCCACAAATGAAAGCAGTGAGTGACCCCACTT  
TCCTTTCTCCTCCAGCACCTCGTTGTTCTGGTAGTCTGCCTGGTGAGGCTCC  
CTTCCTGTTCTCATCTGTGGCTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTCA  
AAGTGGGTTGCTAGGCAGTTAGACAGGCTGTTGGTAACACCCGGTATGAGTTCCATTCA  
GCACAATAAAAGAAATTTGCATTCAAGATGCTAAATTGTTTAACGAAAA

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**FIGURE 162**

MAGLNCGVSIAALLGVLLLGAARLPRGAEAFEIALPRESNITVLIKLGTPTLLAKPCYIVISKR  
HITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMMSGPCPFGEVQLQPSTSLLPTLNRTFI  
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCNSNGTVSRIKM**Q**  
EGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIIESVFEGEGSATLMSANYPEGFPEDELM**TW**  
QFVVPAHLRASVSFLNFNLNCERKEERVEYYIPGSTTNPEVKLEDKQPGNMAGNFNL**LQG**  
CDQDAQSPGILRLQFQVLVQHPQNESSE

**Signal peptide:**

amino acids 1-29

**N-glycosylation sites.**amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,  
310-314, 339-343**Tyrosine kinase phosphorylation site.**

amino acids 276-284

**N-myristoylation sites.**

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309

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**FIGURE 163**

CAACCACACACTGGGAATTGCTGGCCTGACTTCTGACCCCTGACTCCTCATACCCTCCTC  
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCCAGACCACACTGGCCCTTCC  
CCCCCCTGTGGTACTTCATAAAGGTTACTAGCTTCTCCCTGGCCTTGAGACCCACACGAT**T**  
**G**GCCCTGCTGGCTCTGGCCAGTGCCGTCCCTCTGCCCTGCTGGCCCTGGCTGTCTCAGGGT  
GCCCGCCTGGGCTGTCTCCTCTGCTTCACAACCTACTCTGAGGCCCTCCGCATCTGCCAGAT  
GTTTGTGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCTCACGCCGCCTTCCA  
GGGCCTCTGTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTGGGAAG  
GTGCAGAGGGAGGGCAGGAGAGGCCAGAGGGTCAGGCTGAGGGACAGACAGAGAGAAACAGT  
CAGAGGAGAAAGGCTCAAAGACCATGAGAACAAACAGAGACTTAGGGACAGAGAGACACAGACA  
GGGAAAGACAGCAGGGCAAAGACTCAGAGAGGGAGGATGGAGAGTCAGAGAGGGAAAGATGG  
AGACTCAGAGAGAGGGAGGATGGAGACTCAGAGAGAGGAAGATGGAGACTCAGAGGGAAA  
GATGGAGACTCAGGAGTATGGAGAGTCAGAGAGGGAGGATGGACACTCAGGGAGGATGGAG  
AGTCAGGAGGATGGAGACTCATAGAAAGGGGAGGATGGAGAGTCAGGGTGGAAAGATGGAGACTCAA  
AGAGGAATAGAGACCCAGAAAGGGGAGGATGGAGACTCAGAGGGTGGAAAGATGGAGACTCAA  
AGAGGATGGAAACCCAGAGAGAGGGACAGAGA**T****G**AGGCAGAGACTAGGGAAAGCAGGATAG  
CGACTGGTCGGGGCAGAGACTCAGGGAGGATAGAGACTCACAGAGAGGTGAGGATAGAGACT  
TGGGAGGGACTCAGGAAGCATAGCAGTGTGGGCAAAGAGTCAGAGAGGGAGGATACAGAC  
TTGGGAGGGCAGAGACTCAGAAACAGAATGTCGCATTAGGGACATGGTGTGCGGGGAGCTG  
CCTCCCCAGCCCTGCTCCCTCCCTACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA  
CACCTCACCCAGATGACCCATGCCCTGCAGGAGCTGGCTGCTGCCAGGGATCCTTGAGGT  
TGCCTCCCTGATGCTGCAGAGAAATGAAGAAGGTCAATTACACAGCTAAAGAAGCCCAGGC  
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTGCCCGGCTTCCCTGAGCAGGGTGTACTC  
TAGGGTCTGCGACCTCCGCTGGACTGCCAGTTCAAGGATGTGACAGTGACTCGGGCGACCA  
GGCTATGTTTCTTGCATCGTAAACTCCAGCTGCCAAAGGAGGAGATCACCTATTCTGGAA  
GTTCGCAGGAGGAGGTCTCCGACTCAGGACTTGTCTATTCCGAGATATGCCGCGGGCGA  
AGGATAACCTGGCGCGATCCGGCGGCTCAGCTCACGCCACGGGACGTTCTCGTGAT  
CAAGCAAGACCAGCGCCCCCTGGCCCGCTACTTCTTCTTAACGTCTCGGGGCCCCAGCATCTAGC  
ATCAGCGAGTGCAGACTGTTGGCGTGGTGAAGTTCTGGGACTCCGGAGCCACAGT  
TCCCCGCTGTCTCAGATCCCACCGAGAAGTCTGGTTCCAGCAACCTCCAACCCAGGAGGAT  
GTTCTTCGATGGTACTGCAGTGGCAACTAACAAAGGTATCTTCCCTCCCTATCCTATT  
TCCATCCTGAAAATAAGAATATATTCAACTCTAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

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**FIGURE 164**

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRSPKLEECEEAF  
QGLSDTEISEETIHTSSVSGRCRGRAGEAQRVRLDRQRETVRGERLKDHENNRLGTERHR  
QGKTAGQRLREGRMESQRGEDGDSERGEDGDSEEDGDSEGKMETQEYGESERGGWTLRGGW  
RVRRMETHRKGRMESQERLETGEGIETQKGEDGDSEGGRWRLKEDGNPERGGQR

**Signal peptide:**

amino acids 1-26

**N-myristoylation site.**

amino acids 65-71

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**FIGURE 165**

CAGAATCGCAGATTGCCAGCCCTTCCCACCCCTACGGAAAGACGAGTCCAGGGCCGTCC  
TGGCGAGGTAAAACATTAGTCTGGTCTTCAGCGTGACCTGCCAGCAGCCAGGCC**ATG**  
GAGCTCTCTGATGTCACCCCTATTGAGGGTGTGGTAATGAGGTGATGGTGGCAGGTGTG  
GTGGTGTGATTCTAGCCTGGCTTAGCTGGCTCTCACCTACGTAGCAGACAGCGGTAGC  
AACCAAGCTCCTGGCGCTATTGTGTCAGCAGGCAGACACATCCGTCTCACCTGGGCATGTG  
GACCACCTGGTGGCAGGCCAAGGCAACCCCGAGCCAAGTGAACCTCCCCATCCATCAGAGGGT  
AATGATGAGAAGGCTGAAGAGGCGGGTGAAGGTGGGAGACTCCACTGGGAGGCTGGAGCT  
GGGGTGGTGTGAGCCCAGCCTGAGCATCTCCTGACATCCAAGGCCTGCCAAAAGACAA  
GCAGGTGCAGGCAGCAGCAGTCCAGAGGCCCTGAGATCTGAGGATAGCACCTGCCTCCCT  
CCCAGCCCTGGCCTCATCACTGTGCGGCTCAAATTCTCAATGATAACGAGGAGCTGGCTGTG  
GCTAGGCCAGAGGATACCGTGGGTGCCCTGAAGAGCAAATACTTCCCTGGACAAGAAAGCCAG  
ATGAAACTGATCTACCAGGGCCGCCTGCTACAAGACCCAGCCCGCACACTGCCTCTGAAC  
ATTACCGACAACGTGTGATTCACTGCCACCGCTCACCCCCAGGGTCAGCTGTTCCAGGCC  
TCAGCCTCCTGGCCCCCTCGGCCACTGAGCCACCCAGCCTGGTGTCAATGTGGCAGCCTC  
ATGGTGCCTGTCTTGTGGTGTGGTCTGGTACTTCCGAATCAATTACGCCAA  
TTCTCACAGCACCTGCCACTGTCTCCCTGGTGGAGTCACCGTCTTCAGCTTCTAGTA  
TTTGGGATGTATGGACG**TAA**GGACATAGGAAGAAAATGAAAGGCATGGTCTTCTCCTTAT  
GGCCTCCCCACTTTCTGGCCAGAGCTGGGCCAAGGGCCGGGAGGGAGGGTGGAAAGGA  
TGTGATGGAAATCTCCTCCATAGGACACAGGAGGCAAGTATGCCCTCCCTCATCCAC  
AGGAGTACAGATGTCCTCCCGTGCAGCACAACTCAGGTAGAAATGAGGATGTCATCTCCT  
TCACCTTCTGGTCTCTGAAGGAGTCAGGCTGCCAAGCTCAGTGGGAGCCTGGC  
TCTGAGATTCCCTCCCACCTGTGGTCTGACTCTCCAGTGTCCATGTCATGCCCCCAGC  
ACCCAGGGCTGCCCTGCAAGGGCAGCTCAGCATGGCCCCAGCACAACCTCGTAGGGAGCCTGGA  
GTATCCTCCATTCTCAGCCAATACTCATCTTGAGACTGAAATCACACTGGCGGGAAATG  
AAGATTGTGCCAGCCTCTTATGGGCACCTAGCCGCTTCACCTTCTCCTACCCCTTA  
GCAGGAATAGGGTGTCTCCCTTCTTCAAAGCACTTGCTGCTTGCATTTATTTATTTTTA  
AGAGTCCTCATAGAGCTAGTCAGGAAGGGGATGGGGACCAAGCCAAGCCCCCAGCATTGG  
GAGCGGCCAGGCCACAGCTGCTGCCCTACCCACTCCAAGGACTGGGTATGGATCGCTGGCCCTAGG  
CCCTTGGCCAGCGTCCACCCACTCCAAGGACTGGGTATGGATCGCTGGCCCTAGG  
CTCTGCTTCTGGGCTATTGGAGGGTCAGTGTCTGTGACTGAATAAGTCCATTGGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 166**

MELSDVTLLIEGVGNEVMVVAGVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH  
VDHLVAGQGNPEPTELPHPSEGNEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR  
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFPGQES  
QMJKLIYQGRLLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVGS  
LMVPVFVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLVFGMYGR

**Signal peptide:**

amino acids 1-36

**Transmembrane domains:**

amino acids 246-267, 275-301

**N-glycosylation sites.**

amino acids 162-166, 211-215

**N-myristoylation sites.**

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

**Cell attachment sequence.**

amino acids 97-100

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**FIGURE 167**

GGCGGCTGTGTCGCCGGAGCCGAAGCGCGCAGGCCGTCGGCCGGGAGCGGGGGGGTGGGGCGCCA  
TGTGGTTCATGTACCTGCTGAGCTGGCTGCGCTCTCATCCAGGTGGCTTCATCACGCTGGCTGTCGCGCTG  
GACTCTATTACCTGGCAGAAGTGAAGAATAACACAGTGCCACCAGCAGGATCATAAAATACATGATCTGGT  
TCTCCACCGCTGACTGATTGCCCTACGTCTTGAGCCTCCCCACCAGCATGATTGGAGTGGGCCTATTCA  
CCAACCTCGTCTACTTTGCCCTCCAGACCTTCCCTCATCATGCTGACCTCGCTAACCTCATCTGCGT  
GTGGACTAGTGGGGTGAATCATTACCTAGCATTTCAGTTTTGAGAAGAATAATTATCCCTCTCAGAGGTCC  
TGGCCTATTCTCCTGGCTGAGATAATTCTGGCTGCGCTCATTTCCGGCCGGGAGAACGTCC  
TGGCCTATTACCATGAGCAGGAGATGATGTCGTCATCCAAAGGCAAGCAGGGAAACGCTTAG  
GGATCCTGGTTGCTTCTCCTCATCAAAGAGGCCATTCTACCCAGTCAGAAAGATATACTGACCCCCATGCA  
GGCAGGATGTGGGGGCAAGATCAGGAGAGTCAGGCCCTGGCCCTATGCCAGGTGGGGACAGAGTCGGGA  
AGGCACCTACCACCTGCCCTGGCTTCTCCCTCAACTCTGGAGCCCATCCCCACCCCTGGGGGCTCAG  
CTTGGCTCAGATCTGATGCTTAAGAGGCTGTAACCTCAGAGGGCACCAGGAGGGTGGCAGAGCCTGCTTAGCC  
AGGAGGCCGAGGTCCCTCAGTCCCTGGCTCAAGGTGGTCAGGAGGTTCTGGCCCGCTGGGCAGG  
CAGGGCAGGGTCTGAAGCTTAAGAGCAGATGGTACAAGTCTCTGGCAGGTGGGGCATGGGAGGGGCCATG  
GCTTGGCATGTCACAGAAATAGTTTCTGCTGTTGAACGGTGAATTCTGTCAGTCAGATTTCCGTTGAAT  
AAAGCTTCGCTTCTAGGTGGCAGTGTGCTTAATACCCCTGACAGTTCATCTCCCTTCTGGCTGCTAACCTTC  
TGCTCTGGACTGGACTCACTTTCTGCTCAGGGACTCTTCTGGGTTGGCTTCTGCCCTCCAAGGGACT  
GTTCTGTGGCCCTTAATGGGAAGGGGGCAGGGTGAAGCTGACCTGCTCAAGGAGTGGGAAGTGGCTAT  
AGGCAGCCTCTGATGCACTCTTCCATCTCTTCCCAAGGCTCCGTGACTGTCAAACTGGGAGTAGGGAG  
GGGACAAATTAGGACTGGCTAGATTTCAGAAGAACATCTACAATATCTTATTTAAATCTCTGGAAA  
AGGAGTGGTTCTGGCTGAATACTATCTAGGCTCAAGGAGAAACAAAATTTAAATAGCTTCCAGGCAGCTGT  
TTTAAAGAAATGGGACTAATGGGAAGAGCTGTTGCACTCTAAGAGCATCCAAGCCCTGGCCGCTGTGAC  
TCTTGGCTCTGGGAGATATCTGCTTCTTAAGAATACCAAGCTTCCCTTCCCTGAGAGGAAGAGCACATGTTGCTC  
CTCTTGGCTTACCTTCTTAAGAATACCAAGCTTCCCTTCCCTGAGAGGAAGAGCACATGTTGCTC  
CTCTTGGCTTACCTTCTTAAGAATACCAAGCTTCCCTTCCCTGAGAGGAAGAGCACATGTTGCTC  
CTCTTGGCTTACCTTCTTAAGAATACCAAGCTTCCCTTCCCTGAGAGGAAGAGCACATGTTGCTC  
GCCTGCATCATCTCCCATTGGCTGACAGCTGGCCCTACTTCTCCCTGCTGCTGGCCCTCACCTGAT  
GATGTTGGCTTCGCCCTCCACTCTACTGCCAGTGTCTCCAGGGGTTGCTAAATCCAGCAGACCCCTTCC  
TCTTACTAGATCTGGCAGATTGACATGGCTGATCACCCCTGCTTCTGGATGGCACTTCCCTGGCACCT  
GTGGCTAGTTGCTCTACCTCCCTGGCTTCCCTGAGGCTTCCGTCAGGCTTCTCCACTTGGCCATGACAGT  
AGGGTCTTCAGGGTCTGCTGGGCTCCCTAGGGAGCCCACATCCATCTGGATGGTTCAAGGATGGGAG  
TTTAGAGTTGACCTCCAGGCCAACATCTTCTGATCACCTGAACACAGTTTGCTGCCCTCTAGGTGACAG  
ACAATTCAGGTCATGCCCTGAGCTGGTACTTGCTGCTCTGCAAACACTGCCCTCTGGTACTTCCCTGACC  
CCGAGATCACTCAGGAGCCAGACAGGAACATTCTTCTGATCACCCCTGCTTCTGGATGGCACTTCCCTGGCAC  
TCAAAACGGCTCAGGTCTACCTTAACATCTTGTGATTGAGCCACTCCACTGTCATCAGCTTCACCTGGATT  
CGTGCAGGCCCTCTACTGCTTCTCATCATGTCAGGCTATCTCTAAATGCAATTGATGTCAGTTGATCAAG  
TCACTCTCTGGCTTAAACCTTCTGGCTCCCTGCTGCCCTCAGGATAAAAGTCTGGACCCCTCAGCATGGCT  
TGAGACTCATGGTGTCCCTGTCCTGCTCACCTCTGGCTCATCACTTGCTTCTTGCAATTGGTCC  
CTCCCTGATCCAGAGATGCACTGGCTCTCCATTGCCACTCTGATTCTCTTCTGGTACAGAGAAAGGGT  
ACTTCTCTGTCAAATCTCAACTTAGACTTGACTTCCAAAGGAGCTTGGTATAACTCTCTCCGACCC  
CACCCCTGGCATAACTACACAGATCACTCTGGCTCACTTGCTGCCATAATGGTCACTCCCCAGTAGACTGTAAGC  
TCCTTGAGGGCAAGGATTGTGTTGAATTGGTATTAAACAGTGCCTGGCTTGGTGCCTGGCACCTAGAAAGCAC  
TCAATAATGTTGTTAATGAA

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**FIGURE 168**

MWFMYLLSWLSLFIQVAFITLAVAAGLYYLAELIEEYTAVTSRIIKYMIWFSTAVLIGLYVFE  
RFPTSMIGVGLFTNLVYFGLLQTFFIMLTSPNFIILSCGLVVNVHYLAFQFFAEEYYPFSEVL  
AYFTFCLWIIIPFAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGKRGKRLGILVVFSFIKEAIL  
PSRQKIY

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 126-146

**Casein kinase II phosphorylation site.**

amino acids 145-148

**N-myristoylation sites.**

amino acids 73-78, 82-87

**Amidation sites.**

amino acids 168-171, 171-174

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 91-101

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**FIGURE 169**

CAAAGCCCTACCCCTACCATTACCCAGGTCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG  
TTAGAAGGTGCAGAGCGTGGAAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG  
TCCCTGGGCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCCGTGAAATACA  
**CATGGCTCTGTTACGAAAAATTAAATCAGGTGCTGCTGTTCTGATCGTACCCCTGTGT**  
GATTCTGTATAAGAAAGTTCATAGGGACTGTGCCAAGAACATGACGCAGATGATGAATCCGA  
GAACCTGAAGAACTGGAAGAAGAGATTCTGTGGTATTGTGCTGCAGCAGGGAGGATGGG  
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTCTATGT  
AGTGGGACTCCGGAAACTCTGACTCGAATACGAAAATGGATTGAACATTCCAAACTGAGAGA  
AATAAAACTTAAAATCGGAAATTCAACCCGATGGTCCTCAAAGGGAAAGATCAGACCAGACTC  
ATCGAGGCCTGAATTGCTCCAGCCTCTGAACCTTGTGATTATCTCCCTCTACTTATCCA  
CCAACACGAGAAAGTCATCTATTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT  
GTATGACACCACCTTGGCCCTGGGCCACGCCGGCTTCAGATGACTGCGATTGCCCTC  
TGCTCAGGACATAAACAGACTCGTGGACTTCAGAACACATATATGGCTATCTGGACTACCG  
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCCAGCACCTGCTTTCAATCCTGGTGTGAT  
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAAGCAATTGGAGAAATGGATGCA  
AAAGAATGTGGAGGAAAACCTCTATAGCAGCTCCCTGGAGGAGGGTGGCCACCTCCCCAAT  
GCTGATTGTGTTCATGGAAATATTCCACAATTAAACCCCTGTGGCACATAAGGCACCTGGG  
CTGGAATCCAGATGCCAGATATTGGAGCATTCTGCAGGAAGCTAAATTACTCCACTGGAA  
TGGAAAGACATAAACCTGGACTTCCTAGTGGTACAACGACTATGGAAAGCTGGTTGT  
TCCTGACCCCTGCAGGGATATTAAACTCAATCACCCTAGCT**TGATATAACTCTACCC**TTAAAAT  
ATTCCCTGTATAAGAAATGTGGATTGTCCTTGTAGCCAACATAACATTGTCTTTATGAA  
TATTACCTTGTACATATGATCCACAATTAAAAACAAAAACTACTGTGTGCAAATTATAC  
CTTGGACCATATAGGCATTGATTAACCTTTAAGTACATGTGATAACTATGGAAATCAAGAT  
TATGTGACTGAAAACATAAGGAAGAGACCCATCTAGATAACAGCAATCAACCTGCTTAATT  
CTGAATGACAATTATATCCACAAATTAAACTCTACATGTATTTCACATGAAGATCT  
CCTTAACAGGTTGCCAACCTTCTTTATAAAACTATTACATTAAAATATGGACGTCTGAA  
AAATAAAATATTCATCATTTAAAA

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**FIGURE 170**

MALLRKINQVLLFLILLTLCVILYKKVHKGTVPKNDADDESETPEELEEEIPVVICAAAGRMG  
ATMAAINSIYSNTDANILFYVVGLRNLTRIRKWIEHSKLREINFKIVEFNPMVLKGKIRPDS  
SRPELLOPLNLFVRFYLPLLIIHQHEKVIYLDLDDVIVQGDIQELYDTTLALGHAAA  
FSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLGISPTCSFNPGVIVANMTEWKHQ  
RITKQLEKWMQKNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEH  
FLQEAKLLHWRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 234-238

**Tyrosine kinase phosphorylation site.**

amino acids 253-261

**N-myristoylation sites.**amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,  
266-272

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**FIGURE 171**

GGCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAGATGGGCCCCAGCTGGGCCTGAGGCTGCC  
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGTCTCAGCCCTGAGCTGTTCTTCTCC  
TTGCCAGCTTCTCCCTTCTCTGGTCCCCAAGTCAGAACCAAGCTACAATTGGAAGG  
ACTTCCTCGGTCTTGATAAAATGCAATGCCTGCATCGGGACATCTATTGCAAGAAGTTCTT  
AAAGAAGAAATAAGATCTGACAACGGCTGGCTCCACCTGGACTGCCTCCGATTCTTG  
CTTTCTTATCCTGCAAATTACTCAGATGATTCAAATCTGGCGCCCTGTGGAGATCTTAGA  
CTGGTCAGCAAATATCAAACGAGATCTCAGACAGGAGAACTGTGCCTCTGCATCAGCCCC  
AAGACCTGCAGCATTGAGCGTGTCCCTCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC  
AAGCGCCTCACGCCGGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAACTAAAGTTCTG  
TGTATGCTGAGATAAACCCAGTGAAAAGCCTGGCATGGAGGCCAGCACTGAGAACTTCCAGA  
AAGTGTAGCCTCTCCAACTGTGTTACCAACCACATTCAAATAGTAATCATTAAAGA  
GGCTTCTGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 172**

MEPQLGPEAAALRPGWLALLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRFLGLDKCNAC  
IGTSICKKFFKEEIRSDNWLA SHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD  
RRICASASAPKTCSIERVLRKTERFQKWLQAKRLTPDLVQDCHQGQRELKFLCMLR

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 100-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 158-161

**N-myristoylation sites.**

amino acids 56-61, 65-70

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 18-28

**Prenyl group binding site (CAAX box).**

amino acids 179-182

**Leucine zipper pattern.**

amino acids 5-26

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**FIGURE 173**

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTGAAGGTCTAGCCCACCTGGGCTGGCTC  
ACCGCAGACTAGCCGCTCCCATAACAGCACGCCGGACTCTGTCGCTTAAGGCCACTCC  
TATTCTACGGCTGACCCCTGGTGGTACGTGGATCTGTCGCCACGCAAGTCTGGGTCTTCG  
GCGATTGACCGGGGTCCTGCTGTCGGAGCCTCTCCTAAAGCTGCCTGTTCGCGCAGAGAGTT  
TGGAGGGGCGGGTTGGGTGCTGATTGGGCTCGCACCGCAGCACGCTGGAGTCCCG  
CTTAGGTACCAAGTTAGCGTCAGGGAGCTGGTCAGGCAGGTCGCCGGACACCCGTGTGG  
CAGGCAGCGAAGCGCTCGGAGAACTCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC  
GGGAGCCACTGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCCACGGCGCG  
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATTGAAAGGCTGGGTTGGCTGGCC  
TGCTCTGGGGCCCTGCTGGAACCGCCTGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG  
CATGCAGGGCTCGGTGGATGAACTAGAATGGAAATTGCCAGGTGGACCCAAGAACACCA  
TTCAGATGGATCTTCCGGATCAATCCAGATGGCAGCCAGTCAGTGGTGGAGGTGCCTTATG  
CCCGCTCAGAGGCCACCTCACAGAGCTGCTGGAGGAGATATGTGACCGGATGAAGGAGTATG  
GGAACAGATTGATCCTCCACCCATCGCAAGAACTACGTACGTAGTGGGCCGAATGGAG  
AATCCAGTGAACCTGGACCTACAAGGCATCGAATCGACTCAGATATTAGCGGCACCCCTCAAGT  
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTCCGAGAGG  
CTGACAATGTTAAAGACAAACTTGCAAGTAAGCGAACAGATCTTGTGACCATGCCCTGCACA  
TATCGCATGATGAGCTTGAACCACTGGAGCAGCCCACACTGGCTTGATGGATCACCCCCAGG  
AGGGGAAAATGGTGGCAATGCCTTTATATATTATGTTTACTGAAATTAACTGAAAAAATA  
TGAAACCAAAAGT

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**FIGURE 174**

MKGWGLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGS  
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGRNGESSELDLQGIRID  
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

**Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 12-18, 16-22, 29-35

**Endoplasmic reticulum targeting sequence.**

amino acids 179-184

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**FIGURE 175**

CGCAGCGCGCAGTCCTG**ATGG**CCGGCATGGTTACCGCTGCTGCCCTGCTGTCGCTCCTG  
GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGGCTACTAGCATGGTCAA**CTGCAGGGT**GGG  
AGATTCTGATGGAAACAAATTCTCCAGACAGCAGAGATGGTAAGGGCCTGTGCGGGAGGCG  
ACAGTGAAACCCCTTGCCATCGACATATTCCTGTACCCAACAAAGATTTCAGGGATTTGTC  
AGGGAGAAAAGTATCGGACAGAAGCTGAGATGTTGGATGGAGCTTGTCTTGAGGACTTT  
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA  
GTGGAAAAGGCATTTGGAGGCAGCCTGCAGGTCTGGCTCTGGCATCCGAGAGAGACTGGAG  
CACCCAGTGTACACGTGAGCTGGAATGACGCCGTGCCACTGTGCTTGGGGGGAAAACGA  
CTGCCAACGGAGGAAGAGTGGAGTTGCCGCCAGGGGCTTGAAGGGTCAAGTTACCCA  
TGGGGGAACTGGTTCCAGCAAACCGCACCAACCTGTGGCAGGGAAAGTCCCCAAGGGAGAC  
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCAGTGAATGTTCCCCGCCAGAACAACTAC  
GGGCTCTATGACCTCCTGGGAACGTGTGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG  
CAGGACATGCGCGTCCCTCCGGGGGATCCTGGATCGACACAGCTGATGGCTTGCCAATCAC  
CGGGCCCGGGTACCAACCAGGATGGCAACACTCCAGATTGCCAGACAACCTCGGTTTC  
CGCTGTGCTGCAGCGCAGGCCAGGGCCAGGGAGCTG**TAAG**CAGCCGGTGGTACAAGGA  
AAAAAGCCTCTAGGGTCACTGTCATTCCCTGCCATGTTGCAAACAGCGCAATTCAAAGCTC  
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCTCCCTGTCTCCATCCCTGTGGCAGGC  
CTCTCACCAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTGGAGAAGGGGCCAATGTGT  
GACGATGGCTGGGGCCAGGTGTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAA  
CACACAAACAGTTGAAACAGAGCACTCTGAAAGGCCATTAAAGCATTAAAATCTATT  
TCTCCCCCTTCTCCCTGGATGATTAGGAAGCTGACATTGTTCTCAAGGCAGAATT  
TGGTTCTGTTCTCAGCAGTTGCTGTGGAAGGAGAATGCTTCTTGTGGCCTCATCTG  
GTTTGGTGTCCCTCTGAAGGAAACTAGTTCCACTGTGTAACAGGCAGACATGTA  
AAGCACAGTTCAGTCCTAAAGGGCTGGGAGAACCAAGATGATGTACTAGGTGAAGCATT  
TTGTGGGAATCACAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCTATT  
TTTTTTTTTTTTTTGAGACAGGGCTTCTGTGTTGCCAGGCTAGAGTC  
GTGATCACGGCTACTCTAGCCTGAAATTCTGGGCCAAGCAATTCTCCCACCT  
TGAGTAGCTGGACTACAAGTGTGCACCACCATGCCCTGGCTAATT  
ATGGGATCTCGCTCTGTTGCCAGGGTGGTCTCGAACCTCTGCCCAAGCGAT  
TCGACCTCCAAAGTGTGGATTACAGGTGTGAGCCACCTGCCCTGGCCCCCT  
TGCCTCCAAAAACATGTCCTGGAGAGTAGCCTGCTCCACACTGTCA  
CCAATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAA  
AAAAAAAAAA

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**FIGURE 176**

MARHGLPLPLLSSLVGAWLKLGNGQATSMVQLQGGRFLMGTNSPDSRDGEVPVREATVKPFA  
IDIFPVTNKDFRDFVREKKYRTEAEMFGWSFVFEDFVSDELRNKATQPMKSVLWWLPVEKAFW  
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ  
PNRTNLWQGKFPKGDKAEDGFHGSPVNAFPQAQNNGLYDLLGNVWEWTASPYQAAEQDMRVL  
RGASWIDTADGSANHRARVTTRMGNTPDSASDNLGFRCAADAGRPPGEL

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 191-195

**N-myristoylation sites.**

amino acids 23-29, 25-31, 175-181

**Amidation site.**

amino acids 159-163

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**FIGURE 177**

GCCTTCTCGCCCTGACCATGCACCCCTGCATCTCCTGCTGGGCCACAGGCAGCGCTTTAT  
TTCTGGAGCTGAGGGCTAAAACTTTTGACTTTCTCCTCAACATCTGAATCATGCCAT  
GTGCCAGAGGAGCTGGCTGAAACCTTCCGTGGCTCAGCTCCTAACCTGGCGC  
TTTGCTATGGAGACAGCCTCAGCCAGGCCGGTCGCTCCGGACAGGAGGCAAGAGCATT  
TTATCAAGGGCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGCATT  
TTTGTCATATGGCTTGCACTATCCATCACGAGCAGCAGGAGGAAGAGAGATTTGGATGGCT  
CAGAGGACTGGGTGTACTACAGAATTCTCACGAGGAGAAGGACCTGTTTTAACTTGACGG  
TCAATCAAGGATTCTTCCAATAGCTACATCATGGAGAAGAGATATGGAACCTCTCCATG  
TTAAGATGATGGCTTCCCTGCCCCCCTGCCCCATCTCAGTGGCACGGTTCTACAGCAGGGCA  
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTCCAACCTACCAC  
ATGGAGACTTTTCAATTGAACCCGTGAAGAACATCCACTGGTGAGGGAGGGTACCAACCCGC  
ACATCGTTACAGGAGGCAGAAAGTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA  
TTGTGACTCACATGTCCTCTGGGTGAAGAATCTGTTGTTCTTGGTAGTTTATTAAA  
ACATGACCTATTCTACTCAAGTCTTATCTCCTCTGTATTCTTAAATATCTTCA  
TGACATTCAAATCTCTCTGTATTCTTGCAGAAAGTGTACATTCTTGTATAAAA  
CCCTTCACGGTC

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**FIGURE 178**

MPCAQRSLANLSVVAQLLNFGALCYGRQPQPGPVRFPRDQQEHFIKGLPEYHVVGPVRVDAS  
GHFLSYGLHYPISSRRKRDLDGSEDWYYRISHEEKDLFFNLTVNQGFLNSYIMEKRYGNL  
SHVKMMASSAPLCHLSGTVLQQGTRVGTAAALSACHGLTGFFQLPHGDFIEPVKKHPLVEGGY  
PHHIVYRRQKVETKEPTCGLKGIVTHMSSWEEESVLFFW

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 11-15, 105-109, 125-129

**N-myristoylation site.**

amino acids 149-155

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**FIGURE 179**

CAGATTTAAAAGAAAACCTTACTGAATCAGCTGAGTGTAAATAATACGAATTCTTTCT  
TGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGAT**ATGTGTGGATTACAG**TTTCTCT  
GCCTTGCCTACGACTGTTCTGGTTACCTGTATCTTATTACTCCACAAAGAAAT  
ACTTGGATGTCGTCTGTTGTCAGCTCTGCACTGGGAGACAAATTAACTGCCGTAACTTAGG  
CCTTCGAGTATTCTAAGAATTTCCTGAAAGTACAGTTCTGTATCTGACTGGGAATAA  
TATATCTTATATAAATGAAAGTGAATTAAACAGGACTCATTCTCTGTAGCATTGTATTGGA  
TAATTCTAACATTCTGTATGTATCCAAAAGCCTTGTCAATTGAGGCATCTATATTCT  
ATTCTAAATAATAATTCAACAGCTTAGATCCTGGAATTAAAGGGACTTTAAATCT  
TCGTAATTATTTACAGTATAATCAGGTATCTTGTCCGAGAGGAGTATTAAATGATCT  
AGTTTCAGTTCACTAAATCTACAAAGGAATGCCCTCACTGTCCTGGAGTGGTACCTT  
TGTGGTATGGTTGCTCTCGGACTTGATTATCAAACAATAACATTGAGGATATCAGA  
ATCAGGCTTCAACATCTGAAAACCTGCTTGTATTAGGAAGTAATAATTAAACAAA  
AGTACCATCAAATGCCCTTGAAGTACTTAAAGTCTTAAAGGACTTGCCTACGTTGAA  
TATTGAAGCAATACAGCCCTTGCATTAAAGGACTTGCCTACGTTGAA  
AAATTCAAGAATTAGGAATGTTACTAGGGATGGGTTAGTGAATTAAATCTAAACATT  
GATCTTAAGTCATAATGATTAGAGAATTAAATTCTGACACATTCACTGTTAAAGAATT  
AATTACCTTAAGTTAGATAGAAACAGAATAATTGATTGATAATGATAACATTGAAAAT  
GGGAGCATCTTGAAGATCCTTAATCTGTCATTAAATACTTACAGCCTGCACTCAAGGGT  
CCTTAAGCCGTGTCTCATTGATTCTCAGGCAAATTCTAATCCTGGGAATGTAACCTG  
CAAACTTTGGCCTCGAGACTGGCTAGCATCTCAGCCATTACTCTAAACATCTATTGTCA  
GAATCCCCCATCCATGCGTGGCAGAGCATTACGTTATTAACATTACAAATTGTGTACATC  
TTCAATAATGTATCCAGAGCTGGCTGTTAAAATCTCTCATATTCTACACAAGACTAC  
TGCCTAATGATGGCCTGGCATAAAAGTAACCACAAATGGCAGTCCTCTGGAAAATCTGAGAC  
TGAGAACATTACTTCTGGGAACGAATTCTACTTCACCTGCTGGTAGATTTCAGAGAGAA  
TGCCTTGGTAATCCATTAGAGACTACAGCAGTGTACCTGTGCAAATACAACCTACTACTC  
TGTTACCTTGAACTTGGAAAAAAACAGTGCCTACCGAATGATGCTGCTCAATGTCAGGGAA  
AACATCTCTAATTGTACACAAGAAGTTGAGAAGTGAATGAGGCTTTGACATTGCTAGC  
TTTTCTCATCTTAGCTGTGTTAATCATTTTTGATCTACAAAGTTGTCAGTTAAACA  
AAAACCTAAAGGCATCAGAAAACCTCAAGGGAAAATAGACTGAAATACAGCTTTATCAGTC  
AGCAAGGTATAATGTAACTCGCCTCAATTGTAACACTTCCCCTAAATTCTCTAGAAAGTCTGG  
CTTGGAGCAGATCGACTTCATAAAACAAATTGTTCTGAAAATGAGGCACAGGTCAATTCTTT  
TGAACATTCTGCTTT**TAA**CTCAACTAAATTGTCTATAAGAAACTCAGTGCCTGGACAT  
GATTAAAACGAAACCTCTTATATAATTATACCTTAGTTGAAATATAATGAATTATATG  
AGGTTAGCATTATAAAATATGTTTTNTTAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 180**

MCGLQFSLPCLRLFLVVTCYLLLLLHKEILCSSVCQLCTGRQINCRNLGLSSIPKNFPESTV  
FLYLTGNNISYINESELTGLHSLVALYLDNSNILYVYPKAFVQLRHLYFLFLNNNFIKRLDPG  
IFKGLLNLRNLYLQYNQVSFVPRGVFNDLVSVQYLNQQRNRLTVLGSGTFVGVMALRILDLSN  
NNILRISESFGFQHLENLACLYLGSNNLTKVPSNAFEVLKSLRRLSLSHNPPIEAIQPFAFKGLA  
NLEYLLLKNSRIRNVTRDGFSGINNLKHLILSHNDLENLNSDTFSLLKNLTYLKLDRNRIISI  
DNDTFENMGASLKILNLNFNNLTALHPRVLKPLSSLIHLQANSNPWECNCCKLLGLRDWLASSA  
ITLNIYCQNPPSMRGRALRYINITNCVTSSINVSRRAWAVVKSPHIHHKTALMMAWHKVTTNG  
SPLENTETENITFWERIPTSPAGRFFQENAFGNPLETTAVLPVQIQLTTSVTLNLEKNSALPN  
DAASMSGKTSЛИCTQEVEKLNEAFDILLAFFILACVLIIFLIYKVVQFKQKLKASENSRENRL  
EYYSFYQSARYNTASICNTSPNSLESPGLEQIRLHKQIVPENEAQVILFEHSAL

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 530-547

**N-glycosylation sites.**amino acids 71-75, 76-80, 215-219, 266-270, 317-321, 331-335,  
336-340, 400-404, 410-414, 451-455, 579-583**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 231-235

**N-myristoylation sites.**

amino acids 3-9, 69-75, 126-132, 174-180

**ATP/GTP-binding site motif A (P-loop).**

amino acids 506-514

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**FIGURE 181**

GGCCTGGCGCGCGCTCCGTAAGCGTGTGCGGCAGGGCGGGACAGAACCGTCCTCTCG  
GGCTCTGGCGTGTCCGAGACCGCGCTCCCCGCCGAAATCAAGCTCCGAGTCATCCGTGTGGG  
GCATTCGTCCCCCTGGCACAGTTGGCCTCTTCCAGAAGCCGTTTGTGTTTACGTCT  
AAATTGCGTCCGGTCTTATTCTCCCTGGCAAGGTCTGAAGACGGTAGGAGAATAACCT  
GTGTCAGCGTGT **TATGATGCCGTCCGTACCAACCTGGCTACTGGAATCCCAGTAGTAAAGT**  
GAAATATTCAAGGCTCTCCAGCACAGACGATGGCTACATTGACCTTCAGTTAAGAAAACCC  
TCCTAAGATCCCTTATAAGGCCATCGCACTGCCACTGTGCTGTTTGATTGGCGCTTTCT  
CATTATTATAGGCTCCCTCCTGCTGTCAAGGCTACATCAGCAAAGGGGGGGCAGACCGGGCGT  
TCCAGTGCTGATCATTGGCATTCTGGTGTCCCTACCCGGATTTACCACCTGCGCATCGCTTA  
CTATGCATCCAAGGCTACCGTGGTACTCCTATGATGACATTCCAGACTTGATGAC **TAGCA**  
CCCACCCCATACTGAGGAGGAGTCACAGTGGAACTGTCCAGCTTAAGATATCTAGCAGAA  
ACTATAGCTGAGGACTAAGGAATTCTGCAGCTGCAGATGTTAAGAAAATAATGGCCAGATT  
TTTGGGTCTTCCAAAGATGTTAAGTGAACCTACAGTTAGCTAATTAGGACAAGCTCTATT  
TTTCATCCCTGGCCCTGACAAGTTTCCACAGGAATATGTATCATGGAAGAATAGAGGTTA  
TTCTGTAATGGAAAAGTGTGCTGCCACCACCCCTGTAGAGCTGAGCATTCTTTAAATA  
GTCTTCATTGCCAATTGTTCTGTAGCAAATGGAACAATGTGGTATGGCTAATTCTTATTAA  
TTAAGTAGTTATTTAAAAATATCTGAGTATATTATCCTGTACACTTACCTACCTTCATG  
TTCCAGTGGAAAGACCTTAGTAAATCAAAGATCAGTGAGTTCATCTGTAATATTTTTACT  
TGCTTCTTACTGACAGCAACCAGGAATTTCATCCTGCAGAGCAAGTTCAAAATGTAA  
ATACTCCTCTGTTAACAGTCCTGGACCATTCTGATCCAGTTCACCAAGTAGGTTGGACAGC  
ATATAATTGACATTTGCTTAACTGAAATCAAGATGTTCTGCAGATTATCCTTAACGG  
CCGGACTTTGGCTGTTCTAATGAAACATGTAGTGGTTATTATAGAGTTATAGCCGTA  
TTGCTAGCACCTGTAGTATGTCATCATTCTGCTCATGATTCCAAGGATCAGCCTGGATGCCT  
AGAGGACTAGATCACCTAGTTGATTCTATTAGCTTGCAAAAAGTGACTTATATTCCA  
AAGAAATTAAATGTTGAAATCCAATCCTAGAAATAAAATGAGTTNNNTCCA  
AAA

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**FIGURE 182**

MMPSRTNLATGIPSSKVKSRLSSTDGYIDLQFKKTPPKIPYKAIALATVFLIGAFLIIIG  
SLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD

**Transmembrane domains:**

amino acids 45-66, 79-95

**N-myristylation sites.**

amino acids 11-17, 75-81

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**FIGURE 183**

CTAAAAAATACAAAATTAGCTGGCGTGGTGTATGACCTGTAATCCCAGCTACTCAAGAGGCAGGGCAGGA  
GAATCGCTGAACCCAGGAGGCAGAGGTTGCACTGAGCCAAGATAAGTCAGTCCACTCCAGCTGGGTGACAGA  
GCAAGACTCTGTATCAAATAAAATAAAAGTACAACCTCTGGATGGCATGGTGGCTATGTCTGTAATCCCAG  
CACTTGGGAACTTGAGGCGGGTAGATTGCTTAGTCCGGAGTTGAGACCAGTCTGGGTAATATGGTAACCC  
GTCTACCAAAATACAGGTATTAGCCAGTCTCATAACTCGGCTCAAAATAAAATAACATACATAGATG  
AAAATTAACATTTAACAGTCCAACTCAGCGTTTCAGCATATTACAGAGTTGACAATCTCACCACTATCTA  
ATTTCAGAACATTTACATCCCCAAAAGAACCTAACCCATTGACTATCTCTCCATTCCCTCTCCCTAG  
CCTCTGGCAACCAACTAATCTCTTTGCTCTATAGATTGCGCTATTGGACAGTTGATACAAAGGAATCAT  
ACCACATGAGCTTTGCTCCGGCTTCTTGTGTTAATAGAATGTTCAAGGCTCATCTATGCTGTAGCCGT  
ATCAGCACTTCATTCTTCTATGGCTGAATAATAGTCACGTAGGGATGTGCATGTTTCCACTAGCTGAT  
GGACATTGGGTTGTTCCACCTCTGGCTATTAAATATTGCTGCTATAAATATTCAACTACAAGTTGTG  
TGGACATATGTTTATTCTCTGGTATATCCTCGGAGTGGAACTGCTGGATCAGGTGGTAACCTAGGTCTA  
ACCTGGCAGTAAACAGAACATCTATGCATGCTGAGTTGAAATAAACACTTGACCCATAGTAAGTGC  
CAGATCATCTCACAGCAACCAAGTAATTTCACAGATGAGGAATGAAGGCTCCAGAGGTGAACTGGCTT  
TTCCCATTTGAGCAGTCCAAAGTCAGACAGTTAAAAGTGGCAGGACCTGGAAAGGAAGCTAGTTCTTACCC  
GGCATTCTGGGCTCCTGGCTTACGGGCTGGCTATTAGAATAGGCTAAGGCTGCTGCCAAGGCAAGGTGC  
CCCAGTCTGCCCTCTGTCTTATTCCATTCTCTGAGCCCTCCAGGGGACCCCTCTCAGCCACCC  
TCTCTGGTGATGTACAGTGCTGCCGGAGATCAAAGATAAGGTCAGAAACTGGCTCGGACCATAGGACATT  
CACACCACTGTATCCCAGTGGCAAAGCATTGACAGGAACCTGACTCTGAGATCTGTTGTGTCAGAT  
GCGGTGTTGGACGCGCGGGAACAGCAGCAGCAGATCTGAGATGGCATCTGGAACACCTGTATCAGCAGGGC  
ATGCTCAGCGTGGCCAGGAGCTGTGCCAGGAATCAACGCTGAATGTGGACTTGATTTCAAGCAGCCTTC  
GAGTTGAATCGAATCTGGAAACCCCTGCACGAACAAGACCTGGGTCTGCGTTGGAATGGCGTCTCCACAGG  
CAGCGCTCTGGAACTCAACAGCTCCCTGGAGTCAAGCTGCCAGGACTGCACCTCATCCGCTCTGGCAGGA  
GGCCCCCGAAGCAGTGGAGGGCTCAGCTATGCTCGGCACTTCCAGCCCTTGCTCGGCTGCACCAGGGAG  
ATCCAGGTATGATGGCAGCCTGGTACTCGGGCTTGGAGAAGTCAACCTACTGCCACCTGCTGGAC  
AGCAGCCACTGGGAGAGATCTGTGAGACCTTACCCGGGACGCGTGTCCCTGCTGGGTTCTGTGGAGTCC  
CCCCCTAGCTCAGCTTGCTCTGGCTGTGGCGTGCCTGTGATGAACATCAAGGCTGTGATTGAGCAG  
CGGCAGTGCACGGGCTGGAAATCACAAGGAGTTACCGATTGAGATTGAAACTAGGCATGAAGTGTGGTAC  
GCTCATCTGTGGCATGTTATCTCCGAGATGCACTCAATAAGCTCATTAATGGAGGAACACTCCGTGTTGCT  
TGCCCCATCTCCGCCAGCAGACGTCAAGCTTCAACCCCTCCATCAAGCTGAAGTGTCCCTACTGTCCC  
CAGAACCCGGAGATGGAAACGATCATATTTGATTCTACCTGGAAGGAATTGGTGAAGGGTTTCAC  
CTGTGAGCTTGGTCTGCTCGTAGGGTGTCAACTTCAGTGGACTGTGGTGTGTTCAAGAGCGCTGGCTGAG  
GACTTCCACTGAGGGAGCACTGGAGCAGCCCTTGGCAGAGGCTGAGGAGGGAGATGGACCAAGGCCACGCC  
CACCTGGCTCCATGGCATAAGGAAAGGGAGATGCTGGCTCTGTGCTCCCTGCTGTCTTTCCGTTCTGTTGC  
GTTTGACTTAGTGAACCGACAGAGTGGCAAGGGATTGGTCTTCAGCAGTAGACATCCTCCACCCCTGCC  
CAGCCAAGTCTCTTGCTGCCATGCCAATGCTATGTCCACCCCTGCCCAAGAGTGTCCAGCGGTGGCC  
CACCTCTCCCTCCACTACAGCTCAACAGTATGTACCATCTCCACTGTAAATAGTCCAGTTAGAACGGAATG  
CCGTTGTTTATAACTTGAAACAAATGTATTACTGCCCTCTCAAA

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**FIGURE 184**

QCCRKIKDTVQKLASDHKDIHSSVSRCGKAIDRNFSEICGVVSDAVWDAREQQQQILQMAIV  
EHLYQQGMLSVAEELCQESTLNVDLDFKQPFLNRILEALHEQDLGPALEWAVSHRQRLL  
NSSLEFKLHRLHFIRLLAGGPAKQLEALSYARHFQPFARLHQREIQVMMGSLVYLRGLEKSP  
YCHLLDSSHWAECETFTRDACSLLGLSVESPLSVSFASGCVALPVLMNIKAVIEQRQCTGVW  
NHKDELPPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLICGHVISRDALNKLINGGKLKCP  
YCPMEQNPADGKRIIF

**Transmembrane domain:**

amino acids 222-241

**N-glycosylation site.**

amino acids 129-133

**Tyrosine kinase phosphorylation site.**

amino acids 151-159, 184-193

**Amidation site.**

amino acids 327-331

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 222-233

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**FIGURE 185**

GAGCGACGCTGTCTAGTCGCTGATCCAAATGCACCGGCTCATCTTGTCTACACTCTAAT  
CTGCGCAAACCTTTGCAGCTGTCGGGACACTCTGCAACCCCGCAGAGCGCATCCATCAAAGC  
TTTGCACAGCCAACCTCAGCGAGATGACTTGTACCGAAGAGATGAGACCATCCAGGTGAA  
AGGAAACGGCTACGTGCAGAGTCCTAGATTCCGAACAGCTACCCAGGAACCTGCTCCTGAC  
ATGGCGCTTCACTCTCAGGAGAACACGGATAACAGCTAGTGTGACAATCAGTTGGATT  
AGAGGAAGCAGAAAATGATATCTGTAGGTATGATTTGTGGAAGTTGAAGATATATCCGAAAC  
CAGTACCAATTAGAGGACGATGGTGTGGACACAAGGAAGTTCTCCAAGGATAAAATCAAG  
AACGAACCAAATTAAAATCACATTCAAGTCCGATGACTACTTTGTGGCTAAACCTGGATTCAA  
GATTTATTATTCTTGCTGGAAGATTCCAACCCGCAGCAGCTTCAGAGACCAACTGGGAATC  
TGTCAAGCTTATTCAGGGTATCCTATAACTCTCCATCAGTAACGGATCCCCTCTGAT  
TGCAGATGCTCTGGACAAAAAAATTGAGAATTGATACTGGAGATCTGCTCAAGTACTT  
CAATCCAGAGTCATGGCAAGAAGATCTTGAGAATATGTATCTGGACACCCCTGGTATCGAGG  
CAGGTCAACCATGACCGGAAGTCAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCG  
TTACAGTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAAGAGCTGAAGTTGCCAATGT  
GGTCTTCTTCCACGTTGCCCTCGTGCAGCGCTGTGGAGGAAATTGTGGCTGTGGAACTGT  
CAACTGGAGGTCTGCACATGCAATTCAAGGGAAACCGTGAAAAAGTATCATGAGGTATTACA  
GTTTGAGCCTGCCACATCAAGAGGAGGGTAGAGCTAACGACATGGCTTAGTTGACATCCA  
GTTGGATCACCAGAACGATGCGATTGTATCTGCAGCTAACGACACCTCGATAAGAGAATGT  
GCACATCCTTACATTAAGCCTGAGAGAA

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**FIGURE 186**

MHRLIFVYTLLICANFCSCRDTSATPQSASIKALRNANLRRDDLYRRDETIQVKGNQYVOSPRF  
PNSYPRNLLLWRLHSQENTRIQLVFDNQFGLLEAENDICRYDFVEVEDISETSTIIRGRWCG  
HKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLEDFQPAAASETNWESVTSSISGVSY  
NSPSVTDPTLIADALDKKIAEFDTVEDLLKYFNPESWQEDLENMYLDTPRYRGRSYHDRKSKV  
DLDRLNDDAKRYSCTPRNYSVNIREELKLANVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSG  
KTVKKYHEVLQFEPGHIKRRRAKTMALVDIQLDHHERCDCICSSRPPR

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 270-274

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 262-266

**Tyrosine kinase phosphorylation site.**

amino acids 256-265

**N-myristoylation sites.**

amino acids 94-100, 186-192, 297-303, 298-304

**TonB-dependent receptor proteins signature 1.**

amino acids 1-56

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**FIGURE 187**

CATGCCGCTGCCGCCCTGCTGCTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTG  
TGTCTCTGGGGTTGCCCTAACCTGCAAACATCACCTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGCTTCAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGCAAAAGAAATGGCTGAATAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTCTGCTGAAACTCTGACTACGAACACCACTATTATGCCAAAGTTAAGGCCATTG  
GGGAACAAAGTGTCCAATGGCTGAAAGTGGACGGTCTATCCTTTTAGAAACACAAAT  
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGCCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTTGAATACTAAACAGAACGTGGTCCCAGTGTGACCAA  
CCACACGCTGGTGCTCACCTGGCTGGAGCCAACACTCTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAACAGCAGTGTGCCAGGACTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAACATCTGGTATGTTGCCATATCTATTACCGT  
GTTCTTTCTGTGATGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTGATTTGATTATGAAATTGACAAAAGATTCTTGTGCCTGCTGA  
AAAAATCGTATTAACTTATCACCTCAATATCTGGATGATTCTAAATTCATCAGGA  
TATGAGTTACTGGAAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCCAGCAGGAA  
CCTGAGGCCCTCAGGAGGAAGAGGAGGTGAAACATTAGGTATGCTCGCATTGATGGA  
AATTTTTGTGACTCTGAAGAAAACACGGAAGGTACTCTCACCAGCAAGAGTCCCTCAG  
CAGAACAAATACCCCGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCCTGAAAGAGCAGGAGCTCAGTTGCAGGAGGAGGTGTCACACAAGGAACATT  
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCGCAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGCCGGAGGA  
AGAGCCATCGACGCCCTGGCGACTGGATCCCCAAACTGGCAGGCTGTGATTCTCGCT  
GTCCAGCTCGACCAGGATTCAAGAGGCTGCGAGCCTCTGAGGGGATGGCTCGGAGAGGA  
GGGTCTCTATCTAGACTCTATGAGGAGCCGGCTCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTGAGGAATGGGGTTATATGTGCAGATGGAAAACTGATGCCAACA  
CTTCCTTTGCCTTTGTTCTGTGCAAACAAGTGAGTCACCCCTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGTTCAGTTGTCAGTGTGAGAA

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**FIGURE 188**

MPLPPPLLLLLLAAPWGAVPCVSGGLPKPANITFLSINMKNVLQWT PPEGLQGVKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTCKSKWAESGRFYPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNLTYCVHVESFVPGPPRRAQPSEKQCARTLK DQSSEFKAKII FWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHPANLILYGNEFDKRFFVPAEKIVINFITLNISDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEVHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPPDKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQAAALAVLGPQLQYSYTP  
QLQDLDPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE  
GLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMen

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

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**FIGURE 189**

**ATGTGCTGCTGCCGCTGCTCCTGCTGTGGGGCTGCTCCCGGGACGGCGGCGGGGCTCG**  
GGCGAACCTATCCGCACCGGACCCCTCCTGGACTCGGAGGGCAAGTACTGGCTGGCTGGAGC  
CAGGGGGCAGCCAGATCGCCTTCGGCTCCAGGTGCGACTGCAGGCTACGTGGCTTCGGC  
TTCTCGCCCACGGGGCATGGCTCCGCCGACATCGCTGTGGGGGTGGCCCCACGGCGG  
CCCTACCTCCAGGATTATTTACAATGCAAATAGAGAGTTGAAAAAAAGATGCTCAGCAAGAT  
TACCATCTAGAATATGCCATGGAAAATAGCACACACACAATAATTGAATTACCAAGAGCTG  
CATACATGTGACATAAAATGACAAGAGTATAACGGATAGCACTGTGAGAGTGATCTGGCCTAC  
CACCATGAAGATGCAGGAGAAGCTGGTCCAAGTACCATGACTCCAATAGGGCACCAAGAGT  
TTGCGGTTATTGAATCCTGAGAAAATAGTGTCTATCTACAGCCTTACCATACTTTGATCTG  
GTAAATCAGGACGTCCCCATCCAAACAAAGATAACACATATTGGTGCCAAATGTTAAGATT  
CCTGTGTTCAAGAAAAGCATCATGTAATAAAAGGTTGAGGCCAGTGATAACAGAGAGGCCATGAG  
AGTCTGGTGCACCACATCTGCTTACAGTCAGCAACAACCTTAAACGACAGCGTTCTGGAG  
TCCGCCACGAGTGTCTATCACCCCAACATGCCGATGCATTCTCACCTGTGAAACTGTGATT  
TTTGCTGGCTATTGGGGAGAGGGCTTTCTTATCCACCTCATGTTGGATTATCCCTGGC  
ACTCCATTAGATCCGATTATGTGCTCCTAGAAGTCCATTATGATAATCCCACTTATGAGGAA  
GGCTTAATAGATAATTCTGGAAGGTTATTACACAATGGATATAAGGAAATATGATGCT  
GGGGTGATTGAGGCTGGCTCTGGGTGAGCCTTCCATACCACCTCCAGGGATGCCTGAG  
TTCCAGTCTGAGGGTCACTGCACTTGGAGTGCCTGGAAGAGGGCTCTGGAAGCCAAAAGCCA  
AGTGGAAATTCATGTGTTGCTGTTCTCCATGCTCACCTGGCTGGCAGAGGCATCAGGCTG  
CGTCATTTGAAAAGGAAGGAAATGAAATTACTGCTTACAGGAGATCTACAGACAGTCACGACC  
TTCCAGGAGTTTCAGTATCTAAAGGAAGAACAAACAATCTTACAGGAGATAACCTAATTACT  
GAGTGTGCTACAACACGAAAGATAGAGCTGAGATGACTTGGGGAGGACTAACGACCAGGAGT  
GAAATGTGCTCTCATACCTCTTATTACCCAAGAATTAACTTACTCGATGTGCAAGTATT  
CCAGACATTATGGAACAACCTCAGTCATTGGGTTAAGGAGATCTACAGACAGTCACGACC  
TGGCCTTCATTATCAAAGCTCCAAAGCAATATAAAACCTTCTTCATGGATGCTATGAAT  
AAGTTAAATGGACTAAAAGGAAGGTCTCTCCTCAACAAGCTGGCCTCAGCCTGCCAGTG  
AATGTGAGATGTTCAAGACAGACAATGCTGAGTGGTCGATTCAAGGAATGACAGCATTACCT  
CCAGATATAGAAAGACCTATAAACGAGAACCTTGGTGTGGCACGTCTTCTCTTCC  
CTGCACAGAGATTCTCCATCAACTGCTGTTGCCTCTGCTACTCAGCTGACGCTGAGC  
ACCAAGAGCTTGTGATCAAATTCTGTTGGACTTGACAATGTTCTATGATCTGAACCTGTC  
ATTTGAAGTACAGGTTAAAGACTGTGTCACTTGGGATGAGAGTGTGGAGACTTTCTTC  
CCCATTTCCTCCCTTCTTCCATGTTACATGAGAGACATCAATCAGGTTCTCTT  
CTCTTCTTAGAAATACCTGATGTTATATACATGGTCAATAAAACTGGCCTGACTT  
AAGATAACCATTAAAAATTGGGCTGTCATGTGGGAATAAAAGAATTCTTCTTCCTAA  
AAAAAAA

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**FIGURE 190**

MCCWPLLLLWGLLPGTAAGGSGRTYPHRTLLDSEGKYWLGSQRGSQIAFRLQVRTAGYVGFG  
FSPTGAMASADIVVGGVAHGRPYLQDYFTNANRELKKDAQQDYHLEYAMENSTHTIIIEFTREL  
HTCDINDKSITDSTVRVIWAYHHEDAGEAGPKYHDSNRGKSLRLLNPEKTSVLSTALPYFDL  
VNQDVPIPNKDTTYWCQMFKIPVFQEKKHVIKVEPVIQRGHESLVHHILLYQCSNNFNDSVLE  
SGHECYHPNMPDAFLTCTEVIFAWAIGGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEE  
GLIDNSGLRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFQSEGHCTLECLEEALEAEKP  
SGIHFAVLLHAHLAGRIGRLRHFRKGKEMKLLAYDDDFDFNFQEFQYLKEEQTILPGDNLIT  
ECRYNTKDRAEMTWGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEIYRPVTT  
WPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVLSPVNVRCSKTDNAEWSIQGMTALP  
PDIERPYKAEPNVCGTSSSSLHRDFSINLLVCLLLSCTLSTKSL

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 56-73, 378-393, 583-602

**N-glycosylation sites.**

amino acids 114-118, 247-251, 476-480, 517-521

**N-myristoylation sites.**amino acids 11-17, 15-21, 20-26, 45-51, 68-74, 79-85, 290-296,  
316-322, 337-343, 342-348, 456-462, 534-540, 582-588**Copper type II, ascorbate-dependent monooxygenases proteins.**

amino acids 271-321, 422-474

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**FIGURE 191**

GCTTCAGCTGAAGAAAGAGAGGAAATGAAGCGCCTCTGCTCTGTTTGTCTTATAACAT  
TTTCTTCTGCATTCCCTAGTCGGATGACGGAAAATGAAGAAAATGCAACTGGCTCAGG  
CATATCTCAACCAGTTCTACTCTCTGAAATAGAAGGGAAATCATTGTTCAAAGCAAGAATA  
GGAGTCTCATAGATGACAAAATTGGGAAATGCAAGCATTGGATTGACAGTGACTGGAA  
AACTGGACTCAAACACCCCTGAGATCATGAAGACACCCAGGTGTGGGTGCCTGATGTGGGCC  
AGTATGGCTACACCCCTGGTGGAGAAAATACAACCTCACCTACAGAATAATAACTATA  
CTCCGGATATGGCAGCAGCTGCTGGATGAGGCTATCCAAGAAGGTTAGAAGTGTGGAGCA  
AAAGTCACTCCACTAAAATTCAACAGATTCAAAGGGATTGCAGACATCATGATTGCCCTTA  
GGACTCGAGTCCATGGTCGGTGCCTCGCTATTGATGGCCCTGGGAGTGCTTGGCCATG  
CCTTCCTCCTGGTCGGGCTGGTGGTACACTCATTGATGAGGATGAAAATGGACCA  
AGGATGGAGCAGGATTCAACTTGTCTTGCTGCTCATGAATTGGTCATGCACTGGGC  
TCTCTCACTCCAATGATCAAACAGCCTGATGTTCCAAATTATGTCCTGGATCCCAGAA  
AATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGG  
TACCTGCTAACGCAAAGGAACCCACTAACCCATGCCTGTGACCCCTGACTTGACTTTGACG  
CTATCACAACCTTCCGAGAGAAGTAATGTTAAAGGCAGGCACCTATGGAGGATCTATT  
ATGATATCACGGATGTTGAGTTGAATTAAATTGCTTCATTGCTGCCATCTGCCAGCTGATC  
TGCAAGCTGCATACGAGAACCCAGAGATAAGATTGTTAAAGATGAAAATCTGGA  
TGATCAGAGGATATGCTGCTTGCCAGATTATCCAAATCCATCCACATTAGGTTTCCAG  
GACGTGTGAAGAAAATAGATGCAGCGTCTGTGATAAGACCACAAGAAAAACCTACTTCTTG  
TGGCATTGGTGCCTGGAGGTTGATGAAATGACCCAAACCATGGACAAAGGATTCCCGCAGA  
GAGTGGTAAAACACTTCCTGGAATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGAT  
TCTCTTTTCAGCCGTGGATCAAAGCAATTGAAATACAACATTAAGACAAAGAATATTACCC  
GAATCATGAGAACTAATACTGGTTCAATGCAAAGAACCAAGAACACTCCTCATTGGTTTG  
ATATCAACAAGGAAAAGCACATTCAAGGAGGCATAAGATATTGTATCATAAGAGTTAAGCT  
TGTTATTTGGTATTGTTCAATTGCTGAAAAACACTTCTATTATCATAAATTGAC  
CTAAAATAAACCTCAACAGGTCTTTAATATAAATTCTGCTTCAAAATAGAATAAAACCATT  
TTAACACAC

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**FIGURE 192**

MKRLLLLFLFFITFSSAFPLVRMTENEENMQLAQAYLNQFYSLIEGNHLVQSKNRSLIDDKI  
REMQAFFGLTVTGKLDNSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTYRIINYTPDMARAA  
VDEAIQEGLLEVWSKVTPPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLGVLGHAFFFFPGL  
GGDTHFDEDENWTKDGAGFNLFVAAHEFGHALGLSHSNDQTALMFPNYVSLDPRKYPLSQDD  
INGIQSIYGGLPKVPAKPKEPTIPHACDPDLTFDAITTFRREVMFFKGRHLWRIYYDITDVEF  
ELIASFWPSLPAVLQAAVENPRDKILVFKDENFWMIRGYAVLPDYPKSIHTLGFPGRVKKIDA  
AVCDKTTRKTYFFVGIWCWRFDEMTQTMDKGFQRVVKHFPGISIRVDAAFQYKGFFFFSRGS  
KQFEYNIKTKNITRIMRTNTWFQCKEPKNSSFGFDINKEKAHSGGIKILYHKSLSLFIFGIVH  
LLKNTSIYQ

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 55-59, 110-114, 200-204, 452-456, 470-474, 508-512

**N-myristylation site.**

amino acids 71-77, 205-211, 223-229

**Hemopexin domain signature.**

amino acids 171-202, 207-238, 318-334

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 213-223

**Matrixins cysteine switch.**

amino acids 89-97, 207-238

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**FIGURE 193**

CACAATCAGGTCCCATTCTATAGATGGGAAACTGAGGCTTGAGGTACATAGGCCTCGTTCA  
AGGCTGGTATAACCTGCACCCCTCTCCCATGTGAACAACAT**GTTCTGGTAATGGGGCTGTCA**  
TCCAGTCTCCTCCCTGCCCTGCTGGTGCACTCCTGCCCTGCTGGTGCACTTCTGCCCT  
ACTGGTATATTGCTGCCTCTGCTGGGCGCTCCTGCCCTGGCTGGTGTATCCTGCCCT  
GCTGGTGCACTTCTGCCCGCTGATGCACTCCTGCCCTGCTGGTGCACTTCTGGCTCT  
GCTGGCACACTCCTGCCCTGCTGGTGCACTCCTGGCTCTGCTGGCGCACTTCTGCCCT  
TGCTGGTGTATTCCCTGCCCTGCTGGTGTACTCCTCCCTGCTGGTGCACTTCTGCCCT  
TGCTGGCGCACTTCTGCCCTCCAGGCCCTACCT**AGCCTCTCCCTTTATATATGGAAGTCT**  
TCCCAGTTCACTGACACTGGTAACAGGGACTCTGCTCTGGTGTGCTGCCCTGGGAT  
GGGCATCTGTGTCTTCCTTACTACTGCTGGCTCAGGACCCAGAGCTTGAAGCATGTCCAGA  
TGCAGGTCCGGCACCAGAGTCTAAGGAGCCCCAACCCACCAGGATTTCCAATAAGAGA  
TGTTCACCA

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**FIGURE 194**

MVLGNGGCHPVSSLPLLVHFLPLLVHFLPLLVYLLPLLGRFLPRLVYLLPLLVHFLPPLMHL  
PLLVHFLALLAHFLPLLVHFLALLAHFPAPAGVFPAPAGVLPSPAGALPASAGALLASP GPT

**Signal peptide:**

amino acids 1-39

**N-myristylation sites.**

amino acids 4-10, 109-115, 116-122

**Leucine zipper pattern.**

amino acids 14-36, 16-38, 17-39, 21-43, 24-46, 28-50, 31-53,  
35-57, 38-60, 42-64, 45-67, 49-71, 52-74, 56-78, 59-81, 63-85,  
65-87, 66-88

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**FIGURE 195**

GGCAAGGCAGGCGGGCGGCCGGCAGCCGGTGGCGGTGGGAACATCTCGGAGCCA  
CCGCCTTCTCCGCTGGAGCGGGGTCCAGCTTGGCTGCCCTGGCCTTGCCACGTT  
TCGGGTGCCCTGCACCCCCCACCAGGCTCGCTCTCGAAGCGGGAAAGGGCGCTTGCA  
GGATCCTGCCGCCCTCCAACCGGATCTGGTCTAGAGCTCCCAGAGCGAGGCCTCGCCA  
GGACTCCTGCCGCCCAACCTGACCGCCGGGGTGCCTGGGAGCTAGCGCCGGAGAG  
GAAGCGGAAAGGGGACCATGCGGCCCTGACTCGTGGCTGGTCTGCCAGTCTCGGGTG  
CTCTGGATCACGGTGTGCTGTTCTCTGGTAACCAAGAGGAAGTGGAGGTGCCGACGGGA  
CCTGAAGTGCAGACCCCTAACGCTCGGACGCTGACTGGGACGACCTGTGGGACCAGTTGAT  
GAGCGGCGGTATCTGAATGCCAAAAGTGGCGCTGGTGTGACGACCCCTATAAGCTGTATGCT  
TTCAACCAGCGGGAGAGTGAGCGGATCTCCAGCAATCGGCCATCCGGACACTCGCCATCTG  
AGATGCACACTGCTGGTGTATTGCACGGACCTCCACCCACTAGCATCATCACCTCCAC  
AACGAGGCCGCTCCACGCTGCTCAGGACCATCCGAGCTGTATTAAACCGCACCCCTACGCAT  
CTGATCCGGAAATCATATTAGTGGATGACTCAGCAATGACCCCTGATGACTGTAAACAGCTC  
ATCAAGTTGCCAAGGTGAAATGCTTGCACGAACTGACGGCAAGGTCTGGTCCGGTCCGG  
ATTGGGGCGCTGACATGCCAGGGCACCACTCTGACTTTCTCGACAGCCACTGTGAGGTG  
AACAGGGACTGGCTCCAGCCCTGTTGCACAGGGTCAAAGAGGACTACACGCGGGTGGTGC  
CCTGTGATCGATATCATTAACCTGGACACCTCACCTACATCGAGTCTGCCTCGGAGCTCAGA  
GGGGGTTTGACTGGAGCCTCCACTCCAGTGGGAGCAGCTCTCCCAGAGCAGAAGGCTGG  
CGCCTGGACCCACGGAGCCATCAGGACTCCTATCATAGCTGGAGGGCTTCGTGATCGAC  
AAAGCTGGTTGATTACCTGGGAAATATGATATGGACATGGACATCTGGGGTGGGAGAAC  
TTTGAATCTCTTCCGAGTGTGGATGTCGGGGCAGCCTAGAGATCGCCCTGCAGCCGA  
GTGGGGCACGCTTCCGGAAAGCAGCACCCTACGTTTCCCTGATGAAATGCCAACACGTAT  
ATAAAGAACACCAAGCGGACAGCTGAAGTGTGGATGGATGAATACAAGCAATACTATTACGCT  
GCCCGGCCATTGCCCTGGAGAGGCCCTCGGGAAATGTTGAGAGCAGATTGGACCTGAGGAAG  
AATCTCGCTGCCAGAGCTCAAGTGGTACCTGGAGAATATCTACCCCTGAACCTCAGCATCCCC  
AAGGAGTCCCATCCAGAAGGGCAATATCCGACAGAGACAGAAGTGCCTGGATCTCAAAGG  
CAGAACACCAAGAACCCAAACCTAAAGTTGAGCCCTGTGCCAAGGTCAAAGCGAAGAT  
GCAAAGTCCCAGGTATGGCCTCACATACACCCAGCAGATCCTCCAGGAGGAGCTGCCTG  
TCAGTCATCACCTTGTCCCTGGCGCCCACTGGTCTTGTCTTGCAAGAATGGAGATGAC  
CGACAGCAATGGACCAAAACTGGTCCCACATCGAGCACATAGCATCCCACCTCTGCCTCGAT  
ACAGATATGTTGGTGTGGCACCGAGAACGGCAAGGAAATCGTCGTCAACCCATGTGAGTCC  
TCACTCATGAGCCAGCACTGGGACATGGTGAGCTCTTGAGGACCCCTGCCAGAACGAGCAAGG  
GCCATGGGGTGGTCTCCCTGGACAGAACAGACTGGAAACTGGCAGCAAGCAGCCTGCAA  
CCACCTCAGACATCCTGGACTGGAGGTGGAGGCAGAGCCCCCAGGACAGGAGCAACTGTCT  
CAGGGAGGACAGAGGAAACATCACAAGCCAATGGGCTCAAAGACAAATCCACATGTTCTCA  
AGGCCGTTAAGTCCAGTCCTGGCCAGTCATTCCCTGATGGTATCTGGAGACAGAAACCTAA  
TGGGAAGTGTATTGTTCTTCTACAAAGGAAGCAGTCTCTGGAGGCCAGAAAGAAAAG  
CCTTCTTTCACTAGGCCAGGACTACATTGAGAGATGAAGAATGGAGGTGTTCCAAAAGA  
ATAAAGAGAAACTTAGAAGTTGTCTGGAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

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**FIGURE 196**

MRRILTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWDQFDERRYLN  
AKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLRCTLLVYCTDLPPTSIIITFHNEARST  
LLRTIRSVLNRTPTHLLIREIIILVDDFSNDPDDCKQLIKLPVKCLRNNERQGLVRSRIRGADI  
AQGTTLTFLDSHCEVNRDWLQPLLHRVKEDYTRVVCPVIDIINLDFTYIESASELRGGFDWS  
LHFQWEQLSPEQKARRLDPTEPIRTPIIAGGLFVIDKAWFDSLKYDMMDIWGGENFEISFR  
VWMCGGSLEIVPCSRVGHVFRKKHPYVFPDGNNANTYIKNTKRTAEVWMDEYKQYYAARPFAL  
ERPFGNVESRLDLRKNLRCQSFKWYLENIYPELSIPKESSIQKGNIQRQKCLESQRQNNQET  
PNLKLSPCA KVKGEDA KSQV WAFTY TQQILQEE LCLSV ITL FPGAP VV LVL CKNG DDR QQQ WTK  
TGSHIEHIASHLC LDT DMFG DGTENG K EIVVN PCESS LMSQ HWD MVSS

**Transmembrane domain:**

amino acids 475-493

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 2-6

**Tyrosine kinase phosphorylation sites.**

amino acids 68-75, 401-409

**N-myristoylation sites.**

amino acids 178-184, 186-192, 192-198, 346-352, 383-389, 526-532

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**FIGURE 197**

GCAGCTCACCCCTTCGAGCCCGC**GATGGGG**GAAGACGACGCCGCGCTTCGGCTGGCAGCAGGGGCTCTCGACC  
 CGTGGGCAGACTCAGTGGGAGTGCAGCCCGCACCACGGAGCGCACATCGCCGTACACAAGCGGCTTGTGCTGG  
 CCTTCGCTGTGTCCTCGTGGCATTGCTCGCGTACAATGCTCGTGTGCTCAGCCTGCGCTTCGACGAGT  
 CGGGGGCGAGTGCACGCCAGCGCCGACGGTGCCCCCTCAGGCTTCCGGAGCGCCGGCAACGGGAGCCTCC  
 CTGGATCGGCCCGCGCAACCAACCAACGCAAGCGGGGACTCCTGGCAGCCGAGGGGGTGGCCAGTCCGG  
 GGACACGTCGGCCAGCCCGTCCGGAGGGAGCGGGAGCCGTGGAGCCGTGGACGCTGCGCTGTGCG  
 GCCACCTGAAGCCGCTGCACTACAATCTGATGCTCACCGCTTCATGGAGAACATTACACCTTCCGGAGGTCA  
 ACGTGGAGATCGCGTGCAGCCACCGCTACGTAGTGCTCACGCTTCCCAGTGGCGGTGAGAAAGTGC  
 AGCTGGCCAGGGACCCGGCGTCCGGGCTGTCCCTGTAGCCGGTTTTCTCACCCGAAACCCAGGCTTAG  
 TGGTGGCTGAATTAGGACACTGGACGCCAGAGGAATTACAATCTGAAGATTATCTACAAACGCGCTCATCGAGA  
 ATGAGCTCCTGGCTTCTCCGAGCTCTATGCTCCACGGGAGAGAACATTCTGGTGTACTCAGTTT  
 CGCCTACACATGCAGAAAGGCATTTCTGTTTGATGAGCAATCTACAAGGCTACTTCAAACATCAGCATCA  
 AGCATCAAGCAACCTATTATCTTAATATGCCAGTGGAAACTCCGTGTTGAGGAAGATGGATGGGTTA  
 CGGATCATTTCACAGACCCCTCATGTCACATATTATTAGCCTGGGCAATTGCAACTCACATACAGAG  
 AAACATACCAAGAGTGGGTTGAGTACGATTATGCAAGACCTGATGCTATCAGAAGAGGATCCGGGACT  
 ATGCTCTCCATATAACAAAGAGTAAAGAATTGAGACTACTTAAAGTGCCTATTCTTGCCAAAAC  
 TAGATCTTCTAGCTGTGCTTAAGCATCCGTATGCTGTATGGAGAACACTGGGACTAAGTATTGTTGAGATAT  
 GAATACTGCTGGATCCCAGTGTCTCATCTATTGCTTATGCTGGATGTCACCATGGTCTGAGATAT  
 GTCACCAAGTGGTTGGTACAGACTACCTCTATCTGGCTGGAACATGGAAAAGCAGAGGTTCTGACCGATGTT  
 TGCATGAAGTGTGCTGGACGGTTGCCAGTCCCATCCAGTATCACAGGAAGTGTGCTGAGGAAACAGATA  
 TTGACAGGGTGTGACTGGATCGCATATAAAAGGGTGTGCTTTAATAAGAATGCTGGCTAATTGTTATGGG  
 ATTCACTGTTTCCAGAGGGGTTGCAAGATTATTAACCAATTCAAGTATGGTAATGCAGCCAGAAATGATCT  
 GGAATACATTATCGGAGGTTTAAAGGAAATGGAATATACAAGAAGTAATGGATCAGTGGACAC  
 TCCAGATGGGTTATCCTGTTACCCATCTGGGAAACACAAGCAGAAAATAGAATAATAATTACCAACAGC  
 ATTTTATCTATGATATCAGTGTAAACTAAAGCACTTAAACTCAGAATAACGTTACCTGTGGCAGATTCCAT  
 TAACTATTGTGGTAGGAAATAGAAGCCATGTCTCAGAAGCAATTATTGGGTGTCTAACAAATCAGAGC  
 ACAGAATAACTTATTGGACAAAGGAAGCTGGCTGCTGGGAAACATCAATCAAACACTGGCTATTAGAGTCAACT  
 ATGACCTAAAGGAACTGGAGATTATTAATTGATCAATTAACTCGGAATCATGAGGTTCTTCTGCTAGTAACCG  
 CGGGCTTGATCGATGTCAGCTCAGCCAGGGCTGGCTATTGCTCAGAATATTCTCTGGAGATTATCA  
 GATACCTGTGAGGGAGAAGGATTCTTCTTGGCATGCTGCCAGCGAGCTTTATCTCTAGATAAAATTAC  
 TGGACCGCATGGAAAACATAACACATTTCATGAAATATTAAAGCAACTTCAAGGCTAATTCAGGTT  
 GGTGGCCGAAAAATAATTAAATTGATCTTGTGCAAGCATCTAACACATGAAAGACTAACGTTAGAGAAGTT  
 TAATGCTGGCTGCAAGTTTGGCAACAGCACTGTCACCAACAGGCATCAACACTTATTCAGGTT  
 GCAACAGGAACAGAAATACCACTAAATGTTAGAGACATCGTATACTGTCAGGACTGTCACTACTGGATGAGGATG  
 TCTGGGAATTCTATGGATGAAATTCCATTCCACACAGCAGTTCTGAGAAGAAAATATTATTGGAAGCCTTAA  
 CTTGCACTGATGACAGGAATTATTAAACAGGTTCTAAATCTGTCAGTGAATTCTGAGGTTGCTGGATCAAG  
 ATGCAATTGATGTCATAATCCATGCTAGCTCGAAATCCACATGGTCAGACCTGGCTGGAGTTTTTCAGGGATA  
 AATGGAAGATATTAAATACCAAGGTATGGAGAAGCATTGTTATGTATTCCAAACTCATCAGTGGTGTCAACAGAAT  
 TTCTTAATACTGAAGGTGACTCAAAGAGCTCAAGAACATTCTCATGAAACAAACTATGATGGGTTAGCTGCTGCTTCT  
 TCTCACCGAGCTGGAAAATCTGCAAGCCATTGCGCTGGGAAATGTTACCAAGCAGGCTTCCAAATGGT  
 TAGGAAAAGCTCTAACACACT**TAA**ATATGTTATCTTATAACAAACATTCAACTCAGAAGTTATGAGAAGAC  
 GCTTTTGTGGAATGAGGAAAATGACTACCTAGAAAATGGCCAGATTTCAGTGTAACTGTTGGAGGAAATT  
 TTTTTTGTGTTTATTTGGTTGGGGGATATTGTTATGTTGTTCTTCAATTCTGTTCTGTTCTCTAC  
 TGGGTGTCCTCTAAAGAAAACCTTGCAAGTGAACACTAGCCATGATTGCTCAGCTGTACATTCTGCTGTA  
 CAGGACCAATACTATGATGTCAGTGTGATGTTACAGTCATTGAAAACATATTCAAGAATATCTGTCAT  
 GGATATTGTCCTGCTGTGTCAGTCAGCTTATTCAACACGTCAGTGTGTAATATGTTACACC  
 TAGGATGGCATTGCAAAAGCACAAGGATTATATGACAATCAGTATTGCAATGAAAGAAAACATAAAAAC  
 GAAATGATATTCTCAATTGGCAATGTTGAGAGGTTAAAGAGCTTGCACATGACATGAAACATCACTTATTGAGC  
 ACTTGGATTGTCGGCAATGATTACTGTTGCTAACCTATTCTTGTGTTAAAGCTGTGATACATTGTTAAA  
 AGGCATATAGATAGTGTATGCAATTGTTACAGTCAGGAAAGCCCCATATGTTATGAGTGTGACACTGC  
 ACATGTACAAAGAATGCTTCAGATCAAAGAAAATTATCTCTTTTATAACTAAGGACAGTTGCAAAAGGCT  
 TCAAGGAATTATCTCAACATTATTCTTCTATGCTCTAACAAATTCTCAACTGTTATGAGATTGTTACACTGC  
 TTCTGAAACAGTGGCTATTCTGCTACATGAGATGAATACAAACAAATTGTTGATAAAACTCCAAAAAA  
 AAAAAAAAAA

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**FIGURE 198**

MGEDDAALRAGSRGLSDPWADSGVVRPTTERHIAVHKRLVLAFAVSLVALLAVTMLAVLLSL  
RFDECGASATPGADGGPSGFPERGGNGSLPGSARRNHAGGDSWQPEAGGVASPGTTSAQPPS  
EEEREPEWPWTQLRLSGHLKPLHYNLMFTA FMENFTFSGEVNVEIACRNATRYVVLHASRVAV  
EKVQLAEDRAFGAVPVAGFFFLYPQTQVLVVVLNRTLDAQRNYNLKIIYNALIENELLGFFRSS  
YVLHGERRFLGVTQFSPTHARKA FPCFDEPIYKATFKISIKHQATYLSLSNMPVETS VFEEDG  
WVTDHFSQTPLMSTYYLAWAICNFTYRETTTKSGVVVRLYARPDAIRRGSGDYALHITKRLIE  
FYEDYFKVPYSLPKLDLLAVPKHPYAAMENWGLSIFVEQRILLPSVSSISYLLDVTMVIVHE  
ICHQWFGLVTPVWWEDVWLKEGFAHYFEFVGTDYLYPGWNMEKQRFLTDLHEVMLLDGLAS  
SHPVSQEVLIQATDIDRVFDWIAYKKGAALIRMLANFMGHGVFQRGLQDYLTIHKGNAARNDL  
WNTLSEALKRNGKYVNQEVMDQWTLQMGPVITILGNTTAENRIIITQQHEIYDISAKTKAL  
KLQNNSYLWQIPLTIVVGNRSHVSSEAIIWVSNKSEHHRTYLDKGSWLLGNINQTYFRVNY  
DLRNWRLLIDQLIRNHEVLSVSNRAGLIDDAFLSLARAGYLPQNI PLEII RYLSEEKDFLPWHA  
ASRALYPLDKLLDRMENYNIFNEYILKQVATTYIKLGWPKNFNGSLVQASYQHEELRREVIM  
LACSFGNKHCHQQASTLISDWISSNRNRIPLNVRDIVYCTGVSSLDEDVWEFIWMKFHSTAV  
SEKKILLEALTCSDDRNLNRLLNLSLNSEVVLQDAIDVIIHVARNPGRDLAWKFFRDWKW  
ILNTRYGEALFMYSKLISGVTEFLNTEGELKELKNFMKNYDGVAASFSRAVETVEANVRWKM  
LYQDELFWLGKALRH

**Transmembrane domain:**

amino acids 44-63

**N-glycosylation sites.**amino acids 89-93, 160-164, 175-179, 222-226, 338-342, 605-609,  
634-638, 649-653, 663-667, 684-688, 800-804, 906-910**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 362-366

**Tyrosine kinase phosphorylation site.**

amino acids 520-528

**N-myristoylation sites.**amino acids 78-84, 87-93, 90-96, 118-124, 501-507, 604-610,  
825-831, 987-993**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 437-447

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**FIGURE 199**

GGCCCCGGCGCAGCTGGCCAGAGCGACCGCGGGGCTAGCGCGCTCCGCCAGGGGCTCCGAAGCTGGCCC  
GGCCCCGGGCTCCTCCCTCGCTCCGCTTCTCGCTACCGCCGCCCTCTTCCCAAGCTCCCTCGCC  
GTCCGCCCGCCCCACAGCCAGCGCTCCGCCCCCTGCAGCCACGATGGCCGCGGCCGGCCGCCGCCGCC  
ACTCCGGGGATCTCGCTGTTCTCGCTCTGCTCTGGGAGCCGGCGAGCGCTGGAGCGAGATGCTCTTCC  
CGAGGGAGATGCTAGGCCCTTGGCTCTAACCTCTGCCCTCAGGAGGCCGGAGAGGAGCAGTCCTGGCAAAGA  
GCACCTCTGAAGAGAGAGTGGTAACAGCGCCCCCCCAGTCTCTCACAGTCGGCGGAAGTGCTGGGAGCGTGTGCT  
GGATGGGAGCGCACCCTCTGCACATCACGACATCCCAGCCCTGTCACCCTGCTCTTCCAGAGGAGGCCGCCCAA  
GCACGCCCTGCCCTCAAGAAGAAACTGCCTCGCTCAAGCAGGTGAACTCTGCCAGGAAGCAGCTGAGGCCCAA  
GCCACCTCCGAGCCACTGTCAAAGGGCAGGGTCCAGCCAGCGTCCAGGGCTTAGATCTCTCTCC  
CACGGAGAAGCCCTGGCCACCGGGGACCCGACCCCATCGTGGCCTCGAGGAGGCATCAGAAGTGCCCTTGC  
GCTGGATCGAAAGGAGAGTGCCTACAAACACCCGACCCCTGCACAAATCTCCCCCTTCACTTCGAGCCCTA  
TGTGGCCACACACTCCCCAGAGGCCAGAACCCGGGAGCCTGGCTGACATGCCAGGGCCAGGAGGCCAGGAG  
GGACACCAAGCCCCATGGCTGAGAACAGGTGAGAATGAGCTGACTGGTCAAGCTCAGGGAGAGGCCAGGA  
GACCAACTCTCACCATTACCAACACGGCTACACCCAGGACAAGCACCAGCTCTCGTAGTGTGAGCTT  
CTCCAATCTGAGGGTACATTGACTCCAGCAGTACCCACTGTCGCCCTCAACAAACTTCTGGAGTGACATA  
CAACGTGACAGTCTACACTGGCTATGGGTGGAGCTCCAGGTGAAAGAGTGTGAACCTGTCGATGGGAAGTCT  
CTCCATCCGGGGGGTGGACGGCCCTACCCCTGACCGTCTGCCAACAGACACTCTGGTGGAGGGGAGGTAAT  
CCGAAGCCCCACCAACACCATCTCGTCACTTCCGACCTTCCAGGAGCAGGCCCTGGACCTTCCAGCTTCA  
CTACCAGGCCCTCATGCTGAGCTGCAACTTTCCCGCCGCCCTGACTCTGGGATGTCAGGTGATGGACCTGCA  
CTCAGGGGGGTGGCCACTTCACTGCCACCTGGCTATGAGCTCAGGGCGTAAGATGTCAGCATCAA  
TGCCTCAAGCCGCACTGGAGCAGGCCACTCTGCTCAGCTCTGGAGGGGAGCTGCCAACATGGCAC  
CATGCCGGCGCTCTCCCAAGTTACCCCTGAAAACACAAAGGGAGCCAATTCTGACATCTGGACGATTGAAGC  
TCCAGAGGGCCAGAAGCTGACCTGACTTGGAGGGCTGTGCTGACATGACAAGGACAGGTGAGGTTCAAG  
GGGGCAGACCAACAAGTCAGCTCTCTACAGACTCCCTCAACACCGAGAGTGTCCCCCTTGAGGGCTGCTGAG  
CGAAGGCAACACCATCCGACATCGAGTTCACGTCGACCGAGGCCGGGCCCTCACCTCAACATCGGATTGAG  
AGCCTTGGAGAAAGGGCACTGCTATGAGCCCTACATCCAGAACTGGAACTTCACTACATCGGACCCGACCTATAA  
CATTTGGGACTATAGTGGAGTTACCTGGCAGCCCCGGCACTCCCTGGAGCAGGGCCGGCATCATGAATGCA  
CAATGTCGGGGACCCATACTGGATGACACAGAGCCCCCTGCGAGGAGCATGTCGGTGGGAGCTCTGCTG  
GGCTGGGGTGGTATTGTCCTCAAATGGCCCCAGGCTACCTGGAGGATGAAAGATTGTACTCTGCAAGATCCACGT  
GGGAGAAGAGAAACGGATCTTCTTAGATATCCAGTCTCTGAATCTGAGCAACAGTGCACATCTGGACCT  
TGGCGACGGGTCTGGCCACATCTGGGGCACTACCTGGAAACAGTGGCCCCAGAAACTGACTCTCCAC  
GCCAGACTTAACCATCCAGTTCATTGGACCCCTGCTGGCCTCATCTTGGAAAGGGCCAGGGATTATCATGAA  
CTACATAGAGGTATCAAGGAATGACTCTGCTGGATTACCCAGAGATCCAGAACTGGCTGGAAAACACTTCTCA  
CACGGAGTTGGTGCAGGGAGCCAGAACTACCTACCGAGTGTGACCCCGCTATGACATCTGGGAGTGACACCC  
CACCTGCGACTGGGAGCTCAGTGGAGCAGGCCACCCCCCATTTGTGAGAAAATTATGACTGCAACGGGCC  
AGAGGTGGATCACTGGACCCGTTAATTCGATCTGCTGGTGGGGAGCACCATTCAACACACTCTGCCAA  
CCCCGGTTTGTGCTTGAAGGGAGTTCTCTTCTGACCTGCTACAGCCCTGAACAGGGACTCCCCATCTGGACGTC  
TCGCTGCCCACTCGTTGGAGGAGTCTCTGGCATGTGACAAACCCAGGGCTGCCGAAATGGATACCAAA  
CCTGTACAAGCGACTCTACCTGCCAGGAGACTCCCTCACCTCATGTCCTACGAAGGCTTGTGAGCTCATGGCTGA  
AGTGACCATCCGCTGCATCTGGACAGCCATCCACTGGAACGGGCCCTGCCGTGTGAAAGTTAATCAAGA  
CAGTTTGAAACATGCTTGTAGAGCAGAAGCGCAGAGACGTCGCTGGAGGGGAAACATGGCCCTGGCTAT  
CTTCATCCGGTCTCATCATCTCTTACTGCTGGAGGAGCCTACATTACATCACAGATGTCGCTACTATT  
CAACCTCCGGCTGCCCTGCTGATGTAACCTCCACCCCTACAGCCAGATCACCGTGAAACCGAGTTGACAACCC  
TTACGAGACAGGGGAAACCAAGAGAGTATGAGGTTCTATCTAAAGAGAGCTACACTGAGAAGGGACTTGTGAA  
CTCAACACAAATCTCTCGAGACATTCAGCAGAGACCATGTCGCACTGATTGAAACCCAGAAATGTCGACTGT  
CTTTGTTAGACTCTTATCAAGGTTACTGTTCTCCCTGTATTATTATATTAAAGTGAaaaaaaaaaaaaaa  
aaaaaaaaaaaa

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**FIGURE 200**

MPAARPPAAGLRGISLFLALLLGSPAAALERDALPEGDASPLGPYLLPSGAPERGSPGKEHPE  
ERVVTAPPSSSQSAEVLGELVLDGTAPSAAHDIPALSPLLPEEARPKHALPPKKLPSLKQVN  
SARKQLRPKATSAAATVQRAGSQPASQGLDLLSSSTEKGPGPPDPDPIVASEEASEVPLWDRK  
ESAVPTTPAPLQISPFTSQPYVAHTLPQRPEPGEPGPDMAQEAPQEDTSPMALMDKGENELTG  
SASEESQETTTSTIITTVITTEQAPALCSVSFSNPEGYIDSSDYPLLPLNNFLECTYNVTY  
TGYGVELQVKSVNLSDGELLSIRGVDGPTLTVLANQTLLVEGQVIRSPTNTISVYFRTFQDDG  
LGTFLHYQAFMLSCNFPRRPDSGDVTVMDLHSGGVAHFCHLGYLEQGAKMLTCINASKPHW  
SSQEPICSAPCGGAVHNATIGRVLSPSYNPENTNGSQFCIWTIEAPEGQKLHLHFERLLLHDKD  
RMTVHSGQTNKSALLYDSLQTESVPFEGLLSEGNTIRIEFTSDQARAASTFNIRFEAFEKGHC  
YEPEYIQNGNFTTSDPTYNIGTIVEFTCDPGHSLEQGPAAIECINVRDYPWNDEPLCRAMCGG  
ELSAVAGVVLSPNWPEPYVEGEDCIWKIHVGEEKRIFLDIQFLNLSNSDILTIYDGDEVMPhi  
LGQYLGNNSGPQKLYSSTPDLTIQFHSDPAGLIFGKGQGFIMNYIEVRNDSCSDLPEIQNGWK  
TTSHTELVRGARITYQCDPGYDIVGSDTLTCQWDLSWSSDPPFCEKIMYCTDPGEVDHSTRLI  
SDPVLLVGTTIQYTCNPFGVLEGSSLTCYSRETGTPIWTSRLPHCVSEESLACDNPGLPENG  
YQILYKRLYLPGESLTFMCYEGFELMGEVTIRCILGQPSHWNGPLPVCKVNQDSFEHALEAEA  
AAETSLEGGNMALAIFIPVLIISLLGGAYIYITRCRYYSNLRPLMYSHPYSQITVETEFDN  
PIYETGETREYEVSI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 893-915

**N-glycosylation sites.**amino acids 311-315, 328-332, 350-354, 435-439, 458-462, 474-478,  
514-518, 576-580, 618-622, 674-678, 742-746**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 188-192

**N-myristylation sites.**amino acids 23-29, 87-93, 146-152, 454-460, 475-481, 575-581,  
629-635, 695-701, 723-729, 766-772, 877-883, 953-959**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 383-394

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**FIGURE 201**

**GATGGCTACGGCAGGGGGTGGCTCTGGGCTGACCCGGGAAGTCGGGGTCTCCTCGCCTTCT**  
GTCTTCTCGCTCCTACTAGCAGGTTGTGCAGGGAAACTCAGTGGAGAGGAAGATATATAT  
CCCCTTAATAAAACAGCTCCCTGTGTCACGCCACTCATCAGATTGGCTGCCA  
GTCTCAATTAGTGGAGACACAGGGTTATCCACGTAGTAGAGAAAGAGGAGGACCTACAGTG  
GGTATTGACTGATGGCCCCAACCCCCCTTACATGGTCTGCTGGAGAGCAAGCATTACAG  
GGATTTAATGGAGAAGCTGAAAGGGAGAACCGCGAATTGCTGGCTTGAGTGTCCCTGAC  
CAAGCCCAGTCCCTGCCCTCAGGCTCTCCTAGTGTACAGTGCCAAATGATGGTTGGTGT  
TTACTCCAATTCTATGGCCAGAGTTGCTCACTGCAGAGAAATACAGTGGAAATTGGCTGGG  
CAATGGTTGGCTTGAAGACTTAGTTCCCCTTCTTCTTGAAGATGAAAATGAAAC  
CAAAGTCATCAAGCAGTGTATCAAGATCACAAACCTGAGTCAGAATGGCTCAGCACCAACCTT  
CCCACATGTGCCATGCAGCTCTTCACACATGCATGCTGTATCAGCACTGCCACCTGCAT  
GCGCGCAGCTCCATCCAAAGCACCTTCAGCATCAACCCAGAAATCGTCTGTGACCCCCCTGTC  
TGATTACAATGTGTGGAGCATGCTAAAGCCTATAAATACAACGGACATTAAGCCTGACGA  
CAGGGTTGTGGTTGCTGCCACCCGGCTGGATAGTCGTTCTTCTGGAATGTGGCCCCAGG  
GGCTGAAAGCGCAGTGGCTTGTGACCCAGCTGGCTGCTGAGCTTGTGAAAGCTTGC  
ACCTGATGTGACCACCCCTGCCCGCAATGTCTGTTGCTTCTTCAAGGGAAACTTTGA  
CTACATTGGCAGCTCGAGGATGGTCTACGATATGGAGAAGGGCAAGTTCCCGTGCAGTTAGA  
GAATGTTGACTCTTGTGGAGCTGGGACAGGTGGCCTTAAGAACCTTATTAGAGCTTGGAT  
GCACACAGATCCTGTTCTCAGAAAAATGAGTCTGTACGGAACCAAGGTGGAGGATCTCCTGGC  
CACATTGGAGAAGAGTGGTGTGGTGTCCCTGCTGTACATCCTCAGGAGGCCAAATCAGTCCC  
GCCTCTCCCACCATCTTCCCTGCAGCGATTCTCGAGCTGAAACATCTGGCGTTGTTCT  
GGCTGACCAACTCTGGTGCCTTCCATAACAAATATTACAGAGTATTACGACACTGCTGAGAA  
CATTAATGTGAGCTATCCGAATGGTGTGAGCCCTGAAGAGGACCTGAACCTTGTAA  
CAGACAC TGCCAAGGCCCTGGCAGATGTGGCACGGTGTGGACGTGCTCTGTATGAGCTTG  
CAGGAGGAAACCAACTCAGCGACACAGTCAGGCTGATCCCCAACGGTTACCCGCCTGCT  
CTGATTAAAGCCAACAACATGTTCCAGTCTATCCTCAGGCAAGGACCTAAGGTCTACTT  
GGGTGACGGGCCTTCAACATTACATCGCTGTCTCAGCCCCACCAACACCAACTTATGTTGT  
ACAGTATGCCTGGCAAATTGACTGGCACAGTGGTCAACCTCACCCGAGAGCAGTGCAGGA  
TCCAAGTAAAGCTCCAAGTGAAAACAAGGATCTGTATGAGTACTCATGGTCCAGGGCCTT  
GCATTCTAATGAGACGGACCGACTCCCCGGTGTGCGTTCTACTGCACGATTAGCCAGGGC  
CTTGTCTCCTGCCCTTGAACTGAGTCAGTGGAGCTCTACTGAATACTCTACATGGACTGAGAG  
CCGCTGGAAAGATATCGTGGCGATATTCTCATCGCCAGCAAGAGCTTGAGTTGATCAC  
CTGACAGTGGGCTTCGGCATCCTCATCTTCTCCCTCATCGTACCTACTGCATCAATGCCAA  
AGCTGATGTCTTTCAATTGCTCCCCGGAGCCAGGAGCTGTGTCATACT**TGAGGAGGACCC**  
GCTTTCTGCCAGNTCAGCAGTTCACTCCTAGAGCATCTGTCCCCTGGACACAACCACT  
AATTGTCAGTGGAACCTCCCTGGGCTGTCTCAGATTGGGATTAACATAAAAGAGTGGAACT  
ATCCAAAAGAGACAGGGAGAAATAAAATAATTGCCCCCTCCGCTCCCTTCCATCA  
CCCCCTCCCCATTCCCTCTCTACTCATGCCAGATTGGGATTACAAATAGAAGCT  
TCTTGTCTCTGTTAACTCCCTAGTTACCCACCTAATTGCCCTTCAGGACCCCTACTT  
TTCCTCCCTGCCCTGTACCTCTCTGCTCCTCACCCCCACCCCTGTACCCAGGCCACCTCCT  
GACTGGGAAGGACATAAAAGGTTAATGTCAGGGTCAAACACTACATTGAGCCCTGAGGACAGG  
GGCATCTCTGGGCTGAGCTACTGTCTCCTCCACTGTCTTCTCCAGGCCCTCAGATGGC  
ACATTAGGGTGGCGTGCTGCCGGTGGTATCCACCTCCAGGCCACAGTGTCAAGTTGACT  
TTTATTAAAGCTGTAATATCTATTGTTGTTGTCTTTCTTATTCTTTGTAAATAT  
ATATATAATGAGTTCAATTAAATAGATTATCCC

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**FIGURE 202**

MATAGGGSGADPGSRGLRLLSFCVLLAGLCRGNNSVERKIYIPLNKTAPCVRLLNATHQIGCQ  
SSISGDTGVIHVVEKEEDLQWVLTDGPNPYPVMLESKHFTRDLMEKLKGRTSRIAGLAVSLT  
KPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENET  
KVIKQCYQDHNLSQLNGSAPTFPLCAMQLFSHMHAVISTATCMRRSSIQSTFSINPEIVCDPLS  
DYNVWSMLKPINTTGTLPDDRVVVAATRLDSRSFFWNVAPGAESAVASFVTQLAAAELQKA  
PDVTLPRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWM  
HTDPVSQKNESVRNQVEDLLATLEKSGAGVPAILRRPNQSQPLPPSSLQRFLRARNISGVVL  
ADHSGAFHNKYQSIYDTAENINVSYPEWLSPEEDLFNFVTDATAKALADVATVLGRALYELAGG  
TNFSDTVQADPQTVTRLLYGLIKANNSWFQSILRQDLRSYLGDPQLQHYIAVSSPTNTTYVV  
QYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLPRCVRSTARLARA  
LSPAFAELSQWSSTEYSTWTESRWKDIRARIFLIASKELELITLTVGFGILIFSLIVTYCINAK  
ADVLFIAPREPGAVSY

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 671-692

**N-glycosylation sites.**amino acids 45-49, 55-59, 187-191, 200-204, 204-208, 264-268,  
387-391, 417-421, 435-439, 464-468, 506-510, 530-534, 562-566,  
573-577, 580-584, 612-616**Glycosaminoglycan attachment site.**

amino acids 404-408

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 232-236

**N-myristoylation site.**amino acids 5-11, 6-12, 9-15, 29-35, 61-67, 120-126, 146-152,  
168-174, 205-211, 294-300, 438-444, 446-452, 504-510, 576-582

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**FIGURE 203**

GCTAGACCGAGCCCTGGGAGGCATCGGGCTCCCCCGGAAACCCTGCCAGGGAGCCGGGTTT  
GAGCTCAGGCGCCTCTAGCGCGGCCCGAGAAATCTGACTCGCGAGGCCAGAGTTGCAGGGA  
CTGAATAGCAAACGTAGGCTGAGTAGGAAACAGACCATGAGGTCAGTGCAGATCTCCTCTCC  
CAATGCCGTTGCTCCTCTACTAGTTCCGACAATGCTCTTAAGTCTCTGGCGAAGATGTA  
ATTTTCACCCCTGAAGGGGAGTTGACTCGTATGAAGTCACCATTCTGAGAACAGCTGAGCTTC  
CGGGGAGAGGTGCAGGGTGTGGTCAGTCCGTGCTCACCTACTGCAGTTAAAAGGCAAGAAG  
CACGTCCCTCATTGTCGGCCAAGAGACTCTGTGCCCCGACATCTGCGCTTTCTCCTTC  
ACAGAACATGGGAACTGCTGGAGGATCATCCTTACATACCAAAAGGACTGCAACTACATGGG  
TCCGTGAAAGAGTCTCTGGACTCTAAAGCTACTATAAGCACATGCATGGGGGTCTCGAGGT  
GTATTAACTTACATTGATGCCAACATTACCAAAATTGAGCCCCCTCAAGGCCTCTCCAGTTGAA  
CATGTCGTCTATCTCTGAAGAAAGAGCAGTTGGGAACTCAGGTTGTGGCTTAAGTGATGAT  
GAAATAGAATGCCAGATGCCCTTATGAGAATAAGGCAGGCTAAGGGACTTTCTGGATCC  
TATAAACACCCAAAGTACTTGAATTGATCCTACTCTTGATCAAAGTAGGTATAGGTTGTG  
AACACAATCTTCTCAAGTCATACATGATGCCATTCTTGACTGGGATTATGGACACCTAC  
TTTCAAGATGTTGTATGAGGATACACTAAAGGCTCTGAAAGTATGGACAGATTTAACAAA  
ATACCGTTGGATATCCAGAGTTAGCTGAAGTTAGGCAGATTGTAATATATAAAAAAGT  
GTATTAAATGCTCGCCTGTCACTCAGATTGGCACATTATCTCAAAGAAAATATAATGAT  
GCTCTGCATGGCGTTGGAAAAGTGTGTTCTCTAGAAATATGCTGGATCAGTGAGTACTTTA  
CTAGATACAAATATCCTGCCCTGCTACCTGGTCTGCTCATGAGCTGGTCATGCTGTAGGA  
ATGTCACATGATGAACAATACTGCCAATGTAGGGTAGGCTTAATTGCATCATGGCTCAGGA  
CGCACTGGGTTAGCAATTGCAGTTATATCTCTTTAAACATATCTCTCGGAGCAACA  
TGTCTAAATAATATCCCAGGACTAGGTTATGTGCTTAAGAGATGTGAAACAAAATTGTGGAG  
GACAATGAGGAATGTGACTGTGGTCCACAGAGGAGTGTCAAGAAAGATCGGTGTTGCCAATCA  
AATTGTAAGTTGCAACCAGGTGCCAACTGTAGCATTGGACTTGTGCTCATGATTGTCGTTT  
CGTCCATCTGGATACGTGTTAGGCAGGAAGGAAATGAATGTGACCTTGCAAGAGTACTGCGAC  
GGGAATTCAAGTCCCTGCCAAATGACGTTATAAGCAGGATGGAACCCCTGCAAGTATGAA  
GGCGTTGTTCAAGGAAGGGGTGCAGATCCAGATATATGCACTGCCAAGCATTGGACCT  
GATGCCATGGAGGCTCTAGTGAGTCTATGTCAGTTAACTTAATAGGTGATCAATTGGT  
AACTGTGAGATTACAGGAATTGAAACCATCCCTGATTTGCCAGAGCATACTGACTATAATTCT  
ACTCATTTACAGGCAGAAAATCTCATGTGCTGGGCACAGGCTATCATCTATCCATGAAACCC  
ATGGGAATACCTGACCTAGGTATGATAATGATGGCACCTCCTGGAGAACGCCGGTATGT  
TTAAAAAAAAATTGCGTCAATAGCTCAGTCTGCAGTTGACTGTTGCCTGAGAAATGCAAT  
ACCCGGGGTGGTGCACAAACAGAAAAACTGCCACTGCATGTATGGGTGGCACCTCCATTG  
TGTGAGGAAGTGGGTATGGAGGAAGCATTGACAGTGGCCTCCAGGACTGCTCAGAGGGCG  
ATTCCCTCGTCAATTGGGTGTGTCATCATATAATGTTGCCTTATTATTAATCCTTCA  
GTGGTTTTGTGTTTCCGGCAAGTGATAGGAAACCACTTAAACCCAAACAGGAAAAATG  
CCACTATCCAAAGAAAAACTGAACAGGAAGAATCTAAACAAAAACTGTACAGGAAGAATCT  
AAAACAAAAACTGGACAGGAAGAATCTGAAGCAAAACTGGACAGGAAGAATCTAAAGCAAA  
ACTGGACAGGAAGAATCTAAAGCAAACATTGAAAGTAAACGACCCAAAGCAAAGAGTGTCAAG  
AAACAAAAAAAGTAACCGGCAATCCATACTCATTGAGTAACACAGGCTATTATTAACCA  
GCTAATCATTATCCAAAGGCTTCATTCTCCCAATTTTTACTTTAATTTC  
ACAAGTTTGATCAGCAAATAACAGCATTCTGTTGGAAACAAAAA

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**FIGURE 204**

MRSVQIFLSQCRLLLLLVPTMLLKGLEDVIFHPEGEFDSYEVТИPEKLSFRGEVQGVSPVS  
YLLQLKGKKHVHLWPKRLLLPRHLRVFSFTEHGELLEDHPYIPKDCNYMGSVKESLDISKATI  
STCMGGLRGVFNIADAKHYQIEPLKASPSFEHVYLLKEQFGNQVCGLSDDEIEWQMAPYENK  
ARLRDFPGSYKHPKYLELILLFDQSRYRFVNNNLSQVIHDAILLTGIMDTYFQDVRMRIHLKA  
LEVWTDFNKIRVGYPPELAEVLGRFVIYKKSVLNARLSSDWAHLYLQRKYNDALAWSFGKVCSEL  
EYAGSVSTLLDTNILAPATWSAHELGHAVGMSHDEQYCQCRGRLNCIMSGSGRTGFSNCSYISF  
FKHISSGATCLNNIPGLGYVLKRCGNKIVEDNEECDCGSTEECQKDRCCQSNCKLQPGANCSI  
GLCCHDCRFRPSGYVCRQEGNECDLAEYCDGNSSSCPNDVYKQDGTPCKYEGRCFRKGCRSRY  
MQCQSIIFGPDAEAPSECYDAVNLIQDQFGNCEITGIRNFKKCESANSICGRLQCINVETIPD  
LPEHTTIISTHLQAENLMCWGTGYHLSMKPMGIPDLGMINDGTSCGEGRVCFKKNCSVNSSLQ  
FDCLPEKCNTRGVCNNRKNCMYGWAPPCEEVGYGGSIDSGPPGLLRGAIPSSIWWVSIIM  
FRLILLILSVVFVFFRQVIGNHLKPQEKMPLSKAKTEQEESKTKTQVEESKTGTQEESEAK  
TGQEESEKAKTGQEESEKANIESKRPAKSVKKQKK

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 684-705

**N-glycosylation sites.**

amino acids 222-226, 372-376, 438-442, 473-477, 625-629

**N-myristoylation sites.**amino acids 131-137, 168-174, 235-241, 319-325, 364-370, 436-442,  
472-478, 609-615, 642-648, 668-674, 676-680, 680-686, 749-755,  
758-764, 767-773**Amidation site.**

amino acids 69-73

**Disintegrins proteins**

amino acids 429-479

**EGF-like domain proteins**

amino acids 650-662

**Neutral zinc metallopeptidases, zinc-binding region proteins**

amino acids 335-345

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**FIGURE 205**

CGGACGCCGTGGCGGACGCGTGGCGGACGCGTGGGGAAAGGTTGAATGGGTAGAAGGCCG  
TTGTGGAGGGAAACCACCCATCCTCCTGCCCTCACCACCATCATCCTGGCTGGACCGAG  
AGGGTGACGGGGCTGGGAAGGGCAGCTCATGTTCAGGTTCCAGGAGGGCTACCTGTTGA  
CTGTCTTGCAGGAAGAAGAAAACACCTGAGTGACCAGATGTCAGCTCCAGCAGCTCCAGGTGCCCTGGC  
AGATGCCAGAACCACCTCTGAAGAGTGACAGTGCTGAGCATGGTTCTGCACACCT  
GGAATGACTGAAACCCAAAGACTCAAGAAGGAGCTAAAGATCTTGAAGTAGACATGAATAAA  
ACAGAAGGCTGTGGACCACCTGTCAGATGGAGAAGTCCTCTGAGGCTATCCAACACGGAC  
CAGGCCATGAGACCCCAGTACCATCCCTGAATTTCAGAGTCAGTCACACCAGATTGAA  
CTTATCCAGGCCCTCCCATCCAAGAATGGAAAAAGTGGAAATTCTGAATTTCACCAAGCTACT  
ATGAGGCTTGTGCGAAGGCTGAAAATCCTGATCAAGCTGGTTGGAGCGTTCCACGGAG  
TTGGTATCCTGGGGTTAACCTCTGCAAGAGTGGTTATCACTGCTGTTGGTGCACCTAGCCG  
GGGGTCTTGTGTTGGTATTATGCCACCAACTCTGCCAGGGCTTGTCAATATGTCATCACTC  
ATGCCAAAGTGAACATCTGCTGGTTGAGAATGATCAACAGTTACAGAAAATCCTTCGATTC  
CACAGAGCAGCCTAGAGCCCCCTAAAAGCAGTCATCCAGTACAGACTGCCAATGAAGAAGAAC  
ACAACCTGTACTCTGGGATGATTCATGGAACCTGGCAGAAGTATCCCTGACACCCAACTGG  
AGCAGGTACATCGAGAGCCAGAAGGCGAATCAATGCGAGTGCTCATCTACACTCAGGGACCA  
CAGGCATACCCAAGGGAGTGATGCTCAGTCAGACAAACATCACGTGGATTGCAAGGAGCAGTGA  
CAAAGGACTTTAAACTGACAGACAAGCAGTCAGACGGTGGTTAGCTACCTCCACTGCCATA  
TTGCAGCACAGATGATGGACATCTGGGTACCCATAAAGATTGGGCGCTCACATACTTGCTC  
AAGCAGATGCTCTAAGGGCACCTGTAAGTACTCTAAAGGAGGTTAAACCTACTGTCCTCA  
TTGGAGTGCCTCAAATTGGGAGAAGATACATGAGATGGTGAAGAAAAATAGTGCCAAGTCCA  
TGGGCTGAGAAGAAGGCAATTGCTGTTGGCAAGAAACATTGGCTCAAGGTCAACTAAAAAA  
AGATGTTGGGAAATATAATACTCCGTGAGCTACCGATGGCTAACAGACTCTGGTGTTCAGCA  
AAGTCAGACATCCCTGGCTGGATCACTGTCACTCTTATCAGTGGACTGCGCCCCCTCA  
ACCAAGAGACTGCCAGTTCTTCTAACGTTGGACATACCTATAGGGAGTTGATGGTTGA  
GTGAGAGCTGGGACCCCACACGATATCCAACCGAATAACTACAGGCTTCAAGCTGTGGCA  
AGATCTGACTGGGTGTAAGAATATGCTGTTCCAGCAGAACAGGATGGCATTGGGAGATCT  
GCCTCTGGGTAGGCACATCTCATGGCTATCTGAAAGTGAGACTGAAACTACAGAGGCCA  
TCGATGATGAAGGCTGGCTACACTCTGGGATCTGGGCCAGCTGGACGGTCTGGTTCTCT  
ATGTCACCGGCCACATCAAAGAAATCCTTATCACTGCTGGTGTGAAATGTGCCCCCCATT  
CTGTTGAGACCTGGTTAAGAAGAAGATCCCCATCATCAGTAACGCCATGTTAGTAGGAGATA  
AACTGAAGTTCTGAGCATGTTGCTGACGCTGAAGTGTGAGATGAATCAGATGAGCAGGAGAAC  
CTCTGGACAAGCTGAACCTCGAGGCCATCAACTTCTGTCGGGCTGGCAGCCAGGCATCCA  
CCGTGACTGAGATTGTGAAGCAGCAAGACCCCTGGCTACAAAGGCCATCCAGCAAGGCATCA  
ATGCTGTGAACCAGGAAGCCATGAACAAATGCACAGAGGATTGAAAAGTGGTCATCTGGAGA  
AGGACTTTCCATATGGTGGAGAGCTAGGTCAATGATGAAACTTAAGAGACATTTGTTAG  
CCCAGAAATACAAAAACAAATTGATCACATGTACCACTGACTGCTTGTGATGGAGCTGCTCTC  
AGCTGTTCTGATGCCCTCAGCAGGAAGACCTCATTGCAATAAGTGAATGCTGCTTAGGTAG  
AAGCTCCCTGCTGTTTAAGAAGGCCACATTCTCATTGGTCAGTTCTGATTGTTGTC  
TGTTGGAGAGGTGCTCCCTAGAAGAACCTGCCATACGTTCAAAGCAATAAAACTG  
TCTTCTAAGGACCTCAAGTCAGTACCTCCAGGGAAAGCCTATTGGGAAGTCTACTAAAAACTG  
CTGATTACAAGAAGACCTGAACTTGTGGCTCCATTGATTTTTCTCCTCAGGGGAC  
TCAGACATTAGAAGAAAAAGCCTCACAGATTGAAGAAGTGGACCCCCAAATCAACTCACCT  
GCCTGGAAAGCAACTGGGAAACCCCTTCCAATAAGTCCTGATAATAAGCAGCTTCAGGGTCCCAA  
AAAAAAAAAA

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**FIGURE 206**

MTIPEFFRESVNRFGTYPALPSKNGKKWEILNFNQYYEACRKAKSLIKGLERFHGVGILGF  
NSAEWFITAVGAILAGGLCVGIYATNSAEACQYVITHAKVNILLVENDQQQLQKILSIPQSSLE  
PLKAIIQYRLPMKNNNLYSWDDEMELGRSIPDTQLEQVIESQKANQCAVLIYTSGGTGIPKG  
VMLSHDNITWIAGAVTKDFKLTDKHETVVSYPLSHIAAQMMDIWVPIKIGALTYFAQADALK  
GTLVSTLKEVKPTVFIGVPQIWEKIHEMVKKNSAKSMGLKKAFVWARNIGFKVNSKKMLGKY  
NTPVSYRMAKTLVFSKVKTSLGLDHCHSFISGTAPLNQETAEFFLSDLPIGELYGLSESSGP  
HTISQNQNYRLLSCGKILTGCCKNMLFQQNKDGIGEICLWGRHIFMGYLESETETTEAIDDEGW  
LHSGDLGQLDGLGFLYVTGHIKEILITAGGENVPPPIPvetLVKKKIPIIISNAMLVGDKLKFLS  
MLLTLKCEMNQMSGEPLDKLNFEAINFCRGLGSQASTVTEIVKQQDPLVYKAIQQGINAVNQE  
AMNNAQRIEKWVILEKDFSIYGGEGLPMMKLKRHFVAQKYKKQIDHMYH

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 65-86

**N-glycosylation site.**

amino acids 196-200

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 282-286

**Tyrosine kinase phosphorylation sites.**

amino acids 547-555, 608-616

**N-myristoylation sites.**amino acids 15-21, 74-80, 80-86, 84-90, 185-191, 189-195,  
253-259, 337-343, 371-377, 448-454, 536-542**Amidation site.**

amino acids 24-28

**Putative AMP-binding domain signature.**

amino acids 177-189

**Putative AMP-binding domain proteins.**

amino acids 173-190

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## FIGURE 207

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**FIGURE 208**

MAYRVLGRAGPPQP RRARRLLFAFTLSCTS YLCYSFLCCDDLGRSRLLGAPRCLRGPSAGG  
QKLLQKSRPCDP SGPTPSEPSAPSAPAAV PAPRLSGSNHSGSPKLGT KRLPQALIVGVKKGG  
TRAVLEFIRVHPDV RALGTEPHFFDRNYGRGLDWYRS LMPRTLES QITLEKTPSYFVTQEAPR  
RIFNMSRDTKLIVVV RVNPVTRAISDYTQTL SKKPDIPTFEGLSFRNRTLGLVDVSWNAIRIGM  
YVLHLESWLQYFPLAQIHFVSGERLITD PAGE MGRVQDFLGIKRFITDKHFYFNKTKGFPCLK  
KTESSLLPRCLGKSKGRTHVQIDPEVIDQLREFYRPYNIKFYETVGQDFRWE

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 102-106, 193-197, 235-239, 306-310

**Tyrosine kinase phosphorylation site.**

amino acids 296-305

**N-myristoylation sites.**

amino acids 51-57, 100-106, 121-127, 125-131

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 20-31

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**FIGURE 209**

CTTTCTTATCTGTGTACTCTTATCTCACTGTTCTATTTTCTCCTCATTTATTAAC  
CTTTCTTACCTTTCTGAACCTCTAGGCCTCTCTTCCAGAACTGGTGAAGACAATG  
AAACGGCCAAGATGGTAAGAACACAAGCCGATTCCTCCTGGGGAGACTGATAATTAAAAGG  
TTTGTGTGTCAAGAACATTCCCAGCTTCATCACCAACCCCTTCCTCCACCTCTGCCCACTG  
GAGACCACTTACATCCCAGCGGAGCGCAGCTGAAGTCAGGAAACCATGCATCACATTAG  
CAGGAGCCAAGTCAACTTAACTCCGTTCAACATGTGGATGCCAGAGAAA**ATG**ACTGT  
CCAGACAAGCCCCGGCAGCTCATAAACTGGTTCATCTGCTCCCTGTGCGTCCCGCGGGTGC  
AAGCTCTGGAGCAGCCGGTCCAAGGACCCGGAGAAACCTCTGCTGGGACTGCGTGTGCC  
ATCTACTTGGGCTTCCCTGGTGGCCAGGTGGGAGGGCCTCTCCAGCATGGACAGGCGGCT  
GAGAAGGGGCCACATCGCAGCCGCACACCAGCCGAGCCATCCTCCCTGAGATACCCCTGGAT  
GGTACCTGGCCCTCCAGAGTCCCAGGGCAATGGGTCACTCTGCAGCCAATGTGGTGTAC  
ATTACCCCTACGCTCCAAGCGCAGCAAGCCGGCAATATCCGTGGCACCGTGAGGCCAAGCGC  
AGGAAAAAGCATGCAGTGGCAGCGTGGCCAGGGCAGGAGGCTTGGTCGACCATCCCT  
CAGCCGAGGAAGCGCAAGGGAGCTGATGCTGTAGCACCTGGTACGCTCAGGGAGCAAAC  
CTGGTTAAGATTGGAGAGCGACCCCTGGAGGTTGGTGCGGGGTCCGGGAGTGCAGGCCGGG  
CCAGACTTCCCTGCAGCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAGCGCCCC  
TCCTGGCTGAGCAAAGATGACATCCAGGAAGAATGCACTCTGGCGACAGCGCAGTGGCAGGG  
CTCCGGCCTGTGCTCTAGGAGCGAGCCCCTTGCTGGTGCCTGGAGGGGGCGCACCTGGC  
GCTGTGCTCCGTGTGGCCCTAGCCCTGTGGGCTCTCAAGCAGCCCTGGACATGAGTGAG  
GTGTTGCCTTACAGACAGGATCTGGGCTCAACAGGACCCGCGCTGTGAGCAGG  
AAAGCAGAGTTCATCCAAGATGGCCGCATGCCCATCATTCTTGGGATGCATCTTATCT  
TCAGCAAGTAATGACACCCATTCTCTGTTAAGCTCACCTGGGAACTTATCAGCAGTGTG  
AAACAGAAAATGCTGGCAGAATGGCCAGTACCAAGCCTGAATCAGGTTGACTGAAATACAT  
CATCATGAGTGGTCCAAGATGGCACTTTGATTTTGTACAGATTATAATCGCTTAGAT  
ACAAATTGCTGTGGATTCAAGACCTCGCAAGGAAGATGCCGTGTACAGAATGGATTGAGGCC  
AAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAGCGAAAGCATGCCAAGG  
CATTTGGTTTTATAGACAACAAGGTTCTTGACAGGAGTGAAGATAACTAAACTTCAA  
TTGTTAGAAGGCATCAAAGAGTTCCAGCTCTGCAGTTCTGTTGAAGAGCCAGCACTTA  
CGGCAGAAACTTCTTCAGTCTGTGTTCTGATAAAGTGTATTGGGAAAGTCAAGGAGGTTAGA  
CAAGGAATTGAAAAGCTTATCGATGTAATAGAACACAGAGCCAAATTCTTATCACCTATATC  
AATGACACAGGGGCAAAGTATTACCTATGAATGAAT**G**ACAAAAGAATCTCTGGCTAGGGT  
TTAGATATTTATGCTTGGTTGTTAAATCAAGCACATCAACCTCAAGCCCGTT  
TAGCAATGAGGCACTGTAGATGAATACGTAACATTGACTTAAACCAAGTAGCTATAAAGG  
GACTTAGCACTGTATGCATACTTAAAGGTTGAAAACAAACTACTTGAGAAATATTGT  
TTATTTCTCTAACATCATGCTATGTGTCACTGTAACATCTGACAACAGAAATTCTAGT  
TATTCTAGCTAACGTTGAAACATTGTCATGCTGTTAATAGAAAACGAAACTGCAAACAGA  
GATACTGACTCCATTAATAAACATTTGTCGCTTGTGACTGTTCTGACCAAACACTAAT  
GGAAACAATTCTGACGTTCTGCTGATTGTTAACATAGAGCAGTCTACACTACCC  
TGAGGCAACTCTACATTGAAACACTGAGGCTTACAGCCTGCAAGAGCATCAGAGCTGAC  
CATTTAAACAGAAATGCTGGTTATTGCAAACATCACCAGTATATTCTATTGTGTCTATAA  
AAAATCAGTCATTAAGTACAAGAATCATATTCCATTCTTTAGAAATTATTTGTTG  
TCCCTATGGAAATCATTACATCTGACAATTATGTTAAAGAGTTACTCTCTCTATT  
GGTCAAATTGTTAGTGTAGGGCTGAGAAATTAAATTCTAAAGTATGAAGTTACCTATCTG  
AAAATGACTTACAGAGTATCATTAAATGGATGTCTTTAAAAATTGTTACTTTAC  
CAACAATGTAATATAATTATGTTAATGGTTACTGCCAGATATTGAGAAATGGTCAAATAT  
TGAGTGTGTTCAATAA

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**FIGURE 210**

MTCPDKPGQLINWFICSLCVPRVRKLWSSRRPRTRRNLLGTACAIYLGFLVSQVGRASLQHG  
QAAEKGPHRSRDTAEPSPFEIPLDGLAPPESQNGNSTLQPNVVYITLRSKRSKPANIRGTVK  
PKRRKKHAVASAAPGQEALVGPSLQPQEAAREADAVAPGYAQGANLVKIGERPWRLVRGPGVR  
AGGPDFLQPSSRESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGARLLVLEGG  
APGAVLRCGSPCGLLKQPLDMSEVFAFHLDRLGLNRTLPSVRKAEFIQDGRPCPIILWDA  
SLSSASNDTHSSVKLTWGTYQQLLKQKCWQNGRVPKPESGCTEIHHEWSKMALFDPLLQIYN  
RLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAAALAHIIQRKHDPRLVFIDNKGFFDRSEDNL  
NFKLLEGIKEFPASAVSVLKSQHLRQKLLQSLFLDKVYWEQGGRQGIEKLIDVIEHRAKILI  
TYINAHGVKVLPMNE

**Transmembrane domain:**

amino acids 40-56

**N-glycosylation sites.**

amino acids 98-102, 289-293, 322-326

**N-myristoylation sites.**amino acids 8-14, 41-47, 97-103, 187-193, 251-257, 252-258,  
287-293, 484-490

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**FIGURE 211**

GTGGGGTGGTGAGCGCAGGCCGAGGATGAGGAGGTGCAACAGCGCTCCGGGCCGCCGCGCTGCTGCTGC  
TGCTGCTGGCTGCTCGCGGTTCCCGGCCGCTAACCGGCCGCCGCGCTGCTGGCTCCGAGCGCTGGCCGTGGAGTCTCG  
TGACGCTGCTGCAGGCCGACACGGTGCAGGCCGCGCTGGCTCCGAGCGCTGGCCGAAGACGTCAAAGCCTGGAGGC  
CTCCTGGTGCAGGCCACTGCATCGCCTCGCCCGACGTGGAAGGCCGAAGACGTCAAAGCCTGGAGGC  
CGGCCCTGATCTCGCCCGCTGGACTGTGCTGAGGAGACCAACAGTCAGTCTGCAGAGACTTCACATCCCTG  
GCTTCCGACTGTGAGGTTCTCAAGGCCCTTACCAAGAACGCTGGAGCAGTATTCCAGTGGCTGGCTG  
ACGTGAGACGCTGCGGGAGAGGCTATTGACGCCCTGGAGTCCATCATGACAGTGGCCCCAGCCTGCTCC  
CACTGGAGCCTGCAAGCTGGAGGAGATTGATGGATTITTCGAGAATAACGAAGAGTACCTGGCTTGATCT  
TTGAAAAGGGAGGCTCTACCTGGTAGAGAGGTGGCTCTGGACCTGTCCCAGACAAAGGCCGTGGCGGTGCGCA  
GGGTGCTGAACACAGAGGCCAATGTGGTAGAGAAAGTTGGTGTACCGACTTCCCCTTGTACCTGCTGTTCC  
GGAATGGCTGCTCTCCGAGTCCCGCTGCTCATGGAATCCAGGCTTCTATACCGCTAACCTGAGAGACTCT  
CTGGGCTCACCGAGGCTGCCGACAGGACAGTGCACCAACCAGCTAACAAAGATAGCTCCACTGTTTGG  
AATGGCAGATGCCAACATGCTACATGGCTGACCTGGAAATCTGCACTACATCCTGCCGAGTAAAGTGG  
GCAGGTTCCCGGCTCTGGAAAGGGCAGCGCTGGTGGCCCTGAAAAAGTTGTGCTGAGTGTGGCAAGTATTCC  
CTGGCCGGCCCTTAGTCCAGAACTTCTGCACTCCGTAATGAATGGCTCAAGAGGCAGAAGAGAAATAATT  
CCTACAGTTCTTAAAAGTCCCTGGACGACAGGAAGAGGGTGGCTTCTGCCAAGAAGGTGAACTGGATTG  
GCTGCCAGGGAGTGAGCCGATTTCCGGGCTTCCCTGCTCCCTGTGGTCTTCCACTTCTGACTGTGC  
AGGCAGCTCGGAAAATGAGACCACTCACAGGAAGCAGCCAAGGCCAAGGAGGTCTCCAGCCATCCGAGGCT  
ACGTGCACTACTCTCGGCTGCCAGACTGCCACTTCCGAGATGCTGAGCAGATGGCTGCTGCCATGCAACGGG  
TGGGAGTCCCACCGCCGCTGCCCTGGCTCTGGCTAGGCCAACACAGGGCTAACATGCTGCCCTTGAGGTGCC  
CCAGGGAGGACCCCAGTCCCCAACGGTGCAGTGGCACCCTGTAACCTCTCAAGGCCACTTCTCCAGCAATGAACGCC  
TGGATGTGCCCGTGTGGAGCTGGCACCCCTCAACTCTCAAGGCCACTTCTCCAGCAACATCATCC  
TGGACTTCCCTGCACTGGGTCAAGCTGCCGGAGGGATGTGCAAGATGTGGCAGCCGCCAGAGCTGGCATGG  
GAGCCCTGGAGCTGGAAAGCCGAATTCAACTCTGGACCCCTGGAGAGATGATGAAGTCCCCCAAACA  
CCACCCACATGTGCCGGCTGAGGGACCTGAGGCAAGTCGACCCCGAAGCTGCACTGCCATGAGCTGCA  
CAGGCAGGAGGCCAGTCCCCAACGGTGCAGTGGCACAGGCTGAGGAGTGGCAGGAGCAGCCGTTGGCAGTGGCACT  
TGAGCAAGCAGACACAGGGCTGCAATTGCTGGCTGAGTCCAGGGCTGAGAAGAACCCCTCTGGGGCCCTTGG  
AGGTCAAGCGCTGGGGCTGAGCTTCAAGCAGCTGGTCAAGTGGCAGCTGGCATGGCCATCTCTAGGCACCTCAAGGCC  
GGGGCCGAGGCCAGTGGCTGCAAGGTGCTGGAGGGCTCTTACCTGGACATCAGCCTGTGTTGGCT  
ATTCCCTGCTCTCATGGGCCTGCTGGCATGTACACCTACTTCAAGGCCAGATAAGGGCCCTGAAGGCCATG  
CTGGCCACCCCTGCAGCTTGAACCACTGGGAGGGAGGGAGGGAGCTGCCATCTCTAGGCACCTCAAGGCC  
CCTGACCCCATCCCTCCCAACCCCTTGTCTTGTCTGGCTAGAAGTGTGGAAATTCAAGGAAACGAG  
TTGCTCCAGTGAAGCTTCTGGGTTGCTAGGACAGAGAGCTCCCTGACACAAAGACAGGAGCAGGGTCCAGG  
TTCCCTGCTGTGCAAGGGAGGGCAGCCCCGGCAGTGGCAGCTGGCATAGGAGCTCAGTCCTGCCCTTGTGACCAC  
ATTCCCTTTTCAGCTTATTGAAAGTCTGCCCTATTCTCACTGGAGCCTCAGTCTCTCTGCTTGGCTTGG  
CCTCAACTGGGGCAAGTGAAGCCAGAGGAGGGTCCCCAGCTGGTGGGCTGGAATGGAACTCCTCACTAGTGC  
TGGGCTCCGGCCACCCCTGCTCCCTCCGGACAATGAAGAAGCCTTGCACCCCTGGAGGAAGGACCAACGGG  
CCCTCATGCCCTGCCAGCCTCCAGCTCAGACCTCTGGTGGGTTGGCTTCAGGGTGGGTTGG  
TTCTGGAAGTCGTGCTGGCTCCAGGTGAGGCAAGGCATGGTTGCTGGCTGTAGGGTGAGTGGCTTGTG  
GGGACCTGACGAGTTGGTGGCATGGGAAGGATGTGGCTCTAGTGCCTTGCCTTGCAGGAGAAGA  
TGGCTGCTTCACTTCCCCCATTGAGCTGCTCCCTGAGCCTGGTCTTTGTCTTGTCTTGTCT  
CAAGATGAATGCTCATCTTGAGGGTGCAGGTAGAAGCTAGGGAGGGAGTGCTTCTCTCCAGGTTTCAC  
CTTCCAGTGTGCAAGTTAGAAGGGTCTGCCAGTGCCTTACACATGCTTGAATTCCACGCTACCCCT  
GCCTTGGGAGGTGTGGAATAAATTATTGTGTAAGGCA

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**FIGURE 212**

MRRCNSGSGPPSLLLLLWLLAVPGANAAPRSALYSPSDPLTLLQADTVRGAVLGSRSAWAV  
EFFASWCGHCIAFAPTWKALAEDVKAWRPALYLAALDCAEETNSAVCRDFNIPGFPTVRFFKA  
FTKNGSGAVFPVAGADVQTLRERLIDALESHDTWPPACPPLEPAKLEEIDGFFFARNNEEYLA  
LIFEKGGSYLGREVALDLSQHKGVAVRVLNTEANVVRKFGVTDFPSCYLLFRNGSVSRVPVL  
MESRSFYTAYLQRLSGLTREAAQTTVAPTTANKIAPTVWKLADRSKIYMADLESALHYILRIE  
VGRFPVLEGQRLVALKKFVAVLAKYFPGRPLVQNFLHSVNEWLKQRQKRNKIPYSFFKTALDDR  
KEGAVLAKKVNWIGCQGSEPHFRGFPCSLWLFHFLTQARQNVDHQSQEAAKAKEVLPAIRG  
YVHYFFGCRDCASHFEQMAASMHRVGSPNAAVLWLWSHNRVNARLAGAPSEDPQFPKVQWP  
PRELCSACHNERLDVPVWDVEATLNFLKAHFSPSNIIIDFPAAGSAARRDVQNVAAPELAMG  
ALELESRNSTLDPGKPEMMKSPTNTTPHVPAGEASRPPKLHPGLRAAPGQEPPEHMAELQR  
NEQEQLGQWHLSKRTGALLAESRAEKNRLWGPLEVRRVGRSSKQLVDIPEGQLEARAGR  
RGQWLQVLGGGFSYLDISLCVGLYSLSMGLLAMYTYFQAKIRALKGHAGHPAA

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 705-728

**N-glycosylation sites.**

amino acids 130-134, 243-247, 575-579

**Glycosaminoglycan attachment site.**

amino acids 6-10

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 644-648

**N-myristoylation sites.**amino acids 52-58, 56-62, 196-202, 381-387, 392-398, 448-454,  
468-474, 684-690, 702-708**Cytochrome c family heme-binding site signature.**

amino acids 509-515

**Thioredoxin family proteins**

amino acids 62-78

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**FIGURE 213**

GCACGAGGCCGACTTCCAGACCATCTACAAC TGACGGCCTGGAACAGCTTCGGCTCCGACAC  
TGAGATCATCCGGCTCAAGGAGCAAGGTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGA  
GTCTGTGCCGATGGCCGT CATCATTGGGTGGCGTAGGAGCTGGTGTGGCCTCCTCGTCCT  
TATGGCAACCATCGTGGCGTTCTGCTGTGCCGTTCCCAGAGAAATCTCAAAGGTGTTGTGTC  
AGCCAAAATGATATCCGAGTGGAAATTGTCCACAAGGAACCAGCCTCTGGTCGGGAGGGTGA  
GGAGCACTCCACCATCAAGCAGCTGATGATGGACCGGGGAATTCCAGCAAGACTCAGTCCT  
GAAACAGCTGGAGGTCTCAAAGAACAGGAGAAAGAGTTTCAGAACCTGAAGGACCCCACCAA  
TGGCTACTACAGCGTCAACACCTCAAAGAGCACCACTCAACCCGACCATCTCCCTCTCCAG  
CTGCCAGCCCGACCTGCGTCCTGCGGGTAAGCAGCGTGTGCCACAGGCATGTCCCTCACCAA  
CATCTACAGCACCC TGAGCGGCCAGGGCCGCCTCTACGACTACGGCAGCGGTTGTGCTGGG  
CATGGCAGCTCGTCCATCGAGCTTGTGAGCGGGAGTTCCAGAGAGGGCTCCCTCAGCGACAG  
CAGCTCCTCTGGACACCGAGCTGTGACAGCAGCGTCAGCAGCGGCCAGCAGGATGGCTA  
TGTGCAGTTGACAAGGCCAGCAAGGCTTCTGCTTCTCTCCCACCACTCCAGTCCTCGTC  
CCAGAACTCTGACCCAGTCGACCCCTGCAGCGCGGATGCAGACTCACGTCTAAGGATCACA  
CACCGCGGGTGGGACGGGCCAGGGAAAGAGGTCAAGGCACGTTCTGGTGTCCAGGGACGAGG  
GGTACTTTGAGAGGACACCAGAAATTGCCACTTCCAGGACAGCCTCCCAGGCCCTGCCAC  
TGCCTCCTCGAAGCTCTGATCAAGCACAATCTGGGTCCCCAGGTGCTGTGCTGCCAGAGGT  
GGGCGGGTGGGAGACAGACAGAGGTGCGGCTGAGTGCCTGTGCTTAGTGTGGACACCCG  
TGTCCCCGGCCCTTCCTGGAGGCCCTCTACCACCTGCTCTGCCACAGGCACAAGTGGCAG  
CTATAACTCTGCTTCATGAAACTGCGGTCCACTCTCTGGTCTCTGTGGCTCTACCCCTC  
ACTGACCACAAGCTCTACCTACCCCTGTGCCGTGCTCCATACAGCCCTGGGAGAAGGGGA  
TGACGTCTCCAGCACTGAGCTGCCAGAAACCCGGCTCCCACTGCTGCTCATAGCCA  
TACCCCTGGAGGCTGACAAGCCAGAAATGCCCTGGCTAAAGGAGCCTCTCTCACCGAGCTG  
GCCGGGAGCCCACCCCAATTGTTGGTGTGCTACTCTTGCAAGTTCTGTGCTTGTG  
GACTTGATGCCGCTGAACTCTGCGGTGGACGGTCCCGTCAGAGCCTGGTGTACTGGGGGA  
GGGAGGGAGGAGGGAGCCTGTGCTGAGCGACCTCGCCGGTGTGCCCTCTGGCTGTG  
TGACCCAGCCTCCCCACCCACCTCTGCTTGTACTCTCCCTCCCTCAGCACAATC  
GGAGTTCATATAAGAAGTGCAGGGAGCTCTGGTCAGGGTTCTGAAACACTTATGGAGAGA  
GTGCTTCTGGGAAGTGTGGCGTTGAAGGGCTGGAGGGCAGGTCTTAAGATGGCAGACT  
GCCCTCTCAGCTGATAAACACAAGAACGGCGATCCTGCTTCAGTAAGGCTCCACGAGAAGA  
GAGGAAGTATATCTACACCTCAACCCCTCTAGTCACCACCTGAAATAATGTTAGGGAAAAAAA

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**FIGURE 214**

MAVIIGVAVGAGVAFLVLMATIVAFCCARSQRNLKGVVSAKNDIRVEIVHKEPASGREGEEHSTIKQLMMMDRGEFQQDSVLKQLEVLKEEEKEFQNLKDPTNGYSVNTFKEHHSTPTISLSSCQPDLRPAGKQRVPTGMSFTNIYSTLSGQGRLYDYGQRFVLGMGSSSIELCEREFGQRGSLSDSSFLDTQCDSSVSSSGKQDGYVQFDKASKASASSSHHSQSSSQNSDPSRPLQRRMQTHV

**Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 150-154

**N-myristoylation sites.**

amino acids 6-12, 10-16, 36-42, 139-145, 165-171

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 114-125

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**FIGURE 215**

CAGCCCTCCTCCCCAGCCTGAGTGACTACTCTATTCCCTGGTCCCTGCTATTGTCGGGGACG  
ATTGCATGGGCTACGCCAGGAAAGTAGGCTGGGTGACCGCAGGCCTGGTGATTGGGCTGGCG  
CCTGCTATTGCATTATAGACTGACTAGGGGAAGAAAACAGAACAGAAGGAAAAATGGCTGAGG  
GTGGATCTGGGATGTGGATGATGCTGGGACTGTTCTGGGCCAGGTATAATGACTGGCTG  
ATGATGATGATGACAGCAATGAGAGCAAGAGTATAGTATGGTACCCACCTGGCTCGGATTG  
GGACTGAAGCTGGAACCAGAGCTAGGCCAGGGCAAGGCCAGGGCTACCCGGCACGTGGG  
CTGTCCAGAAACGGGCTTCCCCAATTCAAGATGATACCGTTGTCCCCTCAAGAGCTACAAA  
AGGTTCTTGCTTGGTTGAGATGTCGAAAAGCCTATATTCGAAAGCAGCTTAATTGCTC  
TGGGTAACAATGCTGCTTATGCATTAAACAGAGATATTTCGATCTGGGTGGTCTCCAA  
TTGTCGCAAAGATTCTCAATACTCGGATCCCAGTTAAGGAAAGGCTTAATTGCTG  
ATAACTGAGTGTGAATGCTGAAAATCAGCGCAGGCTTAAAGTATACATGAATCAAGTGTG  
ATGACACAAATCACCTCTCGCTGAACTCATCTGCGAGCTGCTGGACTGAGATTGCTTACAA  
ATATGACTGTTACTAATGAGTATCAGCACATGCTGCTAACTTCGACTTGTGACTTTTCGTT  
TATTTCAAGCGGGAAATGAAGAACCAACTTCAGGTTCTGAAACTCCTTGAATTGGCTG  
AAAATCCAGCCATGACTAGGGAACTGCTCAGGGCCAAGTACCATCTCACTGGCTCCCTCT  
TTAATAAGAAGGAGAACAAAGAAGTTATTCTAAACTCTGGTCATATTGAGAACATAAATG  
ATAATTCAAATGGGAAGAAAATGAACCTACTCAGAACATTCGGTGAAGGTTCACTTTTT  
TCTTTTAAAAGAATTCAAGTGTGCTGATAAGGTTCTGGGAATAGAAAGTCACCATGATT  
TTTGGTGAAGTAAAAGTGGAAAATTCACTGCCAAACTGCTGAACATATGTTCCAAAGA  
GCCAGGATAACACCTTGATTTGTAATTAGAACACACATTGAAACTATTCAATTTC  
TCCACCTTGTATATGGTAAAGGAATCCTTCAGCTGCCAGTTGAATAATGAATATCATA  
TTGTATCATCAATGCTGATATTAACTGAGTTGGCTTAAAGATGGATAATGAATA  
TCACTACTTGTCTGAAAACATGTTGCTTTTATCTCGCTGCCTAGATTGAAATATT  
GCTATTCTCTGCATAAGTGACAGTGAACCAATTCAATGAGTAAGCTCCCTGTCATT  
TTCATTGATTAAATTGTGTATCATCAATAAAATTGTATGTTAATGCTGGAAAGA

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**FIGURE 216**

MGYARKVGWVTAGLVIGAGACYCIYRLTRGRKQNKEKMAEGGSGDVDDAGDCSGARYNDWSDD  
DDDSNESKSIVWYPPWARIGTEAGTRARARARARTRARRAVQKRASPNSDDTVLSPQELQKV  
LCLVEMSEKPYILEAALIALGNNAAYAFNRDIIRD LGGLPIVAKILNTRDPIVKEKALIVLNN  
LSVNAENQRRLKVMQNCDDTITSRLNSSVQLAGLRLTNMTVTNEYQHMLANSISDFRRLF  
SAGNEETKLQVLKLLLNLIAENPAMTRELLRAQVPSSLGSLFNKKENKEVILKLLVIFENINDN  
FKWEENEPTQNQFGEGLFFFKEFQVCADKVLGIESHHDFLVKVKVGKFMAKLAEHMFPKSQE

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 68-72, 189-193, 217-221, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-111

**N-myristoylation sites.**amino acids 13-19, 17-23, 19-25, 54-60, 83-89, 147-153, 255-261,  
290-296**Amidation site.**

amino acids 29-33

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## FIGURE 217

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**FIGURE 218**

MAIAQQLATEYVFSDFLLKEPTEPKFKGLRLEAVDKMVTCAVGLPLLLISLAFQAQEISIGTQ  
ISCFSPPSSFSWRQAAFVDSYCWAQQKNSLQSESGNLPWLHKFFPYILLFAILLYLPPLF  
WRFAAAPHICSDLKFIMEELDKVYNRAIKAAKSARDLDMRDGACSVPGVTENLGQSLWEVSES  
HFKYPIVEQYLTKKNSNNLIIKYISCRLLTIIILLACIYLGYYFSLSSLDEFVCSIKSGI  
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVVVLLAPVVVYTLFVFPFRQKTDVLKVYEILPTF  
DVLHFKSEGYNDLSLYNLFLEENISEVKSYKCLKVLENIKSSGQGIDPMLLLNLGMIKMDVV  
DGKTPMSAEMREEQGNQTAELQGMNIDSETKANNGEKNARQRLLDSSC

**Transmembrane domains:**

amino acids 37-55, 108-126, 216-232, 273-290

**N-glycosylation sites.**

amino acids 255-259, 338-342, 394-398

**Glycosaminoglycan attachment site.**

amino acids 357-361

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 203-207

**N-myristoylation sites.**

amino acids 61-67, 174-180, 251-257, 393-399

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 218-229

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**FIGURE 219**

CTGTGAGTGACACACGCTGAGTGGGGTAAGGGAAATGCTGGTGAATTCA~~T~~TTGAGGTGTG  
GGTTGCTGTTAGTCACTCTGTCTTGC~~C~~ATTGCCAAGCACAAGCAATCTTC~~C~~TTCACCAAAA  
GTTGTTACCCAAAGGGAACATTGTC~~C~~CAAGCTGTTGACGCTCTATATCAAAGCAGCATGGC  
TCAAAGCAACGATTCCAGAACAGCCGCATAAAAAAATACGATTATTA~~A~~AAAAGAAAACAAAAA  
AGCAGTTATGAAAAACTGTCAATTCAAGAACAGCTTCTGTC~~C~~TTCATGGAAGACGTT  
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTGTGGAGGACTTCATAGCCTTA  
GGCAGAAATTGAGCCACTGTATTCCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA  
GGATGAAAAGAATATTTATAGGATTGAAACAAAGGAATCTACAAAGCCATCAGTGA~~A~~CTGG  
ATATTCTTCTTC~~C~~GGATTAAAAAATTATTGAAAGCAGTCAGTAAACCAAGCCAAGTACA  
TTGATTTACAGTTTTGAAATACAATAAGAACTGCTAGAAATATGTTATAACAGTCTAT  
TTCTTCTTAAACCTTAA~~C~~ATAACTGACGGCATGTTAGGTGATT~~C~~AGAATAGACAAGAA  
GGATTAGTAAATTAAACGTTGGATATAAGTGTCACTAATTGCACATTCTGTGTTTC  
AAATAATGTTCCATTCTGAACATGTTGTCA~~T~~TCACAAGTACATTGTGTCAACTTAATTAA  
AAGTATGTAACCTGAATTAAC~~T~~CGTGAATATTGTGTGGAGTGGATGTGGGGGTGGAG  
GGGAATGACAGATTCTGGAATGCAATGTAATGTTACTGAGACTAAATAGATGTTATGTAT  
ATGATTGTCTGTTAAGTGTGAAATTGTTAATTGCCAGTGTGA~~A~~CTTAGTACTTAAC  
ACATTGATTAAATTAAATTGGTTCTCAAAAAAAAAAAAAAAA  
AAAAA

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**FIGURE 220**

MLVNFI~~LRCG~~LLVTL~~S~~AI~~A~~KHKQSSFTKSCYPRGTLSQAVD~~ALYIKA~~AWL~~KATI~~PEDRIKN  
IRLLKKKT~~KKQFM~~KNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSLRQKLSHCISCAS  
SAREMKSITRMKRIFYRIGNKGIYKAISEL~~DILL~~SWIKKL~~LESS~~Q

**Signal sequence:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 148-153

**Interleukin-10 proteins.**

amino acids 58-94, 74-102, 128-170

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**FIGURE 221**

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCAGGCCGGCGGCCGTGCCGCTCC  
TGCTGCTGCTGTGTTGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCAGGA  
TGCTGAACCGAATGGTGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA  
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGTCCTGACGG  
CTGCGCACTGCTTCCGAAACACCTCTGAGACGTCCCTGTACCAGGTCTGCTGGGGCAAGGC  
AGCTAGTGCAGCCGGGACCACACGCTATGTATGCCCGGGTGAGGCAGGTGGAGAGCAACCCCC  
TGTACCAAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAGTGCCT  
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTGAGACGGGCATGA  
ACTGCTGGGTCACTGGCTGGGCAGCCCCAGTGAGGAAGACCTCTGCCGAACCGCGATCC  
TGCAGAAACTCGCTGTGCCCATTCGACACACCCAAAGTGCAACCTGCTCTACAGCAAAGACA  
CCGAGTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCCGGCTTCGAGGAGG  
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGCCCTGGTGTGCCTCGTGGGTCAAGTCGT  
GGCTGCAGGCAGGGGTGATCAGCTGGGTGAGGGCTGTGCCGCCAGAACCGCCCAGGTGTCT  
ACATCCGTGTACCGCCCACCAACTGGATCCATCGGATCATCCCCAAACTGCAGTTCCAGC  
CAGCGAGGTTGGCGGCCAGAAGTGAGACCCCCGGGCCAGGAGCCCTTGAGCAGAGCTCG  
CACCCAGCCTGCCGCCACACCATCCCTGCTGGTCCTCCAGCGCTGCTGTTGCACCTGTGAG  
CCCCACCAACTCATTGTAAATAGCGCTCCTCCCTCTCAAATACCCCTTATTTATTT  
ATGTTCTCCAATAAAACCCAGCCTGTGTGCCAGCTGAAAAA

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**FIGURE 222**

MRRPAAVPLLLLCFGSQRAKAATAACGRPRMLNRMVGGQDTQEGERWPWQVSICRNGSHFCGGS  
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA  
LVELEAPVPFTNYILPVCLPDPSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP  
KCNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEG  
CARQNRPGVYIRVTAAHNWIHRIIPKLQFQPARLGGQK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 55-58, 79-82

**Casein kinase II phosphorylation sites.**

amino acids 121-124, 165-168, 167-170, 248-251

**Tyrosine kinase phosphorylation sites.**

amino acids 78-86, 197-203

**N-myristoylation sites.**

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

**Amidation site.**

amino acids 219-222

**Serine proteases, trypsin family, histidine active site.**

amino acids 71-76

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**FIGURE 223**

CAAGATGTGGACAGCTTGTGCTATTGGATTTCTCCTGTCCCTATCTGAAAGCCATGC  
GGCATCCAACGATCCACGCAACTTGTCCCTAACAAAATGTGGAAGGGATTAGTCAGAGGAA  
TGCATCTGTGAAACAGTGATAATAACGTCTGAGGATGTAACCATGGCAGCAGCTTCTCC  
TGTACATTGACCAAAGGGACTTCGGCAGCCCACCTCAACTCTATGGAAGTCACAACAGAGGA  
CACAAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC  
CATTGCTCCCACGGCTGTGGCCTCCAGTACGACTGCGGCCCTCCATTACGACTGCGGCCCTCCAG  
TATGACTGTGGCCTCCAGTGCTCCACGACTGCGCCCTCCAGTACAACGTGGCCTCCATTGC  
TCCCACGACTGCGCCCTCCAGTATGACTGCGCCCTCCAGCAGTACCCATGACACTTGCACCTCC  
CGCGCCCACGTCCACTTCCACAGGGCGGACCCGTCCACTACCGCCACTGGGCATCCATCTCT  
CAGCACAGCCCTCGACAAGTGCACAGAGCAGCGCGTTGCCAAGAACAGCAACCCCTGGCCAC  
ATTGGCCACACGTGCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG  
TCCAAGTCCTTCCAAGCACATGCCAGTGACACCGCGGCAAGCCCTGTACCCCTATGCGTCC  
CCAAGCACAAGGTCCCATTAGCCAGGTGTCAGTGGACCAGCCTGTGGTTAACACAACAAATAA  
ATCCACACCCATGCCCTCAAACACAACCCAGAGCCCGCCCCACCCCCACAGTGGTACCC  
CACCAAGGCACAAGCCAGGGAGCCAAGTGCAGCCAGTACCTCACACCAGCCAAT  
CCCTGAGATGGAGGCCATGTCCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC  
CGCTGGGCCAGGCACATCCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA  
TTCCACTGGCCAACACCCAGGAGCTCAGGGGCACTAACAGATGCCAGCCACGGACTCGTGCCA  
GCCAGCACCAAGGCCAGTACATGGTGGTCACCAACTGAGCCCTCACCCAGGCCGTGGTAGA  
CAAAACTCTCCTCTGGTGGTGTGTTACTCGGGGTGACCCCTTTCATCACAGTCTGGTTTT  
GTTTGCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGACTACTTAAT  
CAACGGGATGTATGCCAGACTCAGAAATGTGA GGGGGCGGGGGCTGGCGGGAGGCCTGGCC  
CTTCCTCGCTTCTTGCCTTGAGACCAAAACCAAGTGTCCAAATTCTTGGTGCA  
ATTGAGGAGATATGCCAGATGCTAAACACATTAATTGCTGTCAAGATTAATTCCATGATCAC  
TAAAGAGTTGCTGCTTTTCAATTATTTGTAAATGATTCTGTGCCAGGAGCAGCTGG  
GGGTTCCACCTCAGGGTGGGCGGGCAGGACCCGTCTCCCCAGGTGTCGGAGCCTGACCTGA  
ATTAAAGTACTGACTGCTCGCCA

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**FIGURE 224**

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAASPV  
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM  
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPCLS  
TALAQVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQ  
AQGPISQVSVDQPVVNTTNKSTPMPSNTTPEPAPTPTVVTTKAQAREPTASPVPVPHTSPIP  
EMEAMSPTTQPSPMPYTQRAAGPGTSQAPEQVETEATPGTDSTGPTPRSSGGTKMPATDSCQP  
STQGQYMVVTTEPLTQAVVDKTLLLVLLGVTLFITVLVLFALQAYESYKKDYTQVDYLIN  
GMYADSEM

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 396-420

**N-glycosylation sites.**

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

**Casein kinase II phosphorylation sites.**

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

**N-myristoylation sites.**

amino acids 68-73, 354-359

**Aldo/keto reductase family putative active site signature.**

amino acids 195-210

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**FIGURE 225**

GGAAGGCCTCAAGGTGCGCGCCGGGGCGCGCTACTGGGGCCTCCGGTGGCAGC  
GCGCCAGGGATCGGCCTGGCAGCCGGGGCGCGAAGGCTGCGCTTCCCTACGGCCCC  
CTCGCTTCCTCCGGCACGGCAACGGAGATTCCTCTCGGGAAACTACGGATCCTTT  
CGGGGATCCTCGCCCCGCCAGTTCTCCGCCCTCCCTTGCTGGGCGCTGGCTGGC  
CCGCGCAGGGGAGGGAGGCTCTGGCAGCCTGGCAGGGAGGCGGGGGCCGGAGCCGCT  
GCCATCGATTCTCCCGCCATGTGACGCCCTTAGCCCTGCAGCCCCAGCGCTCCGG  
GCCTGCGCCTCCGCCCGCCGCAGCGCACG**A**TGCTCTGCCGGACGCGACGCCAACGC  
CGACGCCAGCCCCTGCAGCATCCGCCCTCCGCCGGCAGGTAGAGCCGGGGCAGCTCC  
TGCCTCTTCACTGCACTGCTCTGGCTGCTCCAAAGAGATCTAGCGCTACCGACTTCT  
CTGGTTACCTAACCAAACCTCTGCAAAACCACACCCTATGCCTGTGATGGGACTATTGA  
ATCTACAGTGCCCTCGGATTCTACGATAAGTGTCCAATCGGCATTATGGCAAGATTACC  
AAATGTGTAGTCCCAGAACGCTGCCCTCCAGAGGGAAAGACAGCTTAACCTGTGAGCCA  
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACAGCAGGGCCTGCCACCTCTGGTCAATA  
GCCGTGTTTGGACCTGACCTTGCCAGGAAGCAGTAAATACCTCTGGTCTCTTAAAT  
GCCAACCTAATGAATTAAAAACAAAACCGTGTGAAGACCAGGAGCTGAAACTGCACTGCC  
ATGAATCCAAGTCCCTAACATCTACTCTGCACCTACGGCAGGAGGACCCAGGAAAGGGACA  
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCTTCGATTGCTTACTCAGCTTGAAG  
TCCTATCCCAGGAGTGCTATGGGAAGCAGAGATGCAAAATCATGTCACAAATCACCATTG  
GAAGCCCTGTTGCCAGGGTGAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAACCTCTTGAGCAGAAAGATG  
GTGAATATGGTATAAAACTTCGACCCAGCGGATCGAAGGGTCTGAGGAAAGATGGAATTCTG  
TTAGCAACTCTCTGGCAGCCTTGCTTACATTAGAGCCACCCAGAGAGAGCTGCCCTGCTGT  
TCGTGTCCAGTGTCTGCATGCCCTGCCCTCACACTGTGCCCTGGTCATCAGAGAGCT  
GTGCCAAGGACTCCGCGACTTGCAGCTGGGAGGGAGCAGCTGGTGCAGGAAGTGACAAGG  
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTTGAGTCTGATTCCCAGGG  
AACTGTCGGGTTCTGTAGGACTTCATATCCTATACAGTTCCATAGAAGCTGCAGAGCTCG  
CAGAAAGGATTGAGCGCAGGGAGCAAATCATTAGGAAATATGGATGAACAGTGGTTGGACA  
CCTCGCTCCAAGAACATGGCCAGTTCTACT**TG**AAAACACATGCATCTGATGCGATCGCA  
CTTCTGAAGAAGGAAGGATCCAAATGCCCTCCAGTTGTTCACCTGTACCTCTATGA  
AGGAGAATTGTCATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAAGGGATGTTCAA  
GCTGTTCTAGCACATTCCAAAATAATGAGGAGGGAGGAAAAA  
AAAAAAAAAAAAA

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**FIGURE 226**

MLLPGRARQPPTPQPVQHPGLRRQVEPPGQLLRLFYCTVLVCSKEISALTDFTSGYLTKLLQNH  
TTYACDGDYLNLCPRHSTISVQSAFYGQDYQMCSSQKPASQREDSLTCVAATTFQKVLDECQ  
NQRACHLLVNSRVFGPDLCPGSSKYLLVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA  
TYGRRTQERDICSSKAERLPPFDCLSYSALQVLSRRCYGKQRCKIIVNNHHFGSPCLPGVKKY  
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEYGINFDPSGSKVRKDGILVSNSLAAFAYI  
RAHPERAALLFVSSVCIGLALTLCALVIRESAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE  
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMSGLDTSLPRNMGQFY

**Transmembrane domains:**

amino acids 32-49, 322-343

**N-glycosylation sites.**

amino acids 62-66, 165-169

**Tyrosine kinase phosphorylation site.**

amino acids 280-287

**N-myristoylation site.**

amino acids 302-308, 333-339, 428-434

**Amidation site.**

amino acids 191-195

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**FIGURE 227**

GGCACGAGGTGGAAGGGCTTTACAAACAGATTGCTGGCCCCACCCCCCAGAATTCTCATCA  
GGAGTGGGCAAGACCAATCATTGCATTCTGACAAGTCCCAGGAGCTGCAGCTGCTGGCCC  
TGGAAACCACACTTGAGAACCACTGCTTAGACCAAACACCAAAGGAAGATGCAGCCACCC  
CTTTACATGTCACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG  
CAGCAGCCGAGATTCCCAGTCGCTCCACCATTGGGGCTAGGAGTGAAGCGTGTCA**CCATGG**  
TCAGCTCATGGCCAGGCCAGGAAAGCCTCTGTGCTGTGCGTCTGTGCAGTTCTGTTCTCC  
GGAGGACTCTGGATGCCGTGATCTGGCCAGGAGACCAGGTGCCTGGTCCCTTCCTGGA  
AGGGGACAAGTTACACACCCCCAGCCCCATTTCACCAACTTCTACATGCCCTGGAGAAC  
TTCTACATGTTGGCTGCCCTTCCCTATTCAGCAGTGCCTGCTTATAAACCTGA  
GGCCTGCTCCCCATACCTCCCTGTGCAAGTGCCAGCCGTATTCCAGGCAGCCAATGTTGT  
TGAGGCCAGATGGATTCCCTGGAAGCAGCTGGCCATGGATG**TGAG**TCACTACAGTATTCTAGA  
AACAGAGAAGAGGTCTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCC  
GTCCTTAGCTGATCTAGGTGGAAGCCCAGCTCATGTGCTAGGGGCATGATAATGATAATAA  
AGGAATTGTATCTAGGACTAA

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**FIGURE 228**

MVSSWPARKASLLCVCAVLVLPWRTLGSPIVARRPGAWPSWKTSYTPQPHFPTNFYMPWE  
NLLHVGCPLPLFQQCPVILLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFLLEAGPWM

**Signal peptide:**

amino acids 1-27

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 8-12

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**FIGURE 229**

GGGAAGGGATGCAAGGAAGCCCTCCGGCGCTCGCCTCCAGGCAGGAGACAGCGTCCCCGTGA  
 AAATGTGTGTCTGACATGCAAGCTCAGTGGGCAGAGACCCGTGGATTGCTGTGCCCTGCCCT  
 CCGGACCTGGATC**ATGA**AGGTGTTGGGAAGAAGCTTCTCTGGGTGCTGTTCCGTCTTCC  
 CTGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACGTGACCCGG  
 GCGAGGGGTGGCTGCCATGCAGAGCCGCAGTGGTCCGGACAGCTGCAGGAAGCTCAGG  
 GCTTCCTCCGCCAGAAGAAATGCAGTTCTGAACAAAAGTGAAGAAACTGCAATTGGAGCAGTGGAGAA  
 AGACGTGGGCCTGTCGGATGAAGAGAAACTGTTCAGGTGCACACGTTGAAATTTCAGAA  
 AGAGCTGAATGAAAGTGAAGAAATTCCGTTTCCAAGCTGTCTACGGACTGCAGAGAGCCCTGCA  
 GGGGGATTACAAAGATGTCGTGAACATGAAGGGAGCAGCCGGAGCAGCCTGGAGGAGCCCTGAG  
 AGAGGCTGCAATAAGGAAGAACAGAATATATGAACTTCTGGCAGCAGAAAAACATCAAGT  
 TGAAGCCCTAAAAATATGCAACATCAAACCAAAGTTATCCATGCTTGACGAGATTCTTGA  
 AGATGTAAGAAGGCAGCCGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTGACGACAA  
 TAAATCAGTCAGGGGTCATTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC  
 TAAGAAAATATAACAAAACGAGAAAGTGGAGGATGACTGGGTCTAGCATGCTGATTGACTC  
 CCAGAACAAACCAGTATATTGACCAAGCCCAGAGATTCAACCATCCCACGTGCAGATCACCA  
 CTTTATAAAGGACATTGTAACATAGGAATGCTGTCCTGCCTTGCTGGCTATGTACAGC  
 CATAGGATTGCCTACAATGTTGGTTATATTATTTGTGGTGTACTCTGGACCTTCAGGACT  
 AAATAGTATTAAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTGGGTGTTTTTACTCT  
 TTTCTTGTGGCTTAGAATTCTCAGAAAAGCTAAGAAAGGTGTGGAAGATTCCCTTACA  
 AGGGCGTGTACATGACACTGTTAATGATTGCATTGGCTTGCTGTGGGGCATCTTGC  
 GATCAAACCCACGCAGAGCGTCTTCATTCCACGTGTCTGTCCTGTCAAGCACACCCCTCGT  
 GTCCAGGTTCCATGGGAGTGCCTGGGTGACAAAGAAGGCAGATTGACTACAGCACCGT  
 GCTCCTCGGCATGCTGGTACGCAGACGTGCAGCTCGGGCTTCTCATGGCGTATGCCGAC  
 TCTCATACAGGCGGGGCCAGTGCATCTCTAGCATTGCTGGAAAGTTCTCGAATCCTGGT  
 TTTGATTGGTCAGATTCTTTTCACTAGCGGGTTTTCTTTATGTCTTGTATAAAGAA  
 GTATCTCATTGGACCTATTATCGGAAGCTGCACATGAAAGCAAGGGGAACAAAGAAATCCT  
 GATCTGGGAATATCTGCCTTATCTTAACTGTTAACGGTCACGGAGCTGCTGGACGTCTC  
 CATGGAGCTGGCTGTTCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCACCGA  
 GGAGATGCCACCTCCATCGAACCCATCCGCACTTCTGGCCATCGTTCTGCCTCCAT  
 AGGGCTCCACGTGTTCCCCACGTTGTGGCGTACGAGCTCACGGTCTGGTGTTCCTCACCT  
 GTCAGTGGTGGTGTGAAGTTCTCTGGCGGGCTGGTCTGTCTCATCTGCCGAGGAG  
 CAGCCAGTACATCAAGTGGATCGTCTGCAGGGCTTGCAGGTACGAGTTTCTTGT  
 CCTGGGGAGCCGGCGCGAAGAGCGGGCGTCATCTCTGGAGGTGACCTCTTATACTGAG  
 TGTGACCACGCTCAGCCTTGTCTGGCCCCGGTGTGGAGAGCTGCAATCACGAGGTGT  
 GCCCAGACCGGAGAGACGGTCCAGCCTC**TGA**TGGCTCGGAGATGATGGACCGTGGAGGGAAAG  
 CGTCTGTGGGGAGTGAGCGCTTAGATGGCAGCAGCTGCTCTCTGGGAAGCTCGCACCTG  
 GCAACAGAACAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCGGCTTTACAGAATA  
 TTCTTGCTCTATTAGAATTTCGGAGTAGTTATTGCAAGTGTGATTATGTGCAAGTA  
 GACCCGGACACTGCGTTTACCGATCACCTGAATGTGGTGCCTGGATGTGCCCTTTTT  
 TTCCCTGAAATTATTAAATTCTATTGTGAGTTCATCAGTTCATAGTTTTTAGAA  
 GAAGCAAAATTAAAGGCTTTAAAATGTACAACCTCAGAATTATAATCTGTTAGTCAAATA  
 TTTGTTATTAAACATTCTGTAATATGAAGTTGTAATCCTGGCGTGGAGCTGGAGCTACT  
 TTTGATTCTTAAAGCCTATGTTCTAAAATGAGACAAATACGGATGTCTATTGCCTTTAT  
 TGTAACCTTAAATGAAATAATTGATGTCAATTCTATTAGATATATCACTAAAATATTG  
 GTTTAAATCACAAGAATATGTATTCTTAATAAAGATAATTGATCATGGTAAAAAAAAAA

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**FIGURE 230**

MKVLGRSFFWVLFVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQWVRDSCRKLSGLLRQ  
KNAVLNKLKTAIGAVEKDVGSLDEEKLFQVHTFEIFQKELNESENSVFQAVYGLQRALQGDYK  
DVVNMKESSRQRLEALREAAIKEETEYMELLAAEKHQVEALKNMQHQNQSLSMLEIILEDVRK  
AADRLEEEIEEHAFDDNKSVGVNFCAVLRVEEEANSKQNITKREVEDDLGLSMLIDSQNNQ  
YILTKPRDSTIPRADHHFIKDIVTIGMLS LPCWLCTAIGLPTMFGYIICGVLLGPSGLNSIK  
SIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPCYMTLLMIAFGLLWGHLRIKPT  
QSVFISTCLSSTPLVSRLMGSARGDKEGIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQA  
GASASSSSIVVEVRLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRKHLHESKGKNEILILGI  
SAFIFLMLTVTELLDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV  
FPTFVAYELTVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR  
ARRAGVISREVYLLILSVTTLSSLAPVLWRAAITRCVPRPERSSL

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,  
576-598, 641-660**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 55-59, 673-677

**Tyrosine kinase phosphorylation site.**

amino acids 407-414

**N-myristoylation sites.**amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,  
442-448, 525-531, 530-536**Cell attachment sequence.**

amino acids 404-407

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**FIGURE 231**

GAGAAAAACAACAGGAAGCAGCTTACAAACTCGGTGAACAACTGAGGGAACCAAACCAGAGAC  
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAAGTGGGCAGAGATTCCACCAGGACTG  
GTGCAAGGCGCAGAGCCAGGCCAGATTGAGAAGAAGGCAAAAGATGCTGGGGAGCAGAGCTG  
TAATGCTGCTGTTGCTGCCCTGGACAGCTCAGGGCAGAGCTGCTGCCTGGGGCAGCAGCC  
CTGCCCTGGACTCAGTGCCAGCAGCTTCACAGAAGCTCTGCACACTGGCCTGGAGTGCACATC  
CACTAGTGGCACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC  
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC  
AAAGGATCCACCAGGGCTGATTTTATGAGAAGCTGCTAGGATCGGATATTTCACAGGGG  
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTCATGCCCTCCACTGGCCTCAGCC  
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCCAAGCCTCAGTCCCAGCC  
AGCCATGGCAGCGTCTCCTCTCCGCTTCAAATCCTCGCAGCCTCCAGGCCTTGCTG  
TAGCCGCCCGGGCTTGGCCATGGAGCAGCAACCCTGAGTCCCTAAAGGCAGCAGCTCAAGG  
ATGGCACTCAGATCTCATGGCCCAGCAAGGCCAAGATAAAATCTACCACCCAGGCACCTGTG  
AGCCAACAGGTTAATTAGTCATTAATTTAGTGGACCTGCATATGTTGAAAATTACCAATA  
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGGAAATT  
TGGGGATTATTTATCCTCCTGGGACAGTTGGGAGGATTATTTATTGTATTTATATTGAAT  
TATGTAACCCCCCAATAAGTCTTATTTGTGGCTAAAAAAAAAAAAAA

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**FIGURE 232**

MLGSRAVMLLLLPWTAQGRAVPGGSSPAWTQCQQQLSQKLCTLAWSAHPLVGHMDLREEGDEE  
TTNDVPHIQCGDGCDPQGLRDNSQFCLQRHIHQGLIFYEKLLGSDIFTGEPSLLPDSPVGQLHA  
SLLGLSQLLQPEGHHWETQQIPSLSPSQWPQRLLLRFKILRSLQAFVAVAARVFAHGAATLSP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Casein kinase II phosphorylation site.**

amino acids 64-67

**N-myristylation sites.**

amino acids 25-30, 81-86, 122-127

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**FIGURE 233**

CCCACCGCGTCCGGCCCTGTAACCAAGATACTGACTGACATGGCTGGCGACTCAGGCTGGGTCTGCAGTGCAG  
 CATTAAATGGGCCGCTGACATGAATATGGAGTAGTTCTCTAGCAAAGAGTAATGTGGGCCATGGAGTCAGGCCA  
 CCTCCTCTGGGCTCTGCTGTCATGCAGTCTTGTCAGCTCAACTGACTGATGGAGCCACTCGAGTCTACTACCT  
 GGGCATCCGGGATGTGCAGTGAACATATGCTCCAAAGGAAGAAATGTCATCACGAACCAGCCTCTGGACAGTGA  
 CATAGTGGCTTCCAGCTTAAAGTCTGACAAGAACCGGATAGGGGAACCTACAAGAAGACCATCTATAAAGA  
 ATACAAGGATGACTCATACACAGATGAAGTGGCCAGGCTGCTGGTGGCTCTGGGGCAGTGTGAGGC  
 TGAAGTGGGGATGTCTTCTATTCACTGGAAAGAATTTCGCCACTCGTCCCTATACCATCCACCTCATGGT  
 CTTCTACGAGAAGGACTCTGAAGGTTCCCTATACCCAGATGGCTCTGTCAGCTGAAAGCTGATGACTCTGT  
 TCCCCGGGGGGCAGCCATATCTACAACGGACCATTCAGAAGGGCATGACCCACCGATGCTGACCCAGCGT  
 CTCACCTGGATCTACCATTCTCATGAGATGCTCCACGAGACATTGCACTGGCTAATTGGCCCTCTCATCAC  
 CTGTAAGAGGAGCCCTGGATGGGAACCTCCCTCCTCACGCCAGGATGCTAGACCATGATTCTCCCTCT  
 CAGTGTGGTAGATGAGAACCTCAGCTGGCATCTCAATGAGAACATTGCCACTTACTGCTCAGATCCTGCTT  
 GGACAAAGAAGATGAGACATTCAAGGAGGACATAGGATGCTGCAATCAATGGCTTGGATGGAAATTAC  
 TGAGCTGACATGTGTCAGACAGAACCTGTGGCTGGCAACTTGGCATGGCAATGAAATTGATGTCACAC  
 AGCATTTCATGGACAGATGCTGACTACCCGGACACCACACTGATGTCAGATCTTCCAGCCACCTT  
 TGTGACTGCTGAGATGGTGCCTGGGAACCTGGTACCTGTTAATTAGCTGCCAGTGAACAGTCACTTICGAGA  
 TGGCATGCAGGCACTCTACAAGGTCAAGTCTGCTCATGGCCCTCTGTGGACCTGTCACAGGCAAAGTTCG  
 ACAGTACTTCATTGAGGCCATGAGATTCAATGGGACTATGGCCGATGGGGCATGATGGGAGTACTGGGAAGAA  
 TTGAGAGAGGCCAGGCACTGAGATAAGTTCCAGAAGAGCTCCAGCCGATTGGGGCACTTACTGGAA  
 AGTGGCATATGAACCTTCAAGATGAGAACATTCCAAGAGAAGATGCAATTGGAGGAAGATAGGCATCTTGAAT  
 CCTGGGGCCAGTGTGGGGCTGAGGTGGTGCACCAATTCAAGGTGCTTCTACAACCGTGCCTCCCAGCATT  
 CAGCATGCAGCCCCATGGGGCTTATGAGAAAGACTATGAGGCACTGTGTCATGCTATGTCATCTACCC  
 TGGCTGGTGCAGGCCAGGCTTGGAGAAAGTAACATACCGTGGACAGTCCCCCTCATGCCGGTCCCAGTGTCA  
 GGATCCTGCTGTCACTTGGATGTAATTCTCTGCTGAGATCCCATAAGGACACAAATTCTGGCTGGGG  
 CCCGCTGCTGGTGTGCAGGGCTGGTGCAGATGGCAAGCAGAAAGGGGTGGATAAAGAATTCTTCT  
 TCTCTTCACTGTGGATGAGAACAGAGCTGGTACAGCAATGCCAATCAAGCAGTGTCTATGTTGGATTCCG  
 ACTGCTTCAGAGGATATTGAGGGCTTCAAGACTCCAATCGGATGCTGCCATTATGGGTTCTGTTCTCAA  
 CCTGCCAGGGCTGGACATGTGCAAGGGTGCACAGTCAGGCTGGCACCTGCTGCCAGGGCACAGAGACTGATGT  
 GCATGGACTCATGTCCAGGGCAACACTGTGCAAGGCTGGCACATTGAGATTATGCCCTGACGGAGCTGGGAACGGGA  
 ATGGCACAAACAGTCTGAGAAGGACAGTTATGGTTACATTTCCTGAGCAACAAGGATGGCTCCGGGG  
 ATACAAGAAAGCTTACAGGAAATACACTGATGGTACATTAGGATCCCTGCCAAGGACTGGACCAAGAAGA  
 ACATTTGGGAACTTGGGTCACATTCAAAAGGTGAAGTTGGTGAATCTGACTGTGGTATTCAAGAATAATGC  
 CAGCCGCCCTACTCTGTGCTCATGGAGTGTGCAAGGACTGGCCATGGGGCTGGGCAACTGCTGCTGAGGCTGG  
 TGAGGGTCACTTATGAGGACATCCCAGAGAGGCTGGGCAATGACTCTGCTGCCAGGGACTGGCT  
 GATCTATTATTCTGCACTGGATCCCACAGGACATGTATAGTGGCTGGGGCTGGCTATCTGCCAAAA  
 GGGCATCCTGGAGCCCCATGGAGGACGGAGTGACATGGATGGGAATTGCAATTGCTGGTCTTGATTTGATGA  
 AAATAAGTCTGGTATTGGAGAAAATGGCAACCCATGGGCTCCAGGATCCAGGCACTATTAAACCTACAGGA  
 TGAAACTTCTGGAGAGCAATAAAATGCATGCAATCAATGGAAACTCTATGCCAACCTTAGGGGCTTACCAT  
 GTACCAAGGAGAACAGTGGCTGGTACATGCTGCCATGGGCAAGATGTGGATCTACACACCATCCACTTCA  
 TGCAGAGACTCTCTATCGGAATGGCGAATGGGAGAATACCGGAGATGTGGTGGATCTGTTCCAGGGACTTTGA  
 GGTTGGAGATGGTGGCCAGCAACCTGGACATGGCTGACTGCCATGTGACTGACCATGTCCATGCTGG  
 CATGGAGACCTCTCACTGTTCTCGAACAGAACATTAGGCCCTCAGGCAACAGGAGACTGA  
 AAAAGTCCCCCAGAGACATTGAGAAGGCAATGTGAAGATGCTGGGAGTGGAGCTGGCT  
 GATGCTGGCTCTGTTGGTGCATTAGTGTCACTGGCTGGCTGGGAGATGGCT  
 GTACCAACATCGACAGAGAAAGCTGACGCAATAGGAGGCTCATCTGGATGACAGCTCAAGCTTCTGCTT  
 CAAACAGTAAACATCTGGAGGCCAGTGGAGATCTCTCAGGAAGCACATCTGAGTGCACCTCCAGCAGGCCATGACT  
 AGTCACTAACCCACACTCAAAGGGCATGGGAGTGGAGAAGCAGAAGGGAGCAATCAAGCTTATCTGGATATT  
 CTTTCTTATTATTATGAGGAAATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
 GGCACAAAGGGAGTACCTTATTCTCATGGGAAATTCAACAGCTACATTATATTCTCTGACACTTGA  
 AGGTATTGAAATTCTGAGAATGATCTCTCAGGAAGTGGAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
 ACTTCTTCAAGGACTCAGGAAATTCACTTGAAGTGGGCAAGTGGCTGAGCTGAGCTGTTAAGATAACCCACACTAAAC  
 TAAAGGCTAAGAATATAGGCTGATGGGAAATTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
 CTCCCTGGCAGTGAACACTTGAAGAAGTGGTCAATGGGTTGTCATGCCAGGAGCATGTCACACCTCTGGAGC  
 TAGAAGCTCCTCAGGAAAGCCAGTTCTCAAGTTCTAACCTGTGGCACTGAAAGGAATGTTGAGTTACCTCTTC  
 ATGTTTAGACAGCAAACCTATCCATTAAAGTACTTGTAGACCAAAAAAAAAAAAA

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**FIGURE 234**

MWAMESGHLLWALLFMQLWPQLTDGATRVYLYGIRDVQWNYAPKGRNVITNQPLSDIVASS  
FLKSDKNRIGGYKKTIFYKEYKDDSYTDEVAQPAWLGFGLGPVLQAEVGDVILIHKNFATRPy  
TIHPHGVFYEKDSEGSLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTDADPACLTWIYH  
SHVDAPRDIATGLIGPLITCKRGALDGNSPPQRQDVHDFFLFSVVDENLSWHLNENIATYC  
SDPASVDKEDETFOESNRMHAINGFGVGNLPELNMCQAQKRVVAWLFGMGNEIDVHTAFFHGQM  
LTTRGHHTDVANIFPATFVTAEMLPWEPTGLWILSCQVNHF RDGMQALYKVKS CSMAPPV DLL  
TGKVRQYFIEAHEIQWDYGPMDGHDSTGKNLREPGSISDKFFQKSSRIGGTWVKVRYEAFQD  
ETFOEKMHLEEDRHLGILGPVIRAEVGDTIQVVFYRNASQPFMSQPHGVFYEKDYEGTVNDG  
SSYPGLVAKPFEKVTYRWTVP PHAGPTAQDPACLTWMYFSAADPIRTNSGLVGPLLVCRAGA  
LGADGKQKGVDKEFLLFTVLDENKSWYSANQAAAMLFRLSEDIEGFQDSNRMHAINGFL  
FSNLPRLDMCKGDTVAWHLLGLGETDVHGVMFQGNTVQLQGMRKGAAMLF PHTFVMAIMQPD  
NLGTFEIYCQAGSHREAGMRAIYNVSQCPHQATPRQRYQAARIYYIMAEEVEWDYCPDRSWE  
REWHNQSEKDSYGYI FLSNKDG LLSRYKKAVFREYT DGTFRIPR PRTGPEEH LGILGPLIKG  
EVGDILT VVFKNNASRP YSVHAHVLESTTVWPLAAEPGEVVTYQWNIPERSGPGPNDSACVS  
WIYSAVDPIKDMYSGL VGPLAICQKGILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT  
HGSQDPGSINLQDET FLESNKMHAI NGKLYANLRGLTMYQGERVAWYMLAMQDV DLHTIH FH  
AESFLYRNGENYRADVVDLFP GTFEV VEMVASNP GTWLMHCHVTDHVHAGMETLFTVFSRTEH  
LSPLTVITKETEKVPPR DIEEGNVKMLGMQIPIKNVEMLASVLVAISVTLLL VVLA LGGVVWY  
QHRQRKLRRNRRSILDDSF KLLSF KQ

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 1109-1130

**N-glycosylation sites.**amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,  
876-880, 934-938**Glycosaminoglycan attachment site.**

amino acids 871-875

**Tyrosine kinase phosphorylation sites.**

amino acids 82-90, 137-145, 494-502, 513-521

**N-myristoylation sites.**amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,  
843-849**Multicopper oxidases signature 1.**

amino acids 344-365, 696-717, 1043-1064

**Multicopper oxidases signature 2.**

amino acids 1048-1060

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**FIGURE 235**

GGAAAGAGTGCTGGTACTACAACCAGGAAGTGACAGATAATGTGCTTAAACTACATTAGAAAAGCTTCATAG  
CAAAACTGAGAGATTGAAGCAGTGATTATTTTACATAGTGTGATTAATATTGGAGCTCTGCTGTGCATAGA  
GATGGCAACACATACTTAGAATACACAGCTTCTGGGCCAGAAATTGATCTCTGACTTTGAGCCTTATCTGATTA  
CTGCTTGGTTCATCTTATTGTTAAACTACTCTGTAGGTCAAAGGGAGAGACTCTCCTGGTTGAGAGCC  
TGACTAGACAGGAATTCTGGCAACTGCTCCAGCAGAACTATGGCACTGAGTTAAATGCTGAGGAGATGG  
AAAACTTGTCAGTGTGATTGAGGATGTGAGCCAAGAAGTCCAGGAAGAAGCAGCTGGATGACTCTGGGAGA  
GAGATGAAAAATTATCCAAGTCATCAGTTTACCGAGTGAATCAATTAGTCGGGTTCAAGAACAGAGTCATTG  
ATGGAAATTCACTCAAAGGAGGATTAGGCAAAGAGGACTCCAAAATGAGAACAGACCAAAAGAGTCTTAC  
CAACTTTGGAAAAGAAGTTAACTAGAGTGCATCAAAGTCACTGGACTTGAATAAAATGAATATCTTCTCTGG  
ACAAAAGCAGCACTCAGATTGTTGATGAAGAAAATGTCCTGAGAAAGATCTCATGGAGACTTTTATCA  
ACCGTATTTTCAATATCAGTGTGACAGAAATGTTGAATTGCTCTTACAGTGCAGCTTATGAGAAATTG  
CCAGTCTAGAAATTATAATAGATGTAGTATCTACCCCTGGACTGAGAACATGGAGGTGATCAGCTGAAACGA  
TGACCTACACTATAGTCCTTAATAGTCACCTACTGGAAATGCACTGCTGCCACTGAAAGCAGACACTGTATA  
AAGAAAATCGGGAAAGCACGATTTATTGGTAGATTAGAAGTACTGACACATGATGTCCTTACCATGATTACT  
TCTATACCGTGAACAGATACTGTATCATCCGATCTTCAAAACAGAAATGCAAGGCTAAGAGTTCCACAGATTGA  
AATACAGAAAACAGCCATGGGCTTGTCAATCTTAAATTGAAAAGAATTCTGGAGTTCTGGAGGACTATT  
TCAAACAGCTGAAATCAGATTGTTAATTGAGAAATCTGATTAATTCAGGCCATTGAAAGACCTGGAAAACCTTA  
CTGGCCTACCGAAGGAGAACCTCAACCGAACAGCAGAAACAGTCTCTAAACTTCCCTCTCAGCATTCC  
CTGGAGATGTGGCTTAGGTGCAAAGGGATATTACAGGAAAGAAAAGGAAATGAAAACATAACGTCACTC  
TTATTGTTGTAATGAGTATTGTTGTTATTGTTGAAATGTGACACTGTTCTGAAGCTGTCAAAGA  
TAGAACATGCTGCTCAGTCCTTACCGTCCTGGCTCCAAGAAGAGAAATCTTAAATTAGCCTCTGATATGG  
TGTCAAGAGCAGAAACTATTCAAGAAGATAAAGATCAGGCCATGTTAAAGGGAGTGTGAGACTCCATAG  
TGATGCTGAACAGCTGAAGAGCTCACTCATTGCTCAGAAAACGTTGATCTACTAAATAAGAATAAGACTG  
GCATGGCTGTGAAAGTAGTGATCTGAAGGACTAAACCGCAGAGATACTTGAACCTAAAGAAAATCTGGA  
AGAAAACCCAGACGAATGAAGGATTTGGCATAGAACATTCTATGTTTCTATTGAGATTCTAATATGAA  
CATTTCTTCAGTAACATTATGATAATTAGTCTCTGCTGGCCTTAATAATCCTCTTCACTCTTATAGA  
TATTGTTAAGCTGTGAATTGAGTGTATGGCTCATTTCTACAGTGAAGTCTGATGCTTGTAGCACAGAATCCG  
TACATGCTCAATAGGTCGTTGTAAGTGAAGGATAAACAGGACAATATAAGAAGAAACCTC  
TATGTCATTACTGATTAAAGGTTCTGTTTCAGGCATATAACATTCCAGGTTGTACTGAAAGATTATA  
ATGTCCTCATTTATTAGCATGAAATTAAATAGTCAAACTTTTGAAATCTGATGTTGATGATGATTATCAGAA  
AGGGTCTCTGCCATGCTGATCTTATGAAAGAAATAGTTGTTCTTAAGGTAACTATCAGAGGTGGATT  
ATCTGCTCTCCTCACTTAGAATACCAACAGTCAGGAAAGAACCTCTGAGTTAAAACCAGAAGGTTA  
TGTAAAATCTGGCATTAGTGAAGCAGATCAAATGCTACTGAAACTAAGATGGCTCAGCTTAGCAGTCTTC  
ATGGTGGAAAGTGACACATCTGGTGAAGGAAATTATGTTGATTTCTAGTAAACATGTTGAGATGGCTCCTTATGT  
ATGTGTGACTTGTGTTAATGGTAAGTTAAGCCAGACATAGATTAGCTCTTAAATAAAACTTCAGGGG  
CACGTATGCCCAGTACAAGTGTACTGACTATCAAGTTAACTCAGATGCAAGCTTGCTTTCTAAGG  
TTTTATGCATATGTCCTACAGTGGCTCATTAAAATAAGAACTTTGTAACACTAAACATGAT  
TTTTCAAGAGTTAGGGAAAGTGAAAGTGTGTTTACTGTTGTTCTGAGGCCCTTCTCTGGGGAAAAAATACA  
TATCCATCTATCTATCTATATAAAACTGTGTATACATTCTACTGTTGAAACAACATTGCTTAAATTAAATG  
TTTCATTTCTCCAGAGTCCCCAAAGGCCACATGGCATTATTAGTCAGTCTTGTGAGATGCCGTAGAGAATGAA  
AGTATTGACTCCCTAGAGGGAAAATGGTTCTCTGGGTGAATTCCAACGAAGCATACCTAGGGTAACAGTGA  
ACCTACCTGGGTTGTTGGTAAGGATTATGAGTGTGCTGGCTGAAAGCAAGAATGAGTGGATTATAA  
ACTTGAAGATTCTCTGTTAAAGTCACAAAATGATGCAACAAACATATTGTTGAGTGTGTTATTAAACGTTGT  
ATTTATAACATACCAAGGAAGAGTATGCAAGTAAGTGTGTTATAAAATTAGACTAAATCGTATGGATGCA  
GAATTCAATTAAATAAAATTGAGCCTGTTACGTAATTGAAATTAAATTGAAAATTCAAAA

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**FIGURE 236**

MENLSLSIEDVQPRSPGRSSLDDSGERDEKLSKSISFTSESISRVSETESFDGNSSKGGLGKE  
ESQNEKQTKKSLPTLEKKLTRVPSKSLDLNKNEYLSLDKSSTSVDENVPDKLHGRLF  
NRIFHISADRMFELLFTSSRFMQKFASSRNIIIDVVSTPWTAEELGGDQLRTMTYTI  
VLNSPLTGKCTAATEKQTLYKESREARFYLVDSLHDVPHDYFYTVNRYCIIRSSKQKC  
RLRVSTDLYRKQPWGLVKSLIEKNSSLEDYFKQLESDLLIEESVLNQAIEDPGKLT  
GLRRRRRTFNRTAETVPKLSSQHSSGDVGLGAKGDITGKKEMENYNVTLIVVMSIF  
VLLLVLNVTLFLKLSKIEHAAQSFYRLRLQEEKSLNLASDMVSRAETIQKNKDQAH  
RLKGVLRDSIVMLEQLKSSLIMLQKTFDLLNKNKTGMAVES

**Transmembrane domain:**

amino acids 352-371

**N-glycosylation sites.**

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 81-85, 307-311

**Tyrosine kinase phosphorylation sites.**

amino acids 202-211, 246-254, 341-349

**N-myristoylation site.**

amino acids 259-265

**Amidation site.**

amino acids 339-343

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**FIGURE 237**

CAGGGGCTGGAGGGCAGGGGAGGG**A**T**G**ATGTCATTCCCTGCTCGCGCAATCCTGACCCGTCT  
CTGGGCGCCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC  
AGGCCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTCCTGGCAAGAAGGACCA  
CCTGTCCATGTCCACCAGGGCATCAGGCCACAGAGGAGGGCGGCCTCCACGTCCACATGGA  
GTTCCCGGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGCTCCGAGGG  
ACACTTCAGAGTCCCAGGCTTGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC  
CTTCGCCGTCTTACATCTACAAGGAGCTGGAGGGGCCCTCAGCACCATGGTGCAGCTCTA  
CAGCCGGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTCCAGGACTTCTACCCGACCC  
GGGGCTCCCCAAGGACATGATGGTCATGCTGCCAGTCAGATGCATGCAACCTGAGAGCAA  
GGAGGGCGCC**TGA**ACACTCCGGAGCCCCACCCCCGCCCTCCAGGTGGAGCCAAGCAGCAG  
GCGCCTTGCCCCCTGGAGTCAAGACCCACAGCCCTGGGGACCACCTGGAGTCTCTCCATCCT  
CCACCCCCCGCCTGTGGATGCCTGTGGACGTCTTTCTATTCAATAACAGATGCTGCA  
GCCTCA

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**FIGURE 238**

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMASDCRVFLGKKDHLSMSTRAI  
RPTEEGGLHVHMEFPAGDCNQVDAEYLKVGSEGHFRVPALGYLDVRIVDYSFAVLYIYK  
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

**Signal peptide:**

amino acids 1-20

**Tyrosine kinase phosphorylation site.**

amino acids 110-117

**N-myristoylation sites.**

amino acids 7-13, 79-85, 130-136

**Amidation site.**

amino acids 50-54

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**FIGURE 239**

GGCGCGCTGGTCCAGGTGAGCGGGCGCGTCCCCGCGACGGCGCTGCCCTGCCGAGGCAGTTCA  
CGTAAAGACAGCGAGATCCTGAGGCCAGCCGGAAAGGAGGCAGGATGGAGCTGGCTGCT  
GCCAAGTCCGGGGCCCGCCGCTGCCAGCGCTGGGACTCTGTGGGGACGCCCG  
CGCCGCGCTCGGGACCCGTAGAGCCCAGCGCTGCCGCAATGGCCCTGCTCTCGCGCCCCGC  
GCTCACCCCTCCTGCTCCTCATGGCCGCTGTTGTCAGGTGCCAGGAGCAGGCCAGACCAC  
CGACTGGAGAGCCACCTGAAGACCATCCGGAACGGCGTCAATAAGATAGACACGTACCTGAA  
CGCCGCCTGGACCTCCTGGAGGCAGGACGGTCTGCCAGTATAATGCAGTGACGGATC  
TAAGCCTTCCCACGTTATGGTTATAAACCTCCCCACCGAATGGATGTGGCTCTCCACTGTT  
TGGTGTTCATCTAACATTGGTATCCCTCCCTGACAAAGTGTGCAACCAACACGACAGGTG  
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCAA  
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTCAAGGATGTGAAACAAAC  
AGTGGAGCTTGTGTTGACAGTGTATACATTAGGTTGAAACCATATCTGGACAGCCAACG  
AGCCGCATGCAGGTGTCATTATGAAGAAAAACTGATCTTAAAGGAGATGCCGACAGCTAGT  
GACAGATGAAGATGGAAGAACATAACCTTGACAAATAACTAATGTTTACAACATAAAACT  
GTCTTATTTTGAAAGGATTATTTGAGACCTAAAATAATTATCTTGATGTTAAAAC  
CTCAAAGCAAAAAAGTGGAGGAGATAGTGAGGGAGGGCACGCTGTCTCAGGTATCTT  
CCCCAGCATTGCTCCCTACTTAGTATGCCAAATGTCTTGACCAATATCAAACAGTGCTT  
GTTAGCGGAGAATTTGAAAAGAGGAATATAACTCAATTTCACAACCACATTACCAA  
AAAAGAGATCAAATATAAAATTCACTATAATGCTGTTCAACATTATCTTATTGGAAAATGG  
GGAAATTATCACTTACAAGTATTGTTACTATGAAATTAAATACACATTATGCTAGAA  
GGAACGGACTTTTTCTATTTAATTACACATAATATGTAATTAAAGTACAACATAATAT  
GTTGTTCTCTGTAGCCGTTGAGCATATGAGTAAGTCACATTCTATTAGGACTACTACAA  
GGACAAGGTTCCATTTCAGTTGAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG  
CAACCCAGGATAGCTAAGTGTATGTAATATGCCAGAAGGTGATGTGAATGCGATTCAAA  
GCATAGCCACTCCCATTATGAGCTACTCACATGACAAATGTCATTTGCTATAACCTT  
GCCAAGTTAGAGAAAAGATGGATTAAATGAGATAATGAAAAGATATTAACCTAAAAAAA  
AAAAAAAAAAAAAAA

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**FIGURE 240**

MALLSRPALTLLLLLMAAVVRCQEQAQTTDWRATLKTIRNGVHKIDTYLNAALDLLGGEDGLC  
QYKCSDGSKPFPRYGYKPSPPNGCGSPLFGVHLNIGIPSLTKCCNQHDCYETCGKSKNDCDE  
EFQYCLSKICRDVQKTLGLTOHVQACETTVELLFD SVIHLGCKPYLDSQRAACRCHYEEKTDL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites:**

amino acids 57-63, 93-99

**Phospholipase A2 histidine active site:**

amino acids 106-114

**Neuraxin and MAP1B proteins repeat proteins Block:**

amino acids 109-137

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**FIGURE 241**

GATTCCGAGCGCCTCCACTGCTGGTCCGTTGCCAGATCAACTGCCGCGTGGGCCGGCGTT  
CCCTGAGAGTCTGAGCGCTGCCGCACCCCTCCGAGCTCTATTGCCGTAGCAGACGTCC  
GTCTGCCGCTATCTCCGCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGTG  
TCCAGGCCATGGGCAGCCCTGGCGGCTGGGAGCACGGACGGGGCGCCGCGAGCTGCCTC  
TCGTGCTCACCGCGCTGTGGCCGCGCGTGGCCTGGAGCTGGCTTACGTGCTGGTGCTCG  
GTCCCAGGCCGCCGCGCGCTGGGACCCCTGGCCGGCCTGCAGCTGGCGCTGGCCGCTTCC  
AGCTGCTAACCTGCTGGCAACGTGGGCTCTTCCTGCGCTCGGATCCCAGCATCGTGGCG  
TGATGCTGGCCGGCCGCGGTCTGGGCCAGGGCTGGCTACTGCTACCAATGCCAAAGCCAGG  
TGCCGCCACGCAGGGACACTGCTCTGCCGTGCATCCTGCGTCGGACCACCAACT  
GCCGCCCTGCTGGCCGCTGCGTGGCTTCGGCAACTACCGGCCCTCCTGTGCCTGCTGCTTC  
ATGCCGCCGGCCTGCTCACGTCTGTGCTGGCCCTGCACTGTGGCCCTGCTGC  
GAGCCCACACGCCCTCCACATGGCTGCCCTCCTGCTCCCTGGCTATGTTGCTCACAG  
GCAGAGTGTCTGGCACAGTTGCCTGGCCCTCGTGACGGACACGTGCGTGGCGGGTGC  
TGCTGTGCCGGCTGGCTGCTTCCATGGGATGCTGCTGCCGGGCCAGACCACATGGG  
AGTGGGCTGGGCCAGCACTCCTATGACCTGGGCCCTGCCACAACCTGCAAGGCAGCCCTGG  
GGCCCCGCTGGCCCTCGTCTGGCTCTGGCCCTTCCCTGGCTCCCCATTGCCTGGGATGGGA  
TCACCTTCCAGACCACAGCAGATGTGGACACACAGCCTCCTGATCCAGGAAGAGCCAGAGC  
TGTGCAGGGAGGAAGGGGTGAGAGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT  
GGACCTTAACATCTGCATTGGACAACCTCCACCCCTTCCCTGGCCTTGCCTGCCCTGCCCCTACA  
CTCCTACGTGTCCAGGGCTGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG  
GGGCTGCTCAGGCCGCTAGCTGCCCTTGCAGGTTATAAAAGCACTGACTTGTAA

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**FIGURE 242**

MGQPWAAGSTDGAPAQLPLVLTALWAAVGLELAYVLVLGPGLARALQLALAAFQLL  
NLLGNVGLFLRSDPSIRGVMLAGRGLGQGWAYCYQCQSQVPPRGHCSACRVCILRRDHHCRL  
LGRCVGFNYRPFLCLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLPWLMLLTGRV  
SLAQFALAFVTDTCVAGALLCGAGLLFHGMLLL RGQTTWEARGQHSYDLGPCHNLQAALGPR  
WALVWLWPFLASPLPGDGITFQTTADVGHTAS

**Important features:****Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 51-66, 143-160, 174-191, 198-214

**N-myristoylation sites:**

amino acids 2-8, 8-14, 30-36, 81-87, 88-94, 90-96, 206-212

**Leucine zipper pattern:**

amino acids 143-165, 150-172, 157-179, 164-186

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**FIGURE 243**

CTTGTCTTGTCGGTTGTGATTTCTAATCTGATTTCTCTCGGACGCTCTC  
CCTCTCGGACCCATTCTCCCGTGCCTCATGCCGTAGCCTGGCCCTTCCGGCTTC  
TTCGCTACCGGGGACGCCCTAGTTCTGAATTCTGGCTGGCTCCACCCCTCCGCGTTCAT  
CTTCCTCAAGAGTTGCCCTCTGGGGCTCTGTGTAATCGTCGCCCTCTGGGTATTT  
CTGTGAACTCCGTCTCACACCATCCCACATCTCTGCCTGGCCCTTTCTGTACAG  
CCAGCTCTGTGCTTTCTCCCCCTCTAAAATCGACTCCTCTCCCTGAGAGCCCCA  
CCTTGCCCCACTCCTCATTTCTACGCCCTCTCTGCTGGCTCTCTCCCTG  
CAAGGTTCCATCCATCAATTGTTGCTTTGAGGGTGGCATCCCTCTGACTACTGCT  
CCATCCTTTTTTTTTTTTTGCTTGAGGATTCACCAATTTCTGGT  
TGCCTCCACTGTACTCAGCTTAGGTCCAGGTCCAGTTGTCATCTGAGGCTGGC  
GTGTGCTGTCTCTGATTGCCATTCTCCCTCACCCCGTGAGATCTGTTGTCAGCCTTC  
GTTCTCTTCCGTGCTCCAGCTTCTGCGGGCTTGGCACCTTCTGGCCACAGATTTC  
TGGGTTACAGAGCATGTGCTGAGGCATTGCAGGGCAGAAAAGGGTGGCCGACGTGACCTCT  
AGCTGGACTGCTGGCAGGGAGCTGCCTAGATAAAATTGAAAGAACAGTGACCCAGAGA  
CAGGTGGACAAAGAATTGGGGACTGATGGAACTGAGCTGGATCCAGACTGAAACTGATT  
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGC~~A~~TGGGACCCAGCATTTGAGACT  
TGTGCAAGCTGTTCTGCCTCTAGGGCCATCCCCACTCTGCCTGGGCTGGAGCTTTG  
CTATGAAGCAACAGCCTCAAGATTAGCTGAGCTGTTGCTTCCATAACTGAAAGGGCTTGAT  
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCATTGAGACAGG  
GACTGCAAGGGAGTTGTTGGCTTAAAGGCTGCAGCTCGTCTCGTCTACCCCTGCGCAAAT  
CTCCTACCTTGTTCACCCACCCGGAGTGTCCATTGCCTCTACAGTCGGTCTGCCGGCTTA  
TCTCTGCAACAAACCTCACCAATTGGAGCCTTGTGAAACTCAAGGCCAGCACTCCTAAGTC  
TATCACATCTGCGTCTGTAGCTGCCGACCTGTGTTGGCGAGCAGATGAAGGATTGCCCTCC  
AAATTGTCACCAACTTCTGCCCCCTGGCTGTTCTACGTGTTACAGTTCCACCTTAA  
ATTCAGGCAGGGTTCTCAATACCACCTCCTCATGGGTGTGCTGTGAACATAACCA  
GCTTTAGCAGATTCATCATATTGGGAGCATCAAAGTGAUTGAGGTCTCAACATCTTACA  
GAAGTCTCAGATTGTTGGTGCAGCATCCTCCAGGCAAGATCCTGCTGGGTGTCGTCTTAGG  
CCTCCTGTTGCCCTCAGGGACTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTCA  
CATAACAAATAAAATAGCAGAGTTCCCTTAAAAA  
AAAAAAAAAAAAA  
AAAAAAAAA

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**FIGURE 244**

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE  
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK  
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSLKFQAGFLNTTFLLM  
GCAREHNQLLADFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAWGVVLGLLFAFRD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation sites:**

amino acids 117-121, 183-187

**N-myristoylation sites:**amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,  
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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**FIGURE 245**

GTGGAGTTGGGTGGTCTGGGAGCCTCTCCCTGAGGGCACC CGCTTCAGGAGCTGGCCTCCAGTGCGGC  
GATGTCAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCCGCGCCGTGGCGCTGGCGCTGCCGGCTGCGGGCCTGACCG  
TCCGCTCATGGTGCCGCCACGACGCCATCGCGGGCAGGAAGGCCAGGGGTGCTGAGTTCTCACCTCCTTTAG  
ACTGAGATCTGCCAAGTTTCCGGCATTGCTCTTGAGGATCTCAGAAGGCCCTTAAGACAAGACTGCAAATGGT  
GTGTGTATTTGTCA GAACCGAATGAATTCCCAGAACAGTGGTTCACTCAGGCCAGGCCATGGCTTGGGAT  
TGTTATTCTCTGCTTGTGATGTGATATGGGTTGCTCCTCTGAACCTACTTCGTATGTTTACCCAGTACAA  
CAAACCAATTCTCAGCACCTTGCAAAAACATCTATGTTGTTGTACCTTGGGTTATTATTTGGAAGCC  
ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTGCAAGATGCTGAAGGTTACTTGC  
TGCTTGACAACAGATAACTATGAATAGTTCTTGAGTGAACCTCTGTATGCTGTGAAATTCCATGATCT  
TCCAAGTGA AAAACCTGAGAGCACAAACATTGATACTGAAAAACCCCCAAAAGTCTCGTGTGAGGTTAGTAA  
TATCATGGAGATTGACAGCTCCGTCAAGTCATGCAAGGGAAAGCATGCTGCTTTTTGCAAGATGCTATCCTGTGAA  
AGAACAAAGAATCCATACTGAAAACGTGGGGAAACTTACTGCAACTCAAGTAGCCAAAATTAGCTTTTTTG  
CTTGTGTGGTTTTGGCAAATTGTCATATCAAGAACACTTCAGACACACAAGTTGCTATAGTTAATATTT  
ATCTTCAACTTCCGGACTTTACCTTAATCCTGCTGCAAGTATTCAGTGGAGATAGATTACCT  
TTCTAAAATTTAGCTGTAATTAAAGCATTGGAGGCGTTGACTGGTAAACCTGGCAGGGCTGAAAAACCTGC  
TGGAGAGACACAGTAGGTTCCATTGGTCTCTGCTGGAGCCATGCTCTATGCTGTCTATATTGTTATGATTAA  
GAGAAAAGTAGATAGAGAACAGTGGATATTCAATGTTCTTGGTTGTAGGTTGTTAATCTGCTGCT  
CTTATGCCAGGTTCTTTACTCATTATACTGGATTGAGGACTCGAGTTCCAATAAAGTAGTATTAA  
GTGCATTATCATTAAATGCCATTGGAACAGTACTCTCAGAGTTCTGTGGTTGTGGGCTGCTTCTACCTC  
ATCATTGATAGGCACACTGCAACTAACCTCTGTCCATAATAGCTGACATGTTGATGCAAAGGT  
GCAGTTCTGGTATTGGCAGGCTATCCCTGATTGGTCTTGCAGGAGCTATCCCTGATTGGTCTTGCAGGAGCT  
TTATAATAATTGGATCCTGTGATGGTGGGAATCAGAAGAATATTGCTTTATATGCAAGAAACATCGAATTCA  
GAGAGTCCAGAACAGCGAACAGTGTGAGAGTCTCATTCTATGCACAGTGTCTCAGGAGGATGGAGCTAG  
TAGCTGCTGTTGCTGTAGCCCAGCTGATAATGAACTATACAGCGAACAGAACATCTGGCAAGTTTG  
TAGAAAAAAATGTTCAAGTGCCTAGTCTGAAAAATAACAGTTGAGTTCTTGAAACTCTAAATATTTCTC  
ATACCTGTTCTCATTTCATAATGAAGCACTTGCTATGTTGAGCTGTGACATATCACTACAGTTAGGAAG  
TTTCAGTCTACAGTCCATCAAAGGACCAACCTGCCTTACACATCTCAAGGAATTCAAGCTGTTGAAATCATTGA  
ACTAATCAAGGAATAAACTCTAATGTTCTGGACTTTATTTACATGTTAAATGCTGGAATATATTGAAAT  
GTTTCAGAACATCACTTAAGTGTCTAGAGCCAGTATTCTGACAGGTAATGCTAAAGTACCTGTAA  
TAAGTGTGGATTATTTGGGTTTGAGAATATTGCAAATTAAACACACAAAAATGTTAATTATGCAAC  
AAGCATGTTGTGCAAATTCACTGGACTTTAAAGAATAAGTATTGAGAAATATCTGGTTCACTTACACTA  
CATTTACTGTATTATTCTTATAGCATTAGGTGCCTGATTAAATCTGTGACAAACCATGGCAAATT  
AAGGGGAAGTATTATATAAAATGAAGAAATATGTTGAGGCTATATTGCTGAAACTTAATTGATAAAG  
CTCTGTTAATTAGAGTTGAAGAAATAGTCTCCCTCAATTAGAAATTTCATAATGGAATGATTAAATT  
GAAGTGACAAAGAGTATTATAAAATACAATGTTATAAAAAAA

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**FIGURE 246**

MVPPRRHRGAGRPGVLSSSPPFRLRSAKFGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF  
TQRRLMALGIVILLVDVIWVASSELTSYVFTQYNKPFFSTFAKTSMFVLYLLGFIIWKPWRQ  
QCTRGLRGKHAAFFADAEGYFAACTTDTTMNSSLSEPLYVPVKFHDLPEKPESTNIDTEKTP  
KKSRVRFNSNIMEIRQLPSSHAEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFCFVWF  
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFPSNSGDRFTLSKLLAVILSIGGVVLVN  
LAGSEKPAGRDTVGSIWSLAGAMLYAVYIVMIKRKVDRDKLDIPMFFGFVGLFNLLLWPGF  
FLLHYTGfedfefPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALSLTIPSLIIA  
DMCMQKVQFSWLFFAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRIFAFICRKHRIQRVPEDS  
EQCESLISMHSVSQEDGAS

**Important features:****Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,  
364-379, 399-419, 453-472

**N-glycosylation sites:**

amino acids 157-161, 255-259

**N-myristoylation sites:**

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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**FIGURE 247**

CGTCTGTAGAGATATCATGAACCTCAACTTAGCTTGACTTTCTCCCTGAAGACAGAGGG  
CAGAACTCTGAGTTCCAGAACCATTTCAACTGTATTGGGACCAATCACTGACTCTATTCT  
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTCTAAAATGAA  
TCCTGCTACTAAAATAATTCAAGATGATATATTTCATTCTACAATCTGCTTGTTTAT  
TTAGTTGTTTCTCTCTCTTCCCAGTTCCAGAGACTGGAGCTAAACTGGGCTTCAACA  
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTGAATCTGACTGTTGCTTGGCCTTAATC  
CAGATTACACAGTCAGCTCCACTCCCCCTACTTGGTCTATTGAAATCTGACTACTGCCCT  
GCGCTGGAGTCCTGATCCACCCGCTTGGGTGATCACAGCTGCACACTGCAATTACCAAAGC  
TTCGGGTGATATTGGGGTTACAATCCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG  
GCTATGAGAAGATGATTCATCATCCACACTCTCAGTCACCTCTATTGATCATGACATCATGC  
TAATCAAGCTGAAAACAGAGGGCTGAACCTCAATGACTATGTGAAATTAGCCAACCTGCCCTACC  
AAACTATCTCTGAAAATACCATGTGCTCTGTCTACCTGGAGCTACAATGTGTGATATCT  
ACAAAGAGCCCGATTCACTGCAAACACTGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTGCGCG  
ATGCCCTATAAAACCTACAACATCACGGAAAATATGCTGTGTGGCATTGTGCCAGGAAGGA  
GGCAGCCCTGCAAGGAAGTTCTGCTGCCCGGCAATCTGCAATGGATGCTCAAGGAATCC  
TGTCTTTGCGGATGGATGTGTTGAGAGCCGATGTTGGCATCTATGCCAAATTAACT  
ATATACCCCTGGATTGAAAATGTAATCCAAAATAACTTGAGCTGTGGCAGTTGTGGACCATATGA  
CACAGCTTGTCCCCATCGTTCACCTTAGAATTAAATATAAAATTAACTCCTC

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**FIGURE 248**

MKFILLWALLNLTVVALAFNPDYTVSSTPPYLVYKSDYLPAGVLIHPLWVITAAHCNLPKLR  
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLKTEAELNDYVKLANLPYQT  
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ  
PCKEVSAAPAIICNGMLQGILSFADGCVLRADVGIYAKIFYYIPWIENVIQNN

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites:**

amino acids 11-15, 156-160, 173-177

**Tyrosine kinase phosphorylation site:**

amino acids 108-117

**N-myristoylation sites:**

amino acids 182-188, 203-209

**Amidation site:**

amino acids 185-189

**Serine proteases, trypsin family, histidine active site:**

amino acids 52-58

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**FIGURE 249**

GCGAGGC GGCCGCTGTCTCTGCTGCGGCTTCGGC GACCACAAGTACTGCTGCGACGACCCGC  
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC  
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCCTGTGTGCTCTGCTACCTGT  
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG  
AGGAGGTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA  
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGCAGCTGGAGAGCAATGAGGGGCAGGCTG  
TGAACCTCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG  
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCTAAACATTCA  
ATAAAATGTCTCCATACCATCAA

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**FIGURE 250**

MWWLSIGALIGLSVAAVVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV  
NTGMAAEVPKVSPQQSYSCLNPQLESNEGQAVNSKRLLHHCFMATVTTSDIPGSPEEASVPN  
PDLCGPVP

**Important features:**

**Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 7-13, 11-17, 62-68, 93-99

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**FIGURE 251**

GTGGTTGGATTGAGCCGGGCCGGCGCCGGCGAGTCGGAGGGGTGGCAGTGAGCGGCG  
GCAGAGGCTACGGGCTCGGTTGGCTGACTGGGAGTCGGCAGGCAGGAACC**ATGCGAG**  
GCCAGCGGAGCCTGCTGCTGGGCCGGCCCTCGCCTCCCTCTGCTGCTGGGTT  
ACAGGCGCCGCTGTCCACCTCTACTCCGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT  
GCCTGCGCTCCCTGCTCTACAACCTCCTTGGGGCAGTGACACCGCTGTTGATGCTGCCTTG  
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTGGAGTGGTGGTGTGGTCTGG  
TGATCGTGTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGTCCTGCCTCTCATCCTCC  
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA  
TTGTCTTCCACTACTACCAGGCCATCACCACTCCGCTGGTACCCACCCCAGGGCAGGAATG  
ATATGCCACCGTCTCCATCTGTAAGAAGTGCATTACCCAAGCCAGCCCACACACCACT  
GCAGCATCTGCAACAGGTGTGTGAAGATGGATCACCACGCCCTGGCTAAACAATTGTG  
TGGGCCACTATAACCATCGGTACTTCTCTTCTGCTTTCATGACTCTGGCTGTGTCT  
ACTGCAGCTATGGAAGTTGGGACCTTCCGGGAGGCTATGCTGCCATTGAGACTTATCACC  
AGACCCCACCAACCTCTCCTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT  
GGTCTGTGCAGTTCTGTGGCACTGCCCTGGTGCCCTAACTGTATGGCATGCTGTTCTCA  
TCAGTCGAGGTGAGACTAGCATCGAAAGGCACATCAACAAGAAGGGAGACGTCGGCTACAGG  
CCAAGGGCAGAGTATTAGGAATCCTAACACTACGGCTGCTGGACAACCTGGAAGGTATTCC  
TGGGTGTGGATACAGGAAGGCACTGGCTTACTCGGGTGCTCTTACCTTCTAGTCACCTGCCCT  
ATGGGAATGGAATGAGCTGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG  
CAGT**TGA**GCTGGACTGTGTCAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTCA  
AGGGCCTCCAAGGGCAGTTCTCAGAATCCTGATCAAAAGAGCCAGTGGCCTGCCCTTA  
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTACCACTGCAGAAGAAAGACACAATGT  
GGAGAAATCTTAGGACTGACATCCCTTACTCAGGCAAACAGAAGTTCCAACCCCAGACTAGG  
GGTCAGGCAGCTAGCTACCTACCTTCCAGTGCTGACCCGGACCTCCAGGATACAGCAC  
TGGAGTTGGCCACCAACCTCTTACTTGCTGTGAAAAAACACCTGACTAGTACAGCTGAGA  
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGCTGCTGAGGTCACTGCCACTCTCACA  
TGCTGCTTAAGGGAGCACAAATAAGGTATTCGATTTAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

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**FIGURE 252**

MRGQRSLLLGPARLCLRLLLLGYRRRCPPLLRGLVQRWRYGKVCLRSLLYNSFGGSDTAVDA  
AFEPVYWLVDNVIRWFGVVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFFYSHWNL  
ILIVFHYYQAITTPPGYPPQGRNDIATVSICKCIYPKPARTHHCSICNRCVLKMDHCPWLN  
NCVGHYNHRYFFSFCFFMTLGCVYCSYGSWDLFREAYAAIETYHQTPPPFSFRERMTHKSLV  
YLWFLCSSVALALGALTWWHAVLISGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK  
VFLGVDTGRHWLTRVLLPSSHLPNGNGMSWEPPPWTAHSASVMAV

**Important features:****Transmembrane domain:**

amino acids 88-100, 202-216, 254-274

**N-myristoylation sites:**

amino acids 55-61, 56-62, 92-98, 210-216, 309-315, 319-325, 340-346

**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 201-212

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**FIGURE 253**

GATCAAGCGCCTTCCTTCCCTCCCTCCACTTGGCCTTGCCCCAAGCCAAGACCTGGCCATCAGCCTGGC  
TGCAGGGGCTGCAGGCCAGCTGCACTTTTCAGGTATGGGGAGGGCCAGGCACCATGAAGCCAGTGTGGTC  
GCCACCCCTCTGTGGATGCTACTGCTGGTCCCAGGCTGGGGCCGCCGGAAAGGGTCCCCAGAAGAGGCCCTCC  
TTCTACTATGGAACCTCCCTCTGGCTTCTCCTGGGGCGTGGCAGTTCTGCCTACCAGACGGAGGGCGCCTGG  
GACCAGGACGGAAAGGGCTAGCATCTGGACGTCTCACACACAGTGGAAAGGGAAAGTCTGGGAATGAG  
ACGGCAGATGTAGCTGTGACGGCTACTACAAGGTCCAGGAGGACATCATTCTGCTGAGGGAACTGCACGTCAC  
CACTACCGATTCTCCCTGTCTGGCCCCGGCTCCGTCCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAAGGGA  
ATCGAATTCTACAGTGATCTTATCGATGCCCTCTGAGCAGCAACATCACTCCCATCGTACCTTGACCCACTGG  
GATCTGCCACAGCTGCTCCAGTCAAATACGGTGGTGGCAGAATGTGAGCATGCCAACTACTTCAGAGACTAC  
GCCAACCTGTGCTTGAGGCCTTGGGGACCGTGTGAAGCACTGGATCACGTTAGTGCATCCTCGGGCAATGGCA  
AAAAAAGGCTATGAGACGGGCCACCATGCGCCGGGCTGAAGCTCCGCGCACGGCCTGTACAAGGCAGCACAC  
CACATCATTAAGGCCACGCCAAAACCTGGCATTCTTAAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGT  
GGAATTCACTGAACGTGACTGGGGGAACCTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCAGAGA  
TACCTACAGTTCTGTCTGGCTGGTTGCCAACCCATTATGCCGGTACTACCCCCAAGTCATGAAGGACTAC  
ATTGGAAGAAAGAGTGAGACAGCAAGGCCTGGAGATGTCAGGTTACGGTGTCTCACTCCAGGAGAAGAGCTAC  
ATTAAAGGCACATCCGATTCTGGGATTAGGTCACTTACTACTCGTACATCACGGAAAGGAACTACCCCTCC  
CGCCAGGGGCCAGCTACCAGAACGATCGTACCTGATAGAGCTGGTGAACCAAAGGCCAGATCTGGGTCT  
AAATGGCTATATTCTGTGCCATGGGATTAGGAGGCTCTTAACCTTGCTCAGACTCAATACGGTGAATCTCCC  
ATATATGTGATGGAAATGGAGCATCTCAAAATTCCACTGTACTCAATTATGTGATGAGTGGAGAATTCAATAC  
CTTAAAGGATACATAATGAAATGCTAAAAGCTATAAAAGATGGTCTAATATAAAGGGTATACTTCCTGGTCT  
CTGTTGGATAAGTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTAAACGACAGA  
ATAAGCCTCGTATCCAAAGGCTCAGTTCAATATTACAAGAAGATTATCATTGCCAATGGTTCCCAATCCA  
AGAGAGGGTGGAAAGTTGGTACCTCAAAGCTTGGAAACTTGCTCTATCAACAATCAGATGCTTGCTGCAGAGCCT  
TTGCTAAGTCACATGCAAATGGTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGTCCTCATCACTGCT  
GTTCTACTAATGCTCCTCTGAGGAGGCAGAGCTGAGACAGGATTATCAATTGGAGCTTCATAAGAGAATCTT  
CAGGATCTCCCTCCCTTCTGCTTGAGGGTTCCATACATTGCTGTTTCAGGTTCTACAATAATTACCTTT  
TTCTCTTCTCTTTGGCTTGCTGGATTAAGAATTAGAAAATAAGCAGAAATTA

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**FIGURE 254**

MKPVVWATLLWMLLLVPRLGAARKGSPEEASFYYGTFPLGFSGVGSSAYQTEGAWDQDGKGPSIWDVFTHSGKG  
KVLGNETADVACDGYYKVQEDIILLRELHVNVYRFSLSWRPLLPTGIRAEQVNKKGIEFYSIDLIDALLSSNITPI  
VTLLHHWDLQPQLLQVKYGGWQNVS MANYFRDYANLCFEAFGDRVKHWTFSDPGRAMAEGKYETGHAPGLKLRGTG  
LYKAHHIIKAHAKTWHSYNTTWRSKQQGLVGISLNCDWGEPVDISNPKDEAAERYLQFCLGWFANPIYAGDYP  
QVMKDYIGRKSAEQGLEMSRLPVFSLQEKS YIKGTSDFLGLGHFTTRYITERNYPQRQGPSYQNDRDLIELVDPN  
WPDLGSKWLYSVPWGFRRLLNFAQTQYGDPPYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK  
GYTSWSLLDKFEWEKGYSDRYGFYYVEFNDRNKPYPKASVQYYKKIIIANGFPNPREVESWYLKAETCSINNQ  
MLAAEPLLSHMQMVTEIVVPTVCSCVLITAVLLMLLRRQS

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 541-558

**N-glycosylation sites:**

amino acids 80-84, 171-175, 245-249

**Glycosaminoglycan attachment site:**

amino acids 72-76

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 23-27, 564-568

**Tyrosine kinase phosphorylation sites:**

amino acids 203-211, 347-355, 460-468, 507-514

**N-myristoylation sites:**

amino acids 44-50, 79-85, 167-173, 225-231, 257-263, 315-321

**Amidation site:**

amino acids 307-311

**Glycosyl hydrolases family 1 active site:**

amino acids 407-416

**Glycosyl hydrolases family 1 N-terminal signature:**

amino acids 41-56

**Motif name Glycosyl hydrolases family:**

amino acids 37- 67

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**FIGURE 255**

CGCGAAGATGCAGAAAGGTGGTTTGATCACCGGGCTAGCAGTGGCATGGCTGGCCCTCTG  
CAAGCGGCTGCTGGCGAACGATGATGAGCTTCATCTGTGTTGGCGTGCAGGAACATGAGCAA  
GGCAGAACGCTGTCTGTGCTCTGCTGGCCTCTCACCCCCACTGCTGAGGTACCATTGTCCA  
GGTGGATGTCAGCAACCTGCAGTCGGCTTCCGGGCCTCCAAGGAACCTTAAGCAAAGGTTCA  
GAGATTAGACTGTATATATCTAAATGCTGGATCATGCCTAATCCACAACAAATAATCAAAGC  
ACTTTCTTGCCCTTTCAAGAAAAGTGAATGATGCTGAGCTCAGGAGGTGTTGAGACCAATGTCTTG  
GACCCAGGGTATAAGATCACTGCTGATGGACTTCAGGAGGTGTTGAGACCAATGTCTTG  
CCATTATCCTGATTGGAAACTGGAGCCTCTCCTGTACAGTGACAATCCATCTCAGCT  
CATCTGGACATCATCTCGAGTGCAAGGAACTAATTCAGCCTCGAGGACTTCCAGCACAG  
CAAAGGCAAGGAACCCCTACAGCTCTCCAAATATGCCACTGACCTTGAGTGAGCTGGCTTGAA  
CAGGAACCTCAACCAGCAGGGTCTCTATTCCAATGTGGCTGTCCAGGTACAGCATTGACCAA  
TTTGACATATGGAATTCTGCCCTCGTTATATGGACGCTGTGATGCCGGCAATATTGCTACT  
TCGCTTTTGCAAATGCATTCACTTGACACCATAATGGAACAGAACAGCTCTGGTATGGCT  
TTTCCACCAAAAGCCTGAATCTCAATCCTGTGATCAAATATCTGAGTGCCACCACTGGCTT  
TGGAAAGAAATTATATTGACCCAGAACAGATGGACCTAGATGAAGACACTGCTGAAAAATTAA  
TCAAAAGTTACTGGAACTGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC  
CAGGCTCAGTGGCTCATGCCTTAATCCAGCATTGGGAGGCCAAGGCAGAAGGATCACT  
GAGACCAGGAGTTCAAGACCAGCCTGAGAACATAGTGAGCCCTGTCTACAAAAAGAAAT  
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG  
GGAGGATCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACCTCC  
AGCCTGGGTGACAGCGAGACCCCTGTCTCAAAATATGTATATATTAAATATATATAAAACCA  
GAGCTGACAATGACACTCTGGAACATTGCATACCTCTGTACATTCTGGGTACATGGATTTC  
TACTGAGTTGGATAATATGCATTGTAATAAACTATGAACATATGAA

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**FIGURE 256**

MRKVVLITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD  
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ  
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFQHSKG  
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLMPAILLRF  
FANAFTLTPYNGTEALVWLHQKPESLNPLIKYLSATTGFGGRNYIMTQKMDLDEDTAEKFYQK  
LLELEKHIRVTIQKTDNQARLSGSCL

**Important features:****Transmembrane domain:**

amino acids 234-254

**N-glycosylation sites:**

amino acids 37-41, 178-182, 229-233, 263-267

**Glycosaminoglycan attachment site:**

amino acids 12-16

**N-myristoylation sites:**

amino acids 9-15, 13-19, 15-21, 215-221, 224-230

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**FIGURE 257**

CGGACGGGTGGGGCCGTATGCGCGCTCTGTGGAGTGCACCTGGGTTGGGGCACTGTGCC  
CCAGCCCCCTGCTCCTTGGACTCTACTTCTGTTGCAGCCCCATTGGCCTGCTGGGGAGA  
AGACCCGCCAGGTGTCTCTGGAGGTATCCCTAACTGGCTGGGCCCTGCAGAACCTGCTTC  
ATATACGGCAGTGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCCCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCGATGGGGCCTGATGGTGCCTCCATAAGGACAGCATTAGCTTCTCTG  
CCCTTGTCTTACCAAGGCTGCTTGAGTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC  
CTTGGAAGACCATACTCCATACTCCTGGCCATTCTCTTGGAAACAACATCACTGATT  
CATTGGATCCTGCCACCCCTGAGTGCACATTCAAGGCCACCCATGAACGACCCCTACCAGGA  
CTTTGCCAATGGCAGCCTGGCCTCAGGGTCCAGGCCTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCCGGGAAACCGTTCCCTGTTGGCTGGAGGTAGCCACATTGGCCAGGGCCCTGACT  
GCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTCCAGTTGG  
ACCAGCTACTGTGGGCTCCCTCCATCAGGCTTGCACAGTGGCACCAGTGGCTTACTCCC  
AGAAGCCGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTCCCTTCTCATCCTGCCTTAG  
CATACTCTTCCCCAGTCACCCATTGTCGAGCCTCTTGGTCCCAGAATAACTCTGTG  
CCTTCAATCTGACGTTGGGCTTCCACAGGCCCTGGCTATTGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTTGGCTCCAGTGGACGGCTGTCCCCACTAGTCCTGGCA  
TCATGGCAGTGGCCCTGGGTGCCCAAGGGCTCATGCTGCTAGGGGGCGCTGGTTCTGCTGC  
TGCACCCACAAGAAGTACTCAGAGTACCAAGTCCATAAAATTAAGGCCGCTCTGGAGGGAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTGGAGCATCAAGTTCCAGCC  
GGCCCTTCACCCCCATTTGCTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCCTGG  
AGACCCCCAGGTGGGCTTCCCTCATACTTGTGGGGACTTGGAGGCAGGGACAG  
GGCTATTGATAAGGTCCCCCTGGTGTGCTTGCATCTCCACACATTCCCTGGATGG  
ACTTGCAAGGCCTAAATGAGAGGCATTCTGACTGGTGGCTGCCCTGGAAGGCAAGAAAATAGA  
TTTATTTTTTCACAGGGAAAAAA

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**FIGURE 258**

MRGSVECTWGWHCAPSPLLWTLLLFAAPFGLLGEKTRQVSLEVIPNWLGPLQNLHIRAVG  
TNSTLHYVWSSILGPLAVVMVATNTPHSTLSINWSLLSPEPDGGLMVLPKDSIQFSSALVFTR  
LLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHPMNDPTRTFANGS  
LAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFLEVATLGQGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGSLLPSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYSLPQ  
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPVLGIMAVAL  
GAPGLMLGGGLVLLHHKKYSEYQSin

**Important features:****Signal peptide:**

amino acids 1-35

**Transmembrane domain:**

amino acids 365-386

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern:**

amino acids 371-393

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**FIGURE 259**

CAGGCGGGCCCCCGCGCGCAGGGCCCTGGACCCGCGCGCTCCCGGGG**ATGGT**GAGCAAGGCCTGCTGCCCT  
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGGCATGCCCTGCTGGCCTACGTCGCCTGTTTG  
GGGCAACTCGTTAATATGAGGTCTATCCAGGAAATGGTAACAAAAATTGAAAGCAAGATTGAAGAGATGGT  
TGAACCACTAAGAGAGAAAATCAGAGATTAGAAAAAGCTTACCCAGAAATACCCACCAGTAAAGTTTATC  
AGAAAAGGATCGGAAAAGAATTGATAAACAGGAGGCGCAGGGTTCGTGGCCTCCATCTAACGTGACAAACTCAT  
GATGGACGGCCACGAGGTGACCGTGGTGGACAATTCTCACGGGAGGAAGAGAACGTGGAGCACTGGATCGG  
ACATGAGAACTTCGAGITGATTAACCACGACGTGGTGGAGCCCTACATCGAGGTGACAGATATACCATCT  
GGCATCTCCAGCCTCCCAAACATCATGTATAATCCTATCAAGACATTAAAGACCAATACGATTGGACATT  
AAACATGTTGGGGCTGGCAAAACGAGTCGGCCGTCTGCTCCTGCCATCGAGGTGATGGAGATCC  
TGAAGTCCACCCCTCAAAGTGAGGATTACTGGGCCACGTGAATCAAAGACCTCGGGCTGCTACGATGAAGG  
CAAACGTGTTGCAGAGACCATGTGCTATGCCATGAAGCAGGAAGGCCTGGAAGTGCAGTGGCCAGAACATT  
CAACACCTTGGGCCACGCATGCACATGAACGATGGGCCAGTAGTCAGCAACTCATCCTGCAGGCCCTCAGGG  
GGAGCCACTCACGGTATACGGATCCGGTCTCAGACAAGGGCGTCCAGTACGTACGCGATCTAGTGAATGCC  
CGTGGCTCATGAACAGCAACCGTCAGCAGGCCGGTCAACCTGGGAAACCCAGAAGAACACACAATCCTAGAATT  
TGCTCAGTTAATTAAAAACCTGTTGGTAGCGGAAGTGAATTCACTCTCCGAAGGCCAGGATGACCCACA  
AAAAAGAAAACCGACATAAAAAGCAAAGCTGATGCTGGGTGGAGCCCGTGGCTCCGCTGGAGGAAGGTT  
AAACAAAGCAATTCACTACTCCGTAAGAAACTCGAGTACCGAGCAAATAATCAGTACATCCCCAACCAAAGCC  
TGCCAGAATAAGAAAGGACGGACTGCCACAGC**TGA**ACTCCTCACTTTAGGACACAAGACTACCATTGTACAC  
TTGATGGGATGTATTTGGCTTTGGCTGTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAAC  
TGGAAATTCTGAAGCTGCTTAATGAAATGGATGTGCCTAAAGCTCCCTCAAAAAACTGCAGATTTG  
CCTTGCACCTTTGAATCTCTTTTATGTAAGGCTAGATGCATCTCGCTGTTGAGCTGAAAGCTGAAAGGAA  
CTTAAGCGGACAAAAATGCCGATTTATTTATAAAAGGGTACTTAATAATGAGTCGTATACTATGCAT  
AAAGAAAAATCCTAGCAGTATTGTCAGGTGGTGGTGCGCCGGCATTGATTTAGGGCAGATAAAAGAATTCTGT  
TGAGAGCTTATGTTCTCTTTAATTCAAGAGTTTCCAAGGTCTACTTTGAGTTGCAAACCTGACTTGAAA  
TATTCCCTGTTGGTCATGATCAAGGATATTGAAATCACTACTGTGTTTGTGCATCTGGGGCGGGGGCAGGT  
TGGGGGGCACAAAGTTAACATATTCTGGTTAACCATGGTTAAATATGCTATTTAATAAAATATTGAAACTCA

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**FIGURE 260**

MVSKALLRLVSANRRRMKLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR  
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFGSHLTDKLMMDGHEVTVDNFFTGRK  
RNVEHWIGHENFELINHDVVEPLYIEVDQIYHLASPASPPNYMNPPIKTLKTNTIGTLNMLGL  
AKRVGARLLLASTSEVYGDPEVHPQSEDYWGHNPIGPRACYDEGKRAETMCYAYMKQEGVE  
VRVARIFNTFGPRMHMNDGRVVSNFILQALQGEPLTVYGSGSQTRAFQYVSDLVNGLVALMNS  
NVSSPVNLGNPEEHTILEFAQLIKNLVGSSEIQFLSEAQDDPQKRKPDIKKAKLMLGWEVV  
PLEEGLNKAIHYFRKELEYQANNQYIPPKPKPARIKKGRTRHs

**Important features:****Signal peptide:**

amino acids 1-32

**N-glycosylation site:**

amino acids 316-320

**Tyrosine kinase phosphorylation site:**

amino acids 235-244

**N-myristylation sites:**

amino acids 35-41, 101-107, 383-389

**Amidation sites:**

amino acids 123-127, 233-237

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**FIGURE 261**

GC GTGGTGC GGGGGCGT GGGGAAAT CGGGT GCCCAGCCGT ACTGGTCCGCGCAGTCAGGG  
CAT CCTCCGCAT CCTCCACAT CCTCC **ATGG**C TGAAGAATAAATT CAGTTGTTATGGATC  
TTGGGTCTGTGTTGGTAGCCACTACATCTTCAAAATCCCATCCATCACTGACCCACACTT  
ATAGACAAC TGCA TAGAAGCCCACAACGAATGGCGTGGCAAAGTCAACCCCTCCGGCGAC  
ATGAAATA CATGATTGGATAAAGGTTAGCAAAGATGGCTAAAGCATGGCAAACCAGTGC  
AAATTGAACATAATGACTGTTGGATAAATCATATAATGCTATGCAGCTTGAAATATGTT  
GGAGAAAATATCTGGTTAGGTGGAATAAGTCATTCACACCAAGACATGCCATTACGGCTTGG  
TATAATGAAACCCAATT TATGATTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT  
ACACAGTTAGTTGGCCAATT CATT TATGTCGGTTGTGCAGTTGCAATGTGCTAACCTT  
GGGGGAGCTTCAACTGCAATATTGTATGCAACTACGGACCTGCAGGAAATTGCAAATATG  
CCTCCTTACGCAAGAGGAGAATCTGCTCTGCTCAAAGAAGAGAAATGTGTAAGAAC  
CTCTGCAGGACTCCACAACCTATTATACCTAACCAAAATCCATTCTGAAGCCAACGGGAGA  
GCACCTCAGCAGACAGCCTTAATCCATTCAAGCTTAGGTTCTTCTGAGAATCTT**TAA**  
TGTCATTATACAAAAGAAATTCTCAAATGTTAAATAAGGAATAGTTATTGCTTAATA

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**FIGURE 262**

MALKNKFSCLWILGLCLVATTSSKIPSPIDPHFIDNCIEAHNEWRGKVNPAAADMKYMIWDKG  
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRAITAWYNETQFYDF  
DSLSCSRVCGHYTQLVWANSFYVGCAVAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC  
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLRIF

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site:**

amino acids 119-123

**N-myristoylation sites:**

amino acids 103-109, 150-156, 160-166, 161-167, 175-181

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:**

amino acids 136-156

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:**

amino acids 166-178

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**FIGURE 263**

CGCCCTCCGACCCGCCCGCGCATTGTGGGATCTGTCGGCTTGTCAAGGTGGTGGAGGAAA  
AGGCCTCCGTCATGGGATCCAGACGAGCCCCGTCTGCTGGCCTCCCTGGGGTGGGCTG  
GTCACTCTGCTCGGCTGGCTGTGGCTCTACTTGGTCGGAGGTCCC GCCGGCTCAGGTC  
ACTCTCCTGGACCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCAC  
AACACCAAGAGGTTCCGCTTGCCCTGCCAACGCCACCACACTGGGCTGCCTGTGGC  
AAACATATCTACCTCTCCACCGAATTGATGGCAGCCTGGCATCAGGCCATACACTCCTGTC  
ACCAGTGTGAGGATCAAGGCTATGTGGATCTGTCAAGGTCTACCTGAAGGGTGTGCAC  
CCCAAATTCCTGAGGGAGGGAAAGATGTCTAGTACCTGGATAGCCTGAAGGGTGGGATGTG  
GTGGAGTTCGGGGCAAGCGGGTGCTCACTTACACTGGAAAAGGCATTTAACATTCA  
CCCAACAAGAAATCTCCACCAGAACCCGAGTGGCGAAGAAACTGGAATGATTGCCGGCGG  
ACAGGAATCACCCAATGCTACAGCTGATCCGGGCATCTGAAAGTCCCTGAAGATCCAACC  
CAGTGCTTCTGCTTTGCCAACAGACAGAAAAGGATATCATCTGGGGAGGACTTAGAG  
GAAGTGCAGGCCGCTATCCAATCGCTTAAGCTCTGGTCACTCTGGATCATCCCCAAAA  
GATTGGGCCTACAGCAAGGGTTGTGACTGCCGACATGATCCGGAACACCTGCCGCTCCA  
GGGGATGATGTGCTGGTACTGCTTGTGGCCACCCCAATGGTCAGCTGGCCTGCCATCCC  
AACTTGGACAAACTGGCTACTCACAAAGATGCGATTCACCTACTTAGCATCCTCCAGCTTC  
CCTGGTGCTGTCGCTGCAGTTGTTCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCT  
TTCCTCAGAGTTCAGGTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG  
AACAAATTCCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTGGATGGCCTCCTAAA  
TCTCCCGTGGCAACAGGTCAGGAGAGGCCATGGAGCAGTCTCTCCATGGAGTAAGAAGG  
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCTGATAGCATCTTACTCTCACCTT  
CTTGAGTGTGATGAAAGGAACAGTCTGTGCAATGGTTTACTAAACTCACTGTTCAA  
CCTATGAGCAAATCTGTATGTGAGTATAAGTTGAGCATAGCATACTCCAGAGGTGGTNTT  
ATGGAGATGGCAAGAAAGGAGGAATGATTCTCAGATNTCAAAGGAGTCTGAAATATCATA  
TTCTGTGTGTCTCTCAGCCCTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA  
AACTGCTGTTGTGGCANGAACCCCTGGCTGTGCAAATAATGGGCTGAGGCCCTGTGTGA  
TATTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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**FIGURE 264**

MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKR  
FRFALPTAHHTLGLPGVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLNKGVPKF  
EGGKMSQYLDLSLKVGDVVEFRGPGSLLTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAAGGTG  
ITPMLQLIRAILKVPEDPTQCFLLFANQTEKDIIILREDLEELQARYPNRFKLWFTLDHPPKD  
WAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQKMRFTY

**Important features:**

**Signal peptide:**

amino acids 1-26

**N-glycosylation site:**

amino acids 214-218

**N-myristoylation sites:**

amino acids 22-28, 76-82, 128-134, 180-186

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**FIGURE 265**

CCCGTGCCAAGAGTGACGTAAGTACCGCTATAGAGTCTATAGGCCACTGGCTTCGTAGA  
ACGC GGCTACAATTAATAACATAACCTTATGTATCATAACACATACGATTAGGTGACACTATAG  
ATAAACATCCACTTGCCTTCTCTCCACAGGTGTCCACTCCCAGGTCAACTGCACCTCGGT  
TCTATCGATAATCTCAGCACCCAGCCACTCAGAGCAGGGCACGATGTTGGGGCCCGCCTCAGG  
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCAAATGCC  
TCCCCACTGCTCGGCTCCAGCTGGGTGGCTGATCCACCTGTACACAGCCACAGCCAGGAAC  
AGCTACCACCTGCAGATCCACAAGAATGGCATGTGGATGGCGCACCCATCAGACCATCTAC  
AGTGCCTGATGATCAGATCAGAGGATGCTGGCTTGTGGTGATTACAGGTGTGATGAGCAGA  
AGATAACCTCTGCATGGATTTCAGAGGCAACATTTGGATCACACTATTCGACCCGGAGAAC  
TGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACCTCCTCAGTATCAC  
TTCCCTGGTCAGTCTGGCCGGCGAAGAGAGGCCCTGCCAGGCATGAACCCACCCCCGTAC  
TCCCAGTTCCCTGCCCAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGG  
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGTGCTGAAGCCCCGG  
GCCCGGATGACCCCGGCCCCGGCCCTCTGTTCACAGGAGCTCCGAGCGCCGAGGACAACAGC  
CCGATGGCCAGTGACCCATTAGGGTGGTCAGGGCGGTGAGTGAACACGCACGCTGGGGGA  
ACGGGGCCCGGAAGGCTGCCGCCCTCGCCAAGTTCATCAGGGTCGCTGG

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**FIGURE 266**

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLHYTATARNSYHLQIHKNGHVDG  
APHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRCFHQTLENGYDV  
YHSPQYHFLVSLGRAKRAFLPGMNPPPSQFLSRRNEIPLIHFNTPIP RRHTRSAEDDSERDP  
LNVLKPRARMTPAPASC SQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFAKFI

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 175-179

**N-myristylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

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**FIGURE 267**

GGCTGAGGGGAGGCCGGAGCCTTCTGGGCCTGGGGATCCCTTGCACTGGTGGTGGAGAGAACGCCCTGC  
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTCCCTGGCGCATGTAAGGCTCCACAAAGGAGTTGGAGTTC  
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCAAAGCCCTGGACCTGCCAGCGTGGCACTGAGGCAGCG  
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCAGCCCTGGCCAGCCTG  
CCGGAGCCCTGTGGAGGCAGGCCAGTGGAGGCCAGTGAGGCAGGGCTGCTGGCAGCCACCCGCTGCAACT  
CAGGAACCCCTCCAGGCCATGGACGGCTGCCCCGCTGACGCCAGGGTAAGCATGTGAGGAGGCCGCCCCGG  
AGCCAAGCAGGAGGGAAAGAGGCTTCATAGATTCTATTACAAAGAATAACCACCATTTGCAAGGACCAATGAGG  
CCACTGTGCGTGACATGCTGGGCTCGGACTGCTGGCTGCATGGAGCTGTTGCAGGCCAGGAGGACGGTTTT  
GAGGGCACTGAGGAGGGCTGCCAACAGAGATTCATTTACCTAACAGGTACAAGCGGGCGGGCAGTCCCAGGAC  
AAGTGCACCTACACCTTCATTGTGCCCCAGCAGCGGTACGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG  
GTGCTTCTGGAGAACCGAGTGATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAACGGCAG  
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAC  
CGAACATGAACCTCGCGGTACCGCAGCTACATGCAGCTCCTGCACGAGATCATCCGAAGCGGACAACCG  
TTGGAGCTCTCCAGCTGGAGAACAGGATCTGAACCAGACAGCGACATGCTGCAAGCTGGCAGCAAGTACAAG  
GACCTGGAGCACAAGTACCAAGCACCTGGCCACACTGGCCACAAACCAATCAGAGATCATCGCGAGCTTGAGGAG  
CACTGCCAGAGGTGCCCTGCCAGGCCAGGCCAGCCACCCCCCGCTGCCCGGGCTACCAACCA  
CCCCCTACAACCGCATCATCAACCAGATCTACCAACGAGATCCAGAGTGAAGGTGCTGCCA  
CCCCCTCTGCCACTATGCCACTCTCACCAAGCCTCCATCTTCCACCGACAAGCCGTCGGGCCATGGAGAGAC  
TGCCTGCAGGCCCTGGAGGATGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCTC  
ATGCAGGTGTGGTGCAGAGACACGACCCGGGGCTGGACCGTCATCCAGAGACGCCCTGGATGGCTCTGTT  
AACTTCTCAGGAACTGGAGACGTACAAGCAAGGGTTGGAACATTGACGGCAAACTGGCTGGCCTGGAG  
AACATTTACTGGCTACGAACCAAGCAACTACAAACTCTGGTACCATGGAGGACTGGTCCGGCCGCAAAGTC  
TTTGCAGAAATGCCAGTTCCGCCCTGGAACCTGAGAGCGAGTATTATAAGCTGGGCTGGGGCTACCATGGC  
AATGCCGGTACTCCTTACATGGCACACGCCAACGCCAGTTACCCCTGGACAGAGATCATGATGTCTACACA  
GGAAAATGTGCCACTACCAAGAGGGAGGCTGGTATAACGCCCTGCCACTCAACCTCAACGGGTCTGG  
TACCGGGGGGCCATTACCGGAGCCGCTACCAAGGACGGAGTCACTGGGCTGAGTCCGAGGAGGCTTACTCA  
CTCAAGAAAGTGGTGTGATGATCCGACCGAACCCCAACACCTCCACTAAGCCAGCTCCCCCTCCTGACCTCTC  
GTGGCCATTGCCAGGAGGCCACCTGGTCACGCTGCCACAGCACAAGAACAACTCCTCACCAAGTTCATCCTGA  
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTCCGAAGTCACTGCAGCGGATGATGGAACGTGAATCGATACGGT  
GTTTCTGCTCCCTACTTCCACACCAAGACAGCCCTCATGTCTCCAGGACAGGAGACTACAGACAA  
CTCTTCTTAAATAAGTCTACAAATAAAAAAA

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**FIGURE 268**

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ  
RVTGAICVNSKEPEVLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLRKE  
SRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRILNQTADMLQLASKYKDLHKYQHLATL  
AHNQSEIIAQLEEHQRVPSARPVPQPPPAPPRTVYQPPTYNRIINQISTNEIQSDQNLKVLP  
PPLPTMPTLTSLPSSTDKGSGPWRDCLQALEDGHDTSIIYLVKPENTNRLMQVWCDQRHDPGG  
WTVIQRRLDGSVNFFRNWETYKQGFGNIIDGEYWLGLENIYWLTNQGNYKLLVTMEDWSGRKVF  
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAHYQKGGWWYN  
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLKVVMMIRPNPNTFH

**Important features:****Signal peptide:**  
amino acids 1-22**N-glycosylation sites:**  
amino acids 164-168, 192-196**cAMP- and cGMP-dependent protein kinase phosphorylation site:**  
amino acids 124-128**Tyrosine kinase phosphorylation sites:**  
amino acids 177-184, 385-393, 385-394, 461-468**N-myristoylation sites:**  
amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,  
473-479**Amidation site:**  
amino acids 373-377**Fibrinogen beta and gamma chains C-terminal domain signature:**  
amino acids 438-451**Fibrinogen beta and gamma chains C-terminal domain proteins:**  
amino acids 305-343, 365-402, 411-424, 428-458**Trehalase proteins:**  
amino acids 275-292

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**FIGURE 269**

GCCGAGCTGAGCGGATCCTCACATGACTGTGATCCGATTCTTCCAGCGGCTCTGCAACCAA  
GCGGGTCTTACCCCCGGTCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCACGTCCCCGA  
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAACGAGGATGAGCGGTGCTCCGACGGCCGGGGC  
AGCCCTGATGCTCTGCGCCACCAGCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC  
CAAGTCGCCGCGCTTGCCTGGGACGAGATGAATGTCCTGGCGACGGACTCCTGCAGCT  
CGGCCAGGGCTGCGGAACACCGGAGCGCACCCGAGCTGAGCGCGCTGGAGCGCG  
CCTGAGCGCGTGCAGGGTCCGCTGTCAGGGAACCGAGGGTCCACCGACCTCCGTTAGCCCC  
TGAGAGCCGGTGGACCTGAGGTCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG  
CAGGATCCAGCACTCTTCACAAGGTGGCCAGCAGCAGCGGACCTGGAGAACGAGCACCT  
GCGAATTCACTGCAAAAGCCAGTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT  
GGCCAAGCCTGCCGAAGAAAGAGGCTGCCAGATGGCCAGCCAGTTGACCCGGCTCACAA  
TGTCAGCCGCTGCACGGCTGCCAGGGATTGCCAGGAGCTGTTCAAGGTTGGGAGAGGCA  
GAGTGGACTATTGAAATCAGCCTCAGGGTCTCCGCCATTGGTGAAGTCAAGATGAC  
CTCAGATGGAGGCCTGGACAGTAATTCAAGGGGCCACGATGGCTCAGTGGACTTCAACCGGCC  
CTGGGAAGCCTACAAGGGGGTTGGGATCCCCACGGCGAGTTCTGGCTGGGCTGGAGAA  
GGTGCATAGCATCACGGGGACCGAACAGCCCTGGCGTGCAGCTGCGGACTGGATGG  
CAACGCCAGTTGCTGCAGTTCTCCGTGCACCTGGTGGCGAGGACACGGCCTATAGCCTGCA  
GCTCACTGCACCCGTGGCCGGCCAGCTGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT  
ACCCTCTCCACTGGGACCAAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCT  
CTCTGGAGGCTGGTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC  
CATCCCACAGCAGCGGCAGAACGCTTAAGAAGGGAAATCTCTGGAAAGACCTGGCGGGCCGCTA  
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCG  
TCCTGGCTGGGCTGGTCCCAGGCCACGAAAGACGGTGAETCTTGGCTCTGCCAGGGATGT  
GGCCGTTCCCTGCCCTGGCAGGGGCTCCAAGGAGGGCCATCTGGAAACTTGTGGACAGAGAA  
GAAGACCACGACTGGAGAACGCCCCCTTCTGAGTCAGGGGGCTGCATGCGTTGCCTCTGA  
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCAGTGGACCAAGGGCATGGAGCTTCACT  
CCTTGGCTGGCCAGGGAGTTGGGACTCAGAGGGACCACTGGGCCAGCCAGACTGGCCTCAA  
TGGCGGACTCAGTCACATTGACTGACGGGACCAAGGGCTGTGTGGTCAGAGCGCCCTCAT  
GGTGTGGCTGTGTGTAGGTCCCTGGGACACAAGCAGGCACCAAGTGTGGTATCTGGC  
GGAGCTCACAGAGTTCTTGAATAAAAGCAACCTCAGAACAC

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**FIGURE 270**

MTVIRFFPAASATKRVLPPLRVSSPRTWNPNVPEPRI PAPRLPKRMSGAPTAGAALMLCAA  
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA  
CQGTEGSTDPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLQS  
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFEIQ  
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGD  
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQ  
DHDLRRDKNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQLKKGIFWKTWRGRYYPLQATT  
MLIQPMAAEAAAS

**Important features:****Signal peptide:**

Amino acids 1-13

**Transmembrane domain:**

Amino acids 53-70

**N-glycosylation site:**

Amino acids 224-228

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 46-50;118-122

**N-myristoylation sites:**

Amino acids 50-56;129-135;341-347;357-363

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 396-409

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**FIGURE 271**

CGGACGCGTGGGGAAACCCCTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
AACAAAGATGGCGCGCCGAAGGGAGCCTCTGGGTGAGGACCCAACTGGGCTCCGCCGCTG  
CTGCTGCTGACCATGGCCTTGGCCGGAGGTCGGGACCGCTTCGGCTGAAGCATTGACTCG  
GTCTTGGGTGATACGGCGTCTGCCACCGGCCTGTCAGTTGACCTACCCCTGCACACCTAC  
CCTAAGGAAGAGGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTCAATTGTCAGTT  
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAC  
TATTCCAATCTGATGAGCAAATATGCCATCTGGTGTCCAGAACATCAGCTGCCATTGCT  
GAAC TGAGACAAGAACAACTTATGCCCTGATGCCAAAATGCACCTACTCTTCCTCTAACT  
CTGGTGAGGTATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG  
ACTTTTATCTCAAGCCGATGACGGAAAAATAGTTATTCAGTCTAAGCCAGAAATCCAG  
TACGCACCACATTGGAGCAGGAGCCTACAAATTGAGAGAACATCTCTAAGCAAATGTCC  
TATCTGCAAATGAGAAATTACAAGCGCACAGGAATTCTTGAAGATGGAGAAAGTGTGGC  
TTTTAAGATGCCTCTCTTAACTCTGGGTGGATTAACTACAACCTTGTCCCTCTGGTG  
ATGGTATTGCTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT  
GAGAAGCTGAGTATCTATGGTACTTGGAGTTATGAATGAACAAAAGCTAACAGATATCCA  
GCTTCTCTTGTGGTTAGATCTAAACTGAAGATCATGAAGAACAGCAGGGCCTCTACCT  
ACAAAAGTGAATCTGCTCATTGAAATTTAAGCATTTCTTAAAAGACAAGTGTAAATA  
GACATCTAAAATTCCACTCCTCATAGAGCTTTAAAATGGTTTATTGGATATAGGCCTTAAG  
AAATCACTATAAAATGCAAATAAGTTACTCAAATCTGTG

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**FIGURE 272**

MAAPKGSLWVRTQLGLP<sub>1</sub>LLTMAAGGSGTASAEAFDSVLGDTASCHRACQLTYPLHTYPK  
EEELYACQRGCRLFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL  
RQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEIQA  
PHLEQEPNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTLVLSVMV  
LLWICCATVATAVEQYVPSEKLSIYGDLFMNEQKLNRYPASSLVVVRSKTEDHEEAGPLPTK  
VNLAHSEI

**Important features:****Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site:**

amino acids 90-94

**N-myristoylation sites:**

amino acids 28-34, 29-35, 31-37, 86-92

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**FIGURE 273**

CCCACCGTCCGAACCTCTCCAGCG**ATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGTG**  
CTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACCGA  
CCAGCTGAGCAGGCGGAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT  
GCAGGGTCACCAGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGCTCAT  
AGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAGTACAT  
CTGTATGAACAAGAGGGCAAGCTCATCGGGAAAGCCCAGCGGGAAAGAGCAAAGACTGCGTGT  
CACGGAGATCGTGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGGGCTGGTT  
CATGCCCTCACGCCAGGGCGGGCCAGGCTCCGCAGCCGCCAGAACCGCGCA  
GGCCCACCTCATCAAGGCCCTTACCAAGGCCAGCTGCCCTCCCCAACCACGCCAGAAC  
GAAGCAGTTCGAGTTGTGGGCTCCGCCACCCGCCAGAACGCCACACGGCGGCC  
GCCCTCACG**TAC**TCTGGGAGGCAGGGGCAGCAGCCCCCTGGGCCCTCCCCACCCCTTCC  
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGGCCAGATCCCCGAGGGAGGACCC  
TGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGAAAGGGCAGGCCGGTCCCCAGGGCGGC  
TGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAACGTGAGTGTACCCCTGA  
TCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCCGCTGAAAGGTAGC  
GACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCGGATCT  
CCCTCAGTCTGCCCTAGCCCCAAACTCCTCTGGCTAGACTGTAGGAAGGGACTTTGTT  
GTTTGTGTTTCAGGAAAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCACCTCA  
CATTCCACGACCCAGGCCTGCACCCACCCCAACTCCCAGCCCCGGAATAAAACCATTTCC  
TGC

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**FIGURE 274**

MGAARLLPNLTICLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS  
ATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLGKPSGKSKDGVTEIVLENN  
YTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGS  
APTRRTKRTRRPQPLT

**Important features:**

**Signal peptide:**

Amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

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**FIGURE 275**

TATTTACCATATCAGATTCACATTCA  
GGCTAGAATACTACGGACAGTC  
AGGGGATCCCTCAAGCTCAGCA  
AGTTTCTGAGGAAAATCCAGCG  
TTGGGGTGGACAGATGCCACTGA  
GACAAGATTACAAACTTGTGTTG  
TTACTGCCTGGTAGAACACTA  
TCTTTCTAAAGGTATAGCTGAGC  
AAGGTTAATGA  
ATTGCAATA  
GCTCTGTGAGACTCTGTGAG  
GGCTAGCTCCAGGTGGAGAAGG  
AGCTCCAGCTCCCACATAAAC  
AGTGGATGCCCTCAGGGGAAGAC  
GAGCTGAGACAGGAAACTC  
AGCTGAGTGGATGCCTCAGGG  
GAGCATTCA  
GACTGATGTCAA  
GAGCATTGAGTGTCTTT  
GCTAAAGACAAGAGCAA  
TTGGCTGTTCCATGACTGATTT  
GAGTGCTCTTT  
GTTAATTACAGTGTT  
GATGGCTTTGGGTAGGCAA  
ACACTAATATTGTGTTATTAAA  
GATGGCTTGGCTGAA  
GAGCTTATC  
GAGCAGTGA  
GATCTCTATTTCTCC  
GCTGCTGCG  
AAATTCA  
GCTGCGCAA  
AAATTGCTATAAA

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**FIGURE 276**

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGN  
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKSKKHSVMSRQDLQTLCCTDGC  
SMTDLSALC

**Important features:****Signal sequence:**

amino acids 1-18

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 107-111

**N-myristoylation sites:**

amino acids 3-9, 52-58, 96-102, 125-131

**Insulin family signature:**

amino acids 121-136

**Insulin family proteins:**

amino acids 28-46

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**FIGURE 277**

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTCTGCTGGATTAAAGACGG  
CCCACAGACCAGAACCTCCACTAATCTAAAATACATAGGTGGCTTGTCAAATTCAATTGATTAGTATTGT  
AAAAGGAAAAAGAAGTTCCTCTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT  
CAGATGAACAAACTTCTACACTGATTTTAAATCAAGAATAAGGGCAGCAAGTTCTGGATTCACTGAATCAAC  
AGACACAAAAAGCTGCAATATAGCAACTATGAAGAGAAAAGCTACTAATAAAATAACCCAACGATAGAAC  
TTTTTTCTCTTCTAAAAACAACATAAGTAAAGACTTAAATTAAACACATCATTTACAACCTCATTTCAAAT  
GAAGACTTTTACCTGGACCTAGGTGTCTATTCTCTACTAGTGGACACTGGACATTGAGAGGTGGACAAATT  
CAAATTAACCAAAACAGAGAAGATAACCCCTCGTGCACAGATGTAAGAGAGAAGCAAAGAAATGTGCATA  
CACATTCTGGTACCTGAACAAAGAATAACAGGGCCAATCTGTGTCACACCCAAGGGCAAGATGCAAGTACCAT  
TAAAGACATGATCACCCAGATGGACCTTGAAGGATGTGCTCTCAGGGAGAAGCGGGAGATAGATGT  
TCTGCAACTGGTGGATGTGATGGAAACATTGTGAAGGATGAGTAAGCTGCTGAGAAAGGAAAGCCGTAACAT  
GAACCTCTGTGTTACTCAACTCTATGCAATTATTACATGAGATTATCGTGAAGGGATAATTCACTTGAAC  
TTCCAACGGAAACAAAATCTCAATGTCAACACAGAAATGTTGAAGGATGGCAACAAGATAACAGGGAACTAGA  
GGTGAACATCGCTCCTGACTGATCTGTCAATAACCAATCTGTGATGATCACTTGTGGAAAGAACAGTGCCT  
GAGGATTTTCCCACAAAGACACCCATGTGTCCTCCCCACTTGTCCAGGTGGTCCACAACATATTCCCTAACAG  
CCAACAGTATACTCTGCTGCTGGAGGTAACGAGATTCAAGAGGATCCAGGTTATCCCAGAGATTAAATGCC  
ACCACCTGATCTGGCAACTCTCCACCAAAAGCCCTTCAAGATACCCACCGGTAACTTCAATGAAGGACC  
ATTCAAAGACTGTCAGCAAGCAAAGAGCTGGGATTCCGGTCACTGGGATTTATGATGTTAAACCTGAAAACAG  
CAATGGACCAATGCAAGTGGTGAACAGTTCTGGGACCTTCAAGTGGGACTGTTATTCAAGAAAAGAACAGA  
CGGCTCTGCAACTCTTCAGAAATTGGGAAATTATAAGAAAGGGTTGGAAACATTGACGGAGAAACTGGCT  
TGGACTGGAAATATCTATATGCTTAGCAATCAAGATAATTCAAGTTATTGATTGAATTAGAAGACTGGAGTGA  
TAAAAAGTCTATGCAAAACAGCTTCTGGAACCTGAAAGTGAATTCTATAGACTCGGCCTGGAAC  
TTACCAAGGGAAATGCAGGGATTCTATGATGTGGCATAATGGTAAACAATTACACACTGGACAGAGATAAAGA  
TATGATGCAAGGAAACTGCGCCCACTTCAAAAGGAGGCTGGTACAATGCCGTGACATTCTAACCTAAA  
TGGAGTATGGTACAGAGGAGGCCATTACAGAACGACCAAGATGGAATTCTGGGCGAACATAGAGGCGG  
GTCATACTCTTAAGAGCAGTTCAAGTGTGATCAAGCTATTGACTGAAGAGAGACACTCGCCAATTAAATGA  
CACAGAACCTTCTACTTTCAAGCTTAAATGTAATGTTACATGTATATTACTTGGCACAATTATTTCTAC  
ACAGAAAGTTTAAATGAATTTCACCGTAACTATAAAAGGGAACTTAAATGTTAGTTCTGTCATCTGTCAT  
TACTGCAGAAATTATGTTATCCACAACCTAGTTATTAAATTTATGTTGACTAAATACAAAGTTGTTTC  
TAAAATGTAATATTGCAACATGTAAGCAAATCTTAGCTATATTAAATCATAAAATCATGTTCAAGATA  
CTTAACAATTATTAAATCTAAGATTGCTCTAACGTCTAGTGAACAAATTATTAAATTTCAAGCCAATA  
ATGCATTTTATTAAATACAGACAGAAATTAGGGAGGAAACTCTAGTTGCAATAGAAAATGTTCTT  
CCATTGAATAAAAGTATTCAATTGAAATTGCTCTTACACGTAATGATTAAATCTGAATTCTTAATAAATA  
TATCCTATGCTGATTCTCCAAAACATGACCCATAGTATAAATACATCTATTAAATTTAAATTTCAAGTGT  
AAAATAATGCATGCAATTAAATGGTCAATTATAAAGACAAATCTATGAAATGAAATTCTCAGTGTATCTT  
CATATGATATGCTGAACACCAAAATCTCAGAAATGCAATTATGTTAGTTCTAAATCAGCAAATATTGGTATT  
ACAAAAATGCAGAATATTAGTGTGCTACAGATCTGAATTATGTTCTAATTATTACTTTCTAATT  
ACTGATCTTACTACTACAAAGAAAAACCAACCCATCTGCAATTCAAATCAGAAAGTTGGACAGCTTAC  
AACTTAACTGTCAGAACAGGTGGACTAAACAAACTCAAGGAACACTGTTGGCTGTTTCCGATACTGA  
GAATTCAACAGCTCCAGAGCAGAACGACAGGGCATAGCTTACAGTCCAAAATGCTAATTTCATTTCAAGTGT  
GTAACGCTTAGTCTCACAGTGTCTTAACTCATCTTGCATAACAAACTTACTGACTTTCTGGAAACATT  
TCCATTCAAGGAAATCATATTCACTGCTTAGAGGTGACCTTGCTTAATATATTGTAAGTAAAATTTAAAGA  
TAGCTCATGAAACTTTGCTTAAGCAAAAGAAAACCTCGAATTGAAATGTTGAGGGCAAACATGCACTGGGAAT  
AGCTTAATGTAAGATAATCATTGGACAACCTCAAATCCATCAACATGACCAATGTTTCTGACATCTC  
AAAATAAAACTCTGGTAAACAAATTAAACAAATATCCAAACCTCAAAAAAA

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**FIGURE 278**

MKTFTWTLGVLFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTFLVPEQRITGP  
ICVNTKGQDASTIKDMITRMDLENLKDVLSRQKREIDVLQLVVVDGNIIVNEVKLLRKESRNM  
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTMLKMATRYRELEVKYASLTDLVNNQ  
SVMITLLEEQCLRIFSRQDTHVSPPPLVQVVPQHIPNSQQYTPGLLGGNEIQRDPGYPRDLMPP  
PDLATSPTKSPFKIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSGPMQLWCENSLDP  
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYLGLENIYMLSQNQDNYKLLIELEDWSDKK  
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGGWW  
YNACAHSNLNGWYRGGHYRSKHQDGIFWAEYRGGSYSLRAVQMMIKPID

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation sites:**

Amino acids 160-164; 188-192

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 120-124

**Tyrosine kinase phosphorylation sites:**

Amino acids 173-180; 387-396

**N-myristoylation sites:**Amino acids 70-76; 110-116; 232-238, 343-349; 400-406; 467-473;  
475-487**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 440-453

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**FIGURE 279**

CCCACCGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCTGCCAGTCTGCCCGCGATCCCGC  
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGGCCAGCAGCCCCGCGCGGGAGCCGGACCGCCG  
CCGGAGGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTGCTGAAGCCCGAGTGCAGAAGCC  
CGGGCAAACGCAGGCTAAGGAGACCAAAAGCGCGAAGTCGCGAGACAGCGGACAAGCAGCGA  
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGCAGCAAAAGAAGCGGTGGTGGTGGCGTCG  
**TGGCCATGGCGCGGCTATGCCAGCTCGCTATCCGTCAAGAGAGGCAAGCCCGCGAGCGCG**  
AGAAATCCAACGCCCTGCAAGTGTTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA  
ACAAGTTAAATGTCTTTCCCGGGTCAAACCTCTCGGCTCCAAGAAAGAGGCGCAGAAGAAGAC  
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATAAGCCGACAAGGCTACCAACTTGCGAC  
TGCAGGGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTAAC  
TCATCCCTGTGGGTCTGCAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA  
TGAACAGTGAGGGATACTTGTACACCTCGGAACCTTACACCTGAGTGCAAATTCAAAGAAT  
CAGTGTGAAATTATTATGTGACATATTCAATGATATAACCGTCAGCAGCAGTCAGGCC  
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA  
ACAAGCCTGCAGCTCATTCTGCCTAAACCACTGAAAGTGGCATGTACAAGGAGCCATCAC  
TGCACCGATCTCACGGAGTTCTCCGATCTGGAGCGGGACCCCAACCAAGAGCAGAAGTGTCT  
CTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACG**TAGCCAGTGAGGGCAA**  
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTAGCAGTCCTCA  
CCCCAAAAGTTCAAATTGTCAGTGACATTACAAACAAACAGGCAGAGTTCACTATTCTATC  
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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**FIGURE 280**

MAAAIASSLIROKRQAREREKSACKVSSPSKGKTCDKNKLNFSRVKLFGSKRRRRPE  
PQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLPVGLRVVAIQGVQTKLYLAMN  
SEGYLYTSELFPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK  
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRVSGVLNGGKSMSHNEST

**Important Features:****N-glycosylation site:**

Amino acids 242-246

**Glycosaminoglycan attachment sites:**

Amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site:**

Amino acids 93-100

**N-myristoylation sites:**

Amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 231-239

**HBGF/FGF family proteins:**

Amino acids 78-94, 102-153

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**FIGURE 281**

CCAGGATGGAGCTGGGCCTGTATAAGCCATATTATTGTCTATGCTACTAGACATGGGGGGGA  
CTTGGTAAAAAGGTATTATCCAGCAGAGGGCTGGGAGCCCTGTCTTACTGAACCTGGCA  
ACCTGGATATTCTGAGACATATTTGGGGGATTCAGTAAAAAAGTGGGGATCCCCTCCA  
TTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTGACATTGGCAGTGCC  
AGTAGGGGTGGGATGAGCGAATATTCCAAAGCTAAAGTCCCACACCCCTGTAGATTACAAGAG  
TGGATTGGCAGGAGTGTGCCAAAATACAGTGGAAAGGTGCCTGAAGATATTAAACCACG  
TCTTGAAATTAGTGGTCTTGGCTTGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA  
GGGAAAGGGACGTTTCAATAGGAGGAAAACTCGAGGGTGGGATCCACTGAGGAGTACATA  
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTTAAGTGGCTGCTGTGGAGGG  
GGTACGTGAGGGGGGGCTGGGCTTATCCTCAGGTCCGTGGGTGGGCAAGCGAGTCGGGG  
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGAGCCCAGCGCGCTCCGG  
CGCCTGCCGGTTGGGGTGTCTCCTCCCGGGCGCTATGGCGCGCTGCCAGTAGCCTGAT  
CCGGCAGAACGCGGAGGTCCCGAGCCCCGGGGCAGCCGGCGGTGCGCGCAGCGCGCGT  
GTGTCCCCCGGCCACCAAGTCCCTTGCCAGAACGAGCTCCTCATCCTGCTGTCCAAGGTGCG  
ACTGTGCGGGGGCGGCCGCGCCGGACCGCGCCGGAGCCTCAGCTCAAAGGCATCGT  
CACCAAACGTGTTCTGCCGCCAGGGTTCTACCTCAGGCGAATCCGACGGAAGCATTCCAGGG  
CACCCAGAGGATACCAGCTCCTCACCCACTCAACCTGATCCCTGTGGCCTCCGTGTGG  
CACCATCCAGAGCGCAAGCTGGTCACTACATGCCATGAATGCTGAGGGACTGCTCTACAG  
TTCGCCGCATTCACAGCTGAGTGTGCTTTAAGGAGTGTTGAGAATTACTACGTCT  
GTACGCCCTGCTCTACCGCCAGCGTGTCTGGCCGGGCTGGTACCTCGGCCTGGACAA  
GGAGGGCCAGGTCAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCACTTCTGCC  
CAAGCTCCTGGAGGTGGCCATGTACCAAGGAGCCTCTCCACAGTGTCCCCGAGGCCTCCCC  
TTCCAGTCCCCCTGCCTGAATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA  
GCCAGGCCACCACCAACCTGT

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**FIGURE 282**

MAALASSLIRQKREVREPGGSRPVSAQRRCPRGCKSLCQKQLLILSKVRLCGGRPARPDRG  
PEPQLKGIVTKLFCRQGFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHYMA  
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK  
TKAAAHLPLKLLEVAMYQEPSLHSVPEASPSSPPAP

**Important features:****Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 54-60; 89-95; 131-137

**HBGF/FGF family signature:**

Amino acids 131-155

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**FIGURE 283**

**ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAACGGCAGGCCGGAGCAGCACTGG**  
GACC GGCGTCTGCCAGCAGGAGGCAGCAGCCCCAGCAAGAACCGCAGGCTCTGCAACGGC  
AACCTGGTGGATATCTTCTCAAAGTGCATCTCGGCCTCAAGAAGCGCAGGTTGCAGCGC  
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATTGCAGGAAGGCTACTACTTGCAA  
ATGCACCCCCGATGGAGCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTCAAC  
CTCATACCAGTGGACTACGTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC  
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTTAAAGAA  
TCTGTTTGAAAATTATTGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT  
AGAGCCTGGTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA  
ACCAAACCAGCAGCTATTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT  
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGTGACGCCAAGTAAAAGCACAAAGTGC  
TCTGCAATAATGAATGGAGGCAAACCAGTCACAAAGAGTAAGACAACAT**TAG**

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**FIGURE 284**

MAAAIASGLIRQKRQAREQHWDRPSASRRRSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLRR  
QDPQLKGIVTRLYCRQGYYLQMHPDGALDGTDSTNSTLFNLI PVGLRVVAIQGVKTGLYIA  
MNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK  
TKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASA IMNGGKPVNKS KTT

**Important features:****N-glycosylation sites:**

Amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

**N-myristoylation sites:**

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins:**

Amino acids 104-155, 171-198

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**FIGURE 285**

CGGACCCGTGGCGGACCGTGGCGGACCGTGGCGGACCGTGGCTGGTCAGGTCCAGGTTTGCTTG  
TCCTTTCAAAAATGGAGACACAGAAGAGGGCTTAGAAAAAGTTTGGATGGGATTATGTGGAAACTACCC  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCCTCCACCCCAGTCAGCAGCTCCCTGGCGGTGGTGAAGAGAC  
TCGGGAGTCGCTGCTTCAAAGTCCCCCGCTGAGTGAGCTCTCACCCAGTCAGCCAATGACCTCTCGGG  
TTCTCTGCTGACATCTGCCCTGGCGGCCAGAGACAGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
AGTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTACTAATG  
GAAGTATTACACAGCCAAGGTTCTCTCATACTTATCCAAGAAATACGGCTTGGTATGGAGATTAGCAGTAG  
AGGAAAATGTATGGATACAACCTACGTTGATGAAAGATTGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCCTGGTCTGGTACTGTACCAAG  
GAAAACAGATTCTAAAGGAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTGAACCAGGG  
TCTGCATCCACTACAACATTGTCATGCCACATTACAGAAGCTGTGAGTCCTCAGTGCTACCCCTTCAGCT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTAGTACCTTGAAGACCTTATCGATATCTGAACCA  
AGAGATGGCAGTTGGACTTAGAAGATCTATAGGCCAACTTGGCAACTTCTGGCAAGGTTTGGAA  
GAAAATCCAGAGTGGGATCTGAACCTCTAACAGAGGAGGTAAGATTACAGCTGCACACCTCGTAACCT  
CAGTGTCCATAAGGAAGAACTAAAGAGAACCGATACCATTCTGCCAGGGTCTGGTAAACGCTGTG  
GTGGGAACTGTGCCTGTTGCTCCACAATTGCAATGAATGTCAATGTGCCAAGCAGGTTACTAAAAAATACC  
ACGAGGTCTTCAGTTGAGACCAAAGACCGGTGCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGCAGAGGGAGCACAGGAGGATGCCCATCACCACCAGCAGCTTGT  
GAGCTGTGCAGTGCACTGGCTGATTCTATTAGAGAACGTATGCCTTATCTCCATCCTTAATCTCAGTTGCT  
TCAAGGACCTTCATCTTCAGGATTACAGTGCAATTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGCA  
ACAGCTCTTGAGAGGAGGCCAAAGGACAGGAGAAAAGGTCTCAATCGTGGAAAGAAAATTAAATGTTG  
TAAATAGATCACCAGCTAGTTTCAAGAGTTACCATGTCAGTATTCCACTAGCTGGGTTCTGATTTCAGTT  
GATACTGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGCACCTGATTCCGTTGCCCTGCTTAC  
TCTAAAGCTCCATGCTGGCCTAAATCGTATAAAACTGGATTTTTTTTGCTCATATTACAT  
ATGTAACCAACATTCTATGTAACAAACCTGGTTAAAGGAACATGTTGCTATGAAATTAAACTGT  
GTCATGCTGATAGGACAGACTGGATTTCATATTCTTATTAAAATTCTGCCATTAGAAGAACAGAAACTACA  
TTCATGTTGGAAGAGATAACCTGAAAAGAGACTGGCTTATCTCAGTTATCGATAAGTCAGTTATTG  
TTCTGTTGTAATTCTCCTTTGACATTATAACTGTTGGCTTCTAATCTGTTAAATATATCT  
ATTTTTACCAAAGGTATTTAATATTCTTTTATGACAACCTTAGATCAACTATTAGCTGGTAAATTCT  
AAACACAATTGTTATGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTGACAAAATACATGATTCA  
TTCTCGTATGGGCTAGAGTTAGATTAACTGCAATTAAAAACTGAATTGGAATAGAATTGTAAGTTGCAA  
GACTTTGAAAATAATTAAATTATCATATCTCCATTCTGTTATTGGAGATGAAAATAAAAGCAACTTATGA  
AAGTAGACATTCAAGATCCAGCCATTACTAACCTATTCTTTGGGAAATCTGAGCCTAGCTCAGAAAACAT  
AAAGCACCTTGAAAAGACTTGGCAGCTCCTGATAAACGCGTGTGCTGCAAGTAGGAACACATCCTATT  
TTGTGATGTTGTTATTATCTTAAACTCTGTTCCATACACTGTATAAAATACATGGATATTGTTATGTACA  
GAAGTATGTCCTTAACCAGTTCACTTATTGTAACCTGCAATTAAAAGAAAATCAGTAAAATTTGCTTGT  
AAAATGCTTAATATNGCCTAGGTTATGTGGTCACTTGAATCAAAATGTATTGAATCATCAAATAAAGA  
ATGTGGCTATTGGGAGAAAATTAAAAAAAAAGGTTAGGGATAACAGGGTAATGCC

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**FIGURE 286**

MSLFGLLLTSLAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF  
PHTYPRNTVLWWRILVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEEPESDGTILGRWCGS  
GTVPGKQISKGNQIRIRFVSDNEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNA  
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTP  
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQLRPKT  
GVRGLHKSLTDVALEHHHECDCVCRGSTGG

**Important features:****signal sequence:**

Amino acids 1-14

**N-glycosylation sites:**

Amino acids 25-29;55-59;254-258

**N-myristoylation sites:**

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

**Amidation site:**

Amino acids 229-233

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**FIGURE 287**

CAGCGCTGACTGCGCCGCCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCCTCCC  
CGCTCGGCCTGGCCAGGCCCGCGCT**ATGGAGTTCCCTGGGCCCCCTCTGGGTCTGTGCT**  
GCAGTCTGGCCGCTGCTGATGCCACACCGTCTCTGGAACAGTTCAAATCCAAGTTCCCGA  
ATGAGGACTACACCATACTGTGAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG  
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG  
AGTACCAAGCTGTGCCAGGCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG  
CCAAGCATGGCCGGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTCACCCCTGGCA  
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCAAACCCATCCACCAGCATGAAGACC  
GCTGCTTGAGGTTGAAGGTGACTGTCAGTGGAAAATCACTCACAGTCCTCAGGCCATGACA  
ATCCACAGGAGAAGAGACTTGAGCTGAGCAGATGACCCAGGGTGCAGGTTCTACATAGCATGGTC  
ACAGTGCTGCCAACGCCCTTCCACTTGCTGGACTGTGCTGCTCCTCCACTTCTGCTGC  
**TGCAAACCCCGTGAAGGTGTGCCACACCTGGCTTAAAGAGGGACAGGCTGAAGAGAGGGA**  
CAGGCACTCCAAACCTGTCTGGGCCACTTCAGAGCCCCAGCCCTGGAACCAACTCCCAC  
CACAGGCATAAGCTATCACCTAGCAGCCTAAAACGGTCAATATTAAGGTTCAACCGGAA  
GGAGGCCAACCAGCCGACAGTGCACCTTCCACCTCAGGGATGGAGAAAGAAGTG  
GAGACAGTCCTTCCCACCATTCCTGCCCTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC  
CCTTAAGGCACAGTGGAGCTGAGCTGGAAAGGGCCACGTGGATGGCAAAGCTGTCAAAGA  
TGCCCCCTCAGGAGAGAGCCAGGATGCCAGATGAAGTGAAGGAAAGCAAGAACAG  
TTTCTTGCTTGGAAAGCCAGGTACAGGAGAGGCAGCATGCTGGCTGACCCAGCATCTCCAG  
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTGTAGCCAGGTACTGCATTCTCTCCAT  
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGCTGTGCCAACCTGTCTTAGAGTG  
TAGCTGTAAGGGCAGTGCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCC  
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTCTGCTGATTCTACAACGGAGTTT  
TTTATACAATGTTCTTGTCTAAAATAAGCAATGTGTTTTCGG

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**FIGURE 288**

MEFLWAPLLGLCCSLAAADRHTVEWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM  
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHSY  
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPQEKRЛАADDPEVRVLHSIGHSAAPRLFPL  
AWTVLLLPLLQTP

**Important features:**

**Signal sequence:**

Amino acids 1-17

**N-glycosylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 118-127

**N-myristoylation site:**

Amino acids 10-16

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**FIGURE 289**

CGGACGGCGTGGCGGACGGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTTC  
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAG**ATGG**CCCATGGCCCCGAAGGGC  
CTAGTCCCAGCTGTGCTTGGGCCTCAGCCTTCTCAACCTCCAGGACCTATCTGGCTC  
CAGCCCTCTCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACTGCCGG  
GGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACTTGGAGGTGGA  
AACACTGCCCTGGGAGGAAGAGAATTGTCCAATACAAAGACAGTGAGACCCGCTGGTAGAG  
GTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCACCGCCTGCTGGAGCTGAGTGAG  
GAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTCCAGTGGCTG  
TGCTCAGATTCCCTGAAGCTCTGTCGCCCCGCAGGCACCTTCGGGCCCTCTGCCTCCCTGT  
CCTGGGGAAACAGAGAGGCCCTGCGGTGGTACGGGCAGTGTGAAGGAGAACGGACACGAGGG  
GGCAGCGGGCACTGTGACTGCCAACCGGCTACGGGGTGAGGCCTGTGCCAGTGTGCCCTT  
GGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGTGGCCCTGT  
GCCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAACGGCTGGCCCTGCAT  
CACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCAACGTGGAGCTGACCAA  
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCAGACTGTGCCAAGGCCTGCCTAGGCTGC  
ATGGGGGCAGGGCAGGTGCGTGTAAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGCTCCAAG  
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGAGAGAACAGCAGTGTGAAAAC  
ACCGAGGGCGGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAGATGGAAGGCATCTGTG  
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGACAGAACGAGCTGGTGGTG  
CTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGCCACGCTGGCTGCTAAGGGCAG  
TTGGTGTTCACGCCATCTCATTGGGCTGTGGCGGCCATGACTGGCTACTGGTGTCAAG  
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA**TAA**TCGCGGCCACCACCTGTAGGA  
CCTCCTCCCACCCACGCTGCCCTCAGAGCTTGGCTGCCCTCCTGCTGGACACTCAGGACAGC  
TTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTGCCCTACAGAGCAGGCCAGGTACCC  
AGGCCCGGGCAGACAAGGCCCTGGGTAAAAAGTAGCCCTGAAGGTGGATACCATGAGCTCT  
TCACCTGGCGGGACTGGCAGGTTACAATGTGTGAATTCAAAAGTTTCCCTAATGGTG  
GCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTGGCCTCACAGGGTGGGCCATCACAG  
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCCTGTGTTCAACACATCCCCACACCCCA  
TTGCCACTTATTATTCATCTCAGGAAATAAGAAAGTCTTGGAAAGTTAAAAAAAAAAAA  
AAAAAAAAAAA

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**FIGURE 290**

MAPWPKGLVPAVLWGLSLFLNLPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT  
IRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQQE  
APDLFQWLCSDSLKLCCPAGTFGPSCLPGTERPCGGYGQCEGEGTRGGSGHDCQCAGYGG  
EACGQCGLGYFEAERNASHLVCSCFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTE  
GANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECETEVCP  
GENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFGIIICAL  
ATLAAKGDLVFTAIFIGAVAAMTGYWLRSDRVLEGFIKGR

**Important features:****Signal sequence:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 342-392

**N-glycosylation sites:**

Amino acids 79-83;205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 290-294

**Aspartic acid and asparagine hydroxylation site:**

Amino acids 321-333

**EGF-like domain cysteine pattern signature:**

Amino acids 181-193

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**FIGURE 291**

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**FIGURE 292**

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPANVTLTLSANRLP  
GLPEGAFREVPLQLQSLWLAHNEIRTVAAGALASLSHLKSLDLHNLISDFAWSDLHNLSALQL  
LKMDSNELTFIPRDAFRSILRALRSLQLNHNRHLHTLAEGTFTPLTALSHLQINENPDFDCTCGIV  
WLKTWALTTAVSIPEQDNIACTSPHVLKGTPSLRPLPLPCSAPSVQLSYQPSQDGAELRPGFV  
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLIP  
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP  
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFLTSF

**Important features:**

**Signal peptide:**  
amino acids 1-18

**Transmembrane domain:**  
amino acids 403-418

**N-glycosylation sites:**  
Amino acids 51-55, 120-124, 309-313

**Tyrosine kinase phosphorylation site:**  
amino acids 319-326

**N-myristoylation sites:**  
amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329, 334-340,  
350-356, 394-400

**Amidation site:**  
amino acids 355-359

**Leucine Rich Repeat:**  
amino acids 51-74, 75-98, 99-122, 123-146, 147-170

**Leucine rich repeat C-terminal domain:**  
amino acids 180-230

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**FIGURE 293**

ACTTGGGAGCAAGCGGCCGCGGAGACAGAGGCAGAGGAGCTGGGGCTCCGTCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGGCCGGCTCGAGCCTTGGCCAGGGAGGCGAGGAGCCAGCAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCCAGGCAGGGCTCGAGCCTTGGCCAGGGAGGCGAGGAGCTGGAGAGTTCTGTGAGAACAGCAGGGCT  
GCTTTCTGATCCTCGGACAGATCGCTCCTCCCTGCCAGGGAGGCGAGGAGCTGGAGAGTTCTGTGAGAACAGCAGGGCT  
CTAGGGGAGACACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTTCTGTGAGAACAGCAGGGCT  
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAGGAGTTCATCGTGACA  
TCTTGCAATTCTTGGACATTGGTCTGTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGGAGACCTCAGGACTCTGTGGCCAGGGTGGCTGCTA  
AGGCACGGGACACGGGATCCTAATCTTGGCCATTGGTGTGGGGCAGAGTCAACACCTTGAAGTCCATTG  
GGAGTGGAGCCCCATGAGGACCATGTCTTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGACGGCCCACATGTGCAAGCACCTGGAGCATACTGTGCCACTTCTGCATCAACATCCCTG  
GTCATACGTCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGAATCCAGGATCTG  
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTGAATGTGCCGGCTCTTGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAGAGGTGTGTGGCTGTGGACTACTGTGCCCTAGAAAACACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGGCCAGTGCCTGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTCACAAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGTGCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGTACACTCTGGACCCCATGGCAAAACCTGCAAGGGAGTGACCTGTGCA  
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACGGAGGATTCCTCGTCTGCCAGTGCTAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGTGGATTACTGCCCTGTGAGTGACCATGGTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTGCCTGTCACTGTGCTGAGGGACACGTGCTCCGAGCAGTGAGGAAAGACGTGTG  
CAAATGGACTCTTGTGCTGGGGACACGGTTGTGAACATTGTGTAAGCAGTGAGGATTCGTTGTGTT  
GCCAGTGTGTTGAAGGTTATATACTCGTGAAGATGGAAAACCTGCAAGAAGGAAGATGTCTGCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTAACAGACTGACGACTCATACACGTGCAAGTGTGGAGGGATTCCGGTCG  
CTGAGGATGGGAAACGCTGCCAGGAAGGATGTCTGCAAAATCAACCCACATGGTGTGCAACACATTGTGTTA  
ATAATGGAAATTCTACATCTGCAAAATGCTCAGAGGATTGTTCTAGCTGAGGACCGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAGAGTCTGGAGAAGAGAATTGGAGGTG  
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGACAATTCCCCAAAGCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCAACTCAGCCAAAGACATGAAAAAAGCCGTGCC  
ACATGAAAATACATGGGAAAGGGCTCTGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG  
GAGAAGGGCCAGGGCCCTTCCAACAGGGTGCCAGAGCAGCAGGAGCTTGTTGTCACCGACGGAGGGCTCAGGATG  
ACGTCTCGAGTGGGGAGTAAAGGCAAGGCCAATGGTATCACTATGCTGTTGGGTAGGAAAAGCCATTG  
AGGAGGAACATACAAGAGATTGCCCTGTGAGCCACAAACAAGCATCTTCTATGCCAGACTTCAGCACAATGG  
ATGAGATAAGTGGAAAACCTCAAGAAAGGCACTGTGAGGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCAG  
CAGGGAACTGCCAAAACGGTCCAACAGCAACAGAACTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTCAGTGCACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTT  
CCCATTCAACAAACCTCAGGAAGCCCTTGGAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAAAACGAAGAAGTAAGAAAATTAACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC  
TGGAAAATGCCCTGAGATACAGATGAGATTAGAAAATCGGCACACATTGTTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAGTATAACTAACTTGTATAAATTCTAGGAAAAAAATCCT  
TCAGAATTCTAAGATGAATTACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC  
AACTTGCTTCTGCCCTACCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAGTTGCAAGTCTTACT  
CTGAGAACACTGCCATAGGAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGATTTTATACAATATAAAATTCAACTTCAG

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**FIGURE 294**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIID  
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKR  
MRHLSTGTMGLAIQYALNIAFSEAEAGRPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI  
LIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFOKKLCTAHMCSTLEHNCAGF  
CINIPGSYVCRCQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEEDG  
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGCEHECVN  
MEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTC  
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSQDGKTCALKDSCALGDHGCEHSCVSED  
SFVCQCFCGYILREDGKTCRRKDVCQAIIDHGCEHICVNSSDSYTCECLEGFRLAEDGKRCRK  
DVCKSTHHGCEHICVNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVIDGSKSLGEENF  
EVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKAVAHMKYMGKGSMT  
GLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA  
IEEEELQEIASEPTNKHLYAEDFSTMDEISEKLKGICEALEDSGRQDSPAGELPKTVQQPT  
ESEPVTINIQDLLCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM  
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Important features:****Signal sequence:**

Amino acids 1-23

**N-glycosylation site:**

Amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 115-119; 606-610; 892-896

**N-myristoylation sites:**Amino acids 133-139; 258-264; 299-305; 340-346; 453-459; 494-500;  
639-645; 690-694;  
752-758; 792-798**Amidation sites:**

Amino acids 314-318; 560-564; 601-605

**Aspartic acid and asparagine hydroxylation sites:**Amino acids 253-265; 294-306; 335-347; 376-388; 417-429;  
458-470; 540-552; 581-593

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**FIGURE 295**

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGTGCCTCTCCCGCAGCGCTACCCGC  
**CAT**CGCCTGCCGCCGGCCGCCTGGGCTCCTGCCCTCTGCTGCTGCCGCCGC  
GCCGGAGGCCAAGAACGCCACGCCCTGCCACCGGTGCCGGGGCTGGTGGACAAGTTAA  
CCAGGGATGGTGGACACCGCAAAGAACAGAAACTTGGCGGGAACACGGCTTGGAGGAAAA  
GACGCTGCTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATCCTGGAGGGCTGTGCGA  
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGACCTGGAGGCCTGGT  
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTGTGAAGACACTGAAAGT  
GTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC  
CTGCAGCGGGAAATGCCACTGCAGCGAGATGGGAGCAGACAGGGCGACGGTCCGCCGGTG  
CCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG  
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCTGCAAGACGTGCTCGGCCCTGAC  
CAACAGAGACTGCCGAGTGTGAAGTGGCTGGGTGCTGGACGAGGGCGCTGTGGATGT  
GGACGAGTGTGCCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAAGAACGCCAACGG  
CTCCTACACGTGCAAGAGTGTGACTCCAGCTGTGAGGGCTGCACAGGGAAAGGCCAGGAAA  
CTGTAAAGAGTGTATCTGGCTACCGCAGGGAGCACGGACAGTGTGCAAGATGTGGACGAGTG  
CTCACTAGCAGAAAAACCTGTGAGGAAAACGAAAACGCTACAATACTCCAGGGAGCTA  
CGTCTGTGTGTCCTGACGGCTTCGAAGAACCGAAGATGCCGTGTCGCCGCCAGAGGC  
TGAAGCCACAGAAGGAGAAAGCCGACACAGCTGCCCTCCCGCAAGACCTG**TAA**TGTGCCGG  
ACTTACCCTTAAATTATTCAAGAGGATGTCCCGTGGAAATGTGGCCCTGAGGATGCCGTCT  
CCTGCAGTGGACAGCGCGGGAGAGGGCTGCCTGCTCTAACGGTTGATTCTCATTGTC  
TTAACAGCTGCATTCTGGTTCTAAACAGACTTGTATATTGATAACAGTTCTTGT  
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAA

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**FIGURE 296**

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKNFGGGNTAEEK  
TLSKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKV  
CCSPGTYPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR  
NETHSICTACDESCCKTCSGLTNRDGECEVGWLDEGACDVDECAAEPPPCSAAQFCKNANG  
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY  
VCVCPDGFEETEDACVPPAEAATEGESPTQLPSREDL

**Important features:****Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 190-194; 251-255

**Glycosaminoglycan attachment sites:**

Amino acids 149-153; 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 303-310

**N-myristoylation sites:**Amino acids 44-50; 54-60; 55-61; 81-87; 150-156; 158-164; 164-170;  
252-258; 313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

**EGF-like domain cysteine pattern signature:**

Amino acids 166-178

**Leucine zipper pattern:**

Amino acids 94-116

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**FIGURE 297**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGAGAAAGAGAAAGAGGAAG  
ATGTTGGCAACATTTATTAACATGCTCACAGCCGGACCTGGCATGCTGCTATTCTGCATGACATTT  
AGAACGATGGATTAAATATTTACTTCTAAATAATGAATTACTCAATCTCTATGACCATCTATACATAC  
CACCTCAAAAGTACATCAATATTATATCATTAAGGAATAGTAACCTCTCTCCATATGCATGACATTT  
TTGGACAATGCAATTGTGGCACTGGCACTTATTCAGTGAAGAAAACCTTGTTCTATGGCATTCACTC  
GACAAATGCAAGCATCTCCTTATCAATCAGCTCTTGAACCTACTGACTGACTGTGAATCCTTAAGGGC  
CCATTACATTCGAAGAAGAAGCTAAGATGAAGGACATGCCACTCGAATTCATGTGACTTGGCTAGCTA  
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGT  
TTACACCCAGATCCATTATGGAAGCATTACAGTGGATTGTAATGATTAGGTCTTTAACTTCCCAGCCA  
GATTGCCAGCTAACACACAGATTCTCCTACAGACTAACATATTGAAAAATTGAATACTCCACAGACTTC  
CAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAATATTAAATGTAAGGAGATGC  
CTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGAACTGCCGAAAAATGTCGTCCGAACGTGAGCA  
ACTTACAAGAACTCTATATTAAATCACAACCTGTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATC  
TTCTCGACTTCATCTCAATTCAAATAGATTGCAAGATGATCAACAGTAAGTGGTTGATGCTCTCAAATCTAG  
AGATTCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTAAACCTCTTATCAATCTCGCA  
GCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTGGACTGGAAAACCTAGAAAGCA  
TCTCTTTTACGATAACAGGTTATTAAAGTACCCATGTTGCTCTTCAAAAGTGTAAATCTCAAATTGG  
ATCTAAATAAAAATCCTATTAAATAGAAATACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGG  
TAAATAATATGCCCTGAGCTGATTCCATCGATAGTCTGCTGTGATAACCTGCCAGATTAAAGAAAATAGAAG  
CTACTAACACCCCTAGATTGCTTACATTCCCCAATGCACTTCAAGCTGCCAAGCTGGAACTCATG  
TGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACATTGAGTCTGCTGCCAACCTCAAGGAAATCAGCATA  
ACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTTGGATGAACATGAACAAAACCAACATTGATTGAGC  
CAGATTCACTGTTGCGTGGACCCACCTGAATTCCAAGGTCAGAATGTCGGCAAGTGCATTCAAGGACATGA  
TGGAAATTGCTCCCTTATAGCTCTGAGAGCTTCCCTCTAATCTAAATGTAAGGCTGGAGCTATGTT  
CCTTCACTGTAGAGCTACTGCAAGAACACAGCCTGAAATCTACTGGATAACACCTCTGGTCAAAACTCTG  
CTAATACCCGACAGACAAGTCTATGTCATTCTGAGGGAAACACTAGATATAATGGCTAACTCCAAAGAAG  
GGGGTTATATACTTGATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT  
CTTTCCACAAGATAACAATGGCTTTGAATATTAAAGAGATATTCAAGGCAATTCAAGTTGGTGTCT  
GGAAAGCAAGTTCTAAAATTCTCAAAATCTACTGTTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCATGCTG  
CGCAAAGTGCAGAACCATCTGATGTCAAGGTATATAATCTACTCATCTGAATCCATCAACTGAGTAAAAA  
TTTGATATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAATGTGAAATGTCAACCAAGGTTGCACC  
CTGATCAAAGAGTATGAAAAGATAATACCAACACATTGCGCTGTCAAGACTGAAAATTCTCATGCTG  
GTGTGATATGCTTATCAGCTGCCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACT  
TACAGAAACCAACCTTGCAATTAGGTGAGCTTATCCTCTGATAAAATCTGGGAAGCAGGAAAAGAAAAAA  
GTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGTCCAAAAACCAAGGAAACCTA  
CTCCAAAATGAAC

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**FIGURE 298**

MKDMPLRIHVLLGLAITTLVQAVDKVKDCPRLCCTCEIRPWFTPRSITYMEASTVDCNDLGLLT  
PARLPANTQILLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLEEN  
KLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFDALPN  
LEILMIGENPIIRIKDMNFKPLINRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVP  
HVALQKVVLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPDLRKIE  
ATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRW  
MNMNKTNI RFM EPDSLFCVDPPEFQGQNVHQVFRDMMEICLPLIAPESFPSNLNVEAGSYVS  
FHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTCIATNLVGA  
DLKSVMIKV DGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVKTENSHAAQ  
SARI PSDV KVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTLM  
ACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTS  
LKVKATVIGLPTNMS

**Important features:**

**Signal sequence:**  
amino acids 1-22

**Transmembrane domain:**  
amino acids 633-650

**N-glycosylation site.**  
amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**  
amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**  
amino acids 570-579

**N-myristoylation site.**  
amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**  
amino acids 277-280

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**FIGURE 299**

GCTGTGGAACCTCTCACCGCACGAACTCAGCCAACGATTCTGATAGATTTGGAGTT  
TGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCTACCGTTAGGAACCTGGGGACAGAGCG  
CCCCGGCCGCCTGATGGCCGAGGCAGGGTGCAGCCCAGGACCCAGGACGGCGTCGGGAACCAT  
ACCATGGCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCA  
GTCCTAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCA  
CAGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAACAT  
ACTGGAGCCTGTAACCGTGCACAGAGGGTGTGGATTACACCAACGCTTCAAACAATGAACCT  
TCTTGCTTCCCATGTACAGTTGTAATCAGATCAAAAACATAAAAGTTCCCTGCACCATGACC  
AGAGACACAGTGTGTCAGTGTAAAGAAGGCACCTCCGGAATGAAAACCTCCCAGAGATGTGC  
CGGAAGTGTAGCAGGTGCCCTAGTGGGGAGTCCAAGTCAGTAATTGTACGTCTGGATGAT  
ATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACA  
ATGAACACCAAGCCCCGGGACTCCTGCCCTAGCTGCTGAAGAGACAATGAACACCAGCCCAGGG  
ACTCCTGCCCTAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCTGCCCTAGCTGCT  
GAAGAGACAATGACCACCAGCCGGGACTCCTGCCCTAGCTGCTGAAGAGACAATGACCACC  
AGCCCCGGGACTCCTGCCCTTCTCATACCTCTCATGCACCATGCTAGGGATCATAGTTCTA  
ATTGTGCTTCTGATTGTGTTGTTTGAAAGACTTCAGTGTGGAAGAAATTCCCTTACCTG  
AAAGGTTCAAGTAGGCGTGGCTGAGGGCGGGGGCGCTGGACACTCTGCCCCCTGCCCTCCCT  
CTGCTGTGTTCCACAGACAGAAACGCCCTGC

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**FIGURE 300**

MARIPTKLKFVVVIVAVLLPVlaysATTARQEEVPQQTVAPQQQRHSFKGECPAGSHRSEHT  
GACNPCTEGVDYTNASNNEPSCFPCTVKSDQHKSSCTMTRDVCQCKEGTFRNENSPEMCR  
KCSRCPSGEVQVNCTSDDIQCVEFGANATVETPAAEETMNTSPGT PAPAAEETMNTSPGT  
PAPAAEETMTTSPGT PAPAAEETMTTSPGT PAPAAEETMTTSPGT PASSHYLSCTIVGIIVLI  
VLLIVFV

**Important features:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 240-259

**N-glycosylation site:**

Amino acids 77-81;140-144;156-160

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 126-130

**N-myristoylation sites:**

Amino acids 56-62;72-78;114-120;154-160;233-239

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**FIGURE 301**

CACAAGCATCTTAAATTGAATCCACAAAGTTCATGTAATGAAAAGAAATACATAATTTAAT  
TCAACCCGAGTGTTCAGAACAGAGATTGTATTGCTTAAATTGCTACAGTAATTCAAGAGACA  
GCCCTGTCTGGACACAGAGTTACTGTGGATTTAAGAGACTCAGTTAAAGAATTAGGAATT  
TCTGATTCATTTAAAGGATTACAAATTCAACCCCTGAAAACAAAGCAAATTGAACAGG  
AAAAAAAAAAAAGAAGATGGGTTTTAAGTCCAATATATGTTATTTCTTCTTTGGAGTC  
AAAGTACATTGCCAATATGAAACTTATCAGTGGATGAAGACTATGACCAAGAGCCAGATGAT  
GATTACCAAACAGGATTCCCATTCTGCAAAATGTAGACTACGGAGTCCCTTCATCAGTAT  
ACTTTAGGCTGTGTCAGTGAATGTTCTGTCCAACTAACCTTCATCATCAATGTACTGTGAT  
AATCGCAAACACTCAAGACTATCCAAATATTCCGATGCACATTCACTACCTTCAGTTC  
AATGAAATTGAGGCTGTGACTGCAAATTCAATTCAATGCAACTCATCTTAAAGAAATTAAAC  
CTCAGCCACAACAAAATTAAATCTCAAAAGATTGATTATGGTGTGTTGCTAAGCTTCAAAT  
CTACTACAACCTTCATCTAGAGCATAATAATTAGAAGAATTCCATTCCCTTCCTAAATCT  
CTGGAAAGACTCCTCTGGTTACAATGAAATCTCAAACACTGCAGACAAATGCTATGGATGG  
CTAGTAAACTTGACCATGCTGATCTCTGTTATAATTATCTCATGATTCTCTGCTAAAGAC  
AAAATCTTGCCAAAATGGAAAAACTAATGCAGCTCAACCTCTGCAGTAACAGATTAGAATCA  
ATGCCTCCTGGTTGCCTCTTCACTTATGTATCTGCTTAGAAAATAATTCAATTCTCT  
ATACCCGAAAATACCTCGACAAACTTCAAAACTTCATACTCTAAGAATGTACACAACAAA  
CTACAAGACATCCCATAATAATTTTAATCTTCAACATTGTAGAAACTCAGTGTGGACAC  
AACAAATTGAAGCAAGCATCTATATTCAAGAAATTGGAACACCTATACCTACAAAATAAT  
GAAATAGAAAAGATGAATCTTACAGTGATGTGCTTCTATTGACCCACTACATTACCACCAT  
TTAACATACATTGTTGACCAAAATAAAACTAAAAGAACCAATAAGCTCATACATCTCT  
TGCTTCCCTCATACACACTATTATTGGTGAACAACGAAGCACTAATGGTCAAACAATA  
CAACTAAAGACACAAGTTTCAGGAGATTCCAGATGATGATGATGAAAGTGAAGATCACGAT  
GATCCTGACAATGCTCATGAGAGGCCAGAACAAAGAGCAGAAGGGCACTTGACCTTCAT  
TATTATGAAAATCAAGAATAGCAAGAAACTATATAGGTATACACTACGACTTCACAAAACCTA  
TACTTAATATAGTAAATCTAAGTAAACATGTATTACTCAAAGTAATATATTAGAATTATGTA  
TTAGTATAAGATCAGAATTGAATTAAAGTTGTTGGTGACATCTGCATCATTCAAGGATTAG  
AACTTACTCAAAATAATGTAATCTTAAAAATATAAATTAGAATGACAAGTGGAAATCATAA  
ATTAAACGTTAATGGTTCTTATGCTCTTTAAATATAGAAATATCATGTTAAAGAAAAAAA  
AAAAAAA

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**FIGURE 302**

MGFLSPIYVIFFFFGVKVHCQYETYQWDEDYDQEPPDDYQTGFPFRQNVDYGVPFHQYTLGCV  
SECFCPTNFPSSMYCDNRKLKTIPNIPMHIQQLYLQFNEIEAVTANSFINATHLKEINLSHNK  
IKSQKIDYGVFAKLPNLLQLHLEHNNLEEFPPPLPKSLERLLLGYNEISKLQTNA MDGLVNLT  
MLDLCYNYLHDSSLKDKitAKMEKLMQLNLCSNRLESMPPGLPSSLMYLSLENNSISSIPEKY  
FDKLPKLHTLRMSHNKLQDIPYNIFNLPNIVELSVGHNKLKQAFYIPRNLEHLYLQNNEIEKM  
NLTVMCPSIDPLHYHHLTYIRVDQNLKEPISSYIFFCFPHIHTIYYGEQRSTNGQTIQLKTQ  
VFRRFPDDDESEDHDDPDNAHESPEQEGAEGHFDLHYHENQE

**Important features:****N-glycosylation sites:**

Amino acids 113-117; 121-125; 187-191; 242-246; 316-320

**Tyrosine kinase phosphorylation sites:**

Amino acids 268-275; 300-307

**N-myristoylation site:**

Amino acids 230-236

**Leucine zipper patterns:**

Amino acids 146-168; 217-239

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**FIGURE 303**

GCCCAGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAGC  
TGCAGCCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTACCA  
CGCTTGTGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGAATCTGGT**  
AGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTATGAT  
ACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGGGTTT  
AAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGAAACAGT  
CTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGGACCTCCA  
TCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCATGCCTCAA  
AGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAGTGTGCACAA  
AAATGCCTTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACAACCCCTGGCACTGCGACTG  
TACTCTACAGCAAGTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCACAACGTGATCTG  
TAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGCCAACGACGCTGA  
CCTTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCATGTTGGCTGGT  
CACTATGGTATCTCATATGTGGTATTATGTGAGGAAAATCAGGAGGATGCCGGAGACA  
CCTCGAATACTTGAATCCCTGCCAAGCAGGAGAAGCAGATGAACCTGATGATATTAG  
CACTGTGGT**ATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAAGTAGTTGCGATTGCA**  
GTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAAACTTGTATTCAGTTT  
TTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACATAAAATAATTGAGTTAG  
GTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGTAAGCTACTATCTGAACATT  
AGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTAATTAAAAGCAAATAAAAG  
CTTAACCTTGAACCATGGAAAAAAAAAAAAAAAAAAAAACAA

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**FIGURE 304**

MNLVDLWLTRSLSMCLLQS FVLMILCFHSASMC PKG CLSSSGGLNVTC SANLKEIPRDLP  
PETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSNRIQ  
SVHKNAFNNLKARARIANPWHCDCTLQQVLRSMASN HETAHN VICKTSVLDEHAGR PFLNAA  
NDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKKADEP  
DDISTVV

**Important features:**

**Signal sequence:**

Amino acids 1-33

**Transmembrane domain:**

Amino acids 204-219

**N-glycosylation sites:**

Amino acids 47-51; 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation sites:**

Amino acids 37-43; 45-51; 110-116

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**FIGURE 305**

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCTAGGGTTTCCACTTGTGAATTGTTCT  
ATACTAAAATTCGACCAAGACACCTTGTCTCCAAATGCAAATGAAATACCAATGAAATTGAGCCTGCT  
ATTGCAACATGGGATTTCAAGGAAATGGTGTACAATTGTGAAGATGATAATGAATGTGAAATTAACTCAGT  
CCTGTGGCAAAATGCTAATTGCACTAACACAGAAGGAAGTTATTGTATGTGTACCTGGCTTCAGATCCA  
GCAGTAACCAAGACAGGTTTATCACTAATGATGGAACCGTGTATAGAAAATGTGAATGCAAACGTCCATTAG  
ATAATGTCGTATAAGCTGAAATATTAATAAAACTTAAACAAAATCAGATCCATAAAGAACCTGTGGCTTG  
TACAAGAAGTCTATAAGAAAATTCTGTGACAGATCTTCACCAACAGATAATTACATATAGAAAATATTAGCTG  
AATCATCTTCAATTACTAGGTACAAGAACACATATCTCAGCAAGGACACCCTTCAACTCAACTCTTACTG  
AATTGTAAGGACCGTGAATAATTGTTCAAGGGATACTTGTGATTTGGGAAAGTTATCTGTGAATCATA  
GGAGAACACATCTAACAAACTCATGCACACTGTTGAACAAGCTTAAAGGATACTCCAGAGCTTCCAAAAGA  
CCACAGAGTTGATAACAAATTCAACGGATATAGCTCTCAAAGTTCTTTGATTCAATAACATGAAACATA  
TTCATCCTCATATGAATATGGATGGAGACTACATAAAATATTTCAAAGAGAAAAGCTGCATATGATTCAAATG  
GCAATGTTGCAAGTTGCATTTTATATTATAAGAGTATTGGCTTTGCTTCATCATCTGACAACCTTCTATTGA  
AACCTCAAATTATGATAATTCTGAAGAGGGAGAAAGACTCATATCTCAGTAATTCTAGTCAATGAGCTCAA  
ACCCACCCACATTATGAACTTGAAGGAAATTAAACATTACATTAACTGATCGAAAGGTACAGATAAGGTATAGGA  
GTCTATGTCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCTCAGAGGGCTGTGAGCTGACAT  
ACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTGCAATTGATGTCCTCTGGCTT  
CCATTGGTATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTT  
CCATATGCATTTTACCTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAACAAATTCTTGC  
GTAGCCTATTTCTGCTGAACCTGTTTCTGGATCAACAAACTAATAAGCTTCTGTCATCA  
TTGCCGACTGCTACACTACTCTTTAGCTGCTTTGATGGCATTGAGGACATACATCTATCTCA  
TTGTTGGGTGTCATCTACAACAAGGGATTGGCACAAGAATTTTATATCTTGGCTATCTAAGCCCAGCCG  
TGGTAGTTGGATTTCGGCAGCACTAGGATACAGATATTATGGCACAACAAAGTATGTTGGCTTAGCACCAGAAA  
ACAACATTATTGGAGTTTATAGGACAGCATGCTAACATTCTGGTTAATCTTGGCTTTGGAGTCATCA  
TATACAAAGTTTCGTCACACTGCAGGGTTGAAACCAAGTACTGGCTTGAGAACATAAGGTCTTGCAA  
GAGGAGCCCTGCTTCTGTCCTCTCGCACCCACCTGGATCTTGGCTTCCATGTTGTCACGCATCAG  
TGGTTACAGCTTACCTCTCACAGTCAGCAATGCTTCCAGGGATGTTCATTTTTATTCCGTGTGTTT  
CTAGAAAGATTCAAGAAGAATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAGGTAAACAT  
AGAGAATGGGATAATTACAACGTGACAAAAAATCCAAAGCTGTGGATGACCAATGATAAAAATGACT  
CATCAAATTATCCAATTATTAACACTAGACAAAAAGTATTTAAATCAGTTTCTGTTATGCTATAGGAAC  
GTGATAATAAGGAAATTATGTTATCATAGATAACTATGTTTCTATGTGAAATAGTTCTGTCAAATA  
GTATTGAGATATTGGAAAGTAATTGGTTCTCAGGAGTGTATCTGACCCAGGAAAGATTGTTGACAT  
ACACGAGAAGTATATGAATGTCCTGAAGGAAACACTGGCTGATATTCTGTGACTCGTGTGCTTGAACAT  
AGTCCCCTACCACTCGGTAAATGAGCTCCATTACAGAAAGTGGAAACATAAGAGAATGAAAGGGCAGAATATCAA  
CAGTGAAGGAAAGGAAATGATAAGATGTATTTGAATGAATGAACTGTTTCTGTAGACTAGCTGAGAACATTGTTGACAT  
AAAATAAGAATTGAAGGAAACACATTTCACCAATTGTAATTGTTCTGAACTTAATGTCCACTAAACAACTT  
AGACTTCTGTTGCTAAATCTGTTCTTTCTAATATTCTAAAAAAAAAAAGGTTACCTCCACAAATTGA  
AAA

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**FIGURE 306**

MKRLPLLVVFSTLLNCSYTQNCKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNECGNLTQSCGENANC  
TNTEGSYYCMCVPGFRSSNQDRFITNDGTVCIENVANCHLDNVRIAANINKTLTKIRSIKEPVALLQEVRNS  
VTDLSPDOIITYIEILAESSSLLGYKNNTISAKDTLSNSTLTEFVKTVNNFVQRDTFVWWDKLSVNHRRTHLTKL  
MHTVEQATLRLISQSFKTTEFDTNSTDIAKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFL  
YYKSIGPLSSSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAFVN  
SPDTMNGSWSSEGCELTYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLGIIISLICLAICTFW  
FFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGLHYFFLAFAWMCIEGIHLYLIVGVVIYN  
KGFLHKNFYIFGYLSPAVVVGFSAAALGYRYGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHT  
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLVHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEY  
YRLFKNVPCCFGCLR

**Important features:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 431-450; 494-515; 573-594; 619-636; 646-664

**N-glycosylation sites:**Amino acids 15-19; 21-25; 64-68; 74-78; 127-131; 177-181;  
188-192; 249-253; 381-385; 395-399**Glycosaminoglycan attachment site:**

Amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 360-364

**Tyrosine kinase phosphorylation sites:**

Amino acids 36-44; 670-677

**N-myristoylation sites:**Amino acids 38-44; 50-56; 52-58; 80-86; 382-388; 388-394;  
434-440; 480-486; 521-527**Aspartic acid and asparagine hydroxylation site:**

Amino acids 75-87

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**FIGURE 307**

CCAGGCCGGGAGGCACGCCAGCCGTCAAACGGGAACAGCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGT  
ATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCATGGC  
CCGGAGGAGCGCCTCCCTGCCGCCGCGCTGGCTGGAGCATCCTCTGTGCCTGCTGGCACTGCCGGCGGA  
GGCCGGGCCGCCAGGAGGAGGCTGTACCTATGGATCGATGCTACCAGGAAGAGTACTCATAGGATTGAGA  
AGAAGATATCCTGATTGTTTCAGAGGGAAAATGGCACCTTACACATGATTGAGAAAAGCGAACAGAGAAT  
GCCAGCTATTCCCTGTCATAATCCATTCCATGAATTTCACCTGGCAAGCTGCAGGGCAGGAGAACATTCATGA  
ATTCCCTGCTTGCCTCCCTGGATAAAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGT  
GCCTCACAAAGGCATCAGTTGTTCAAGTTGGTTCCATGCTTGAAAACAGGATGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCTTCTTAAACATG  
TCAACAAGCTGAGTGCCCAGGGGTGCCAAATGGAGGCTTTGTAATGAAACACGCATCTGCAGTGCTGA  
TGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTGACCCACGATGTATGAATGGTGGACTTGTGACTCC  
TGGTTCTGCATCTGCCACCTGGATTCTATGGAGTGAATGTGACAAAAGCAAACGCTCAACCACCTGCTTAA  
TGGAGGGACCTGTTCTACCCTGGAAAATGTTGCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAA  
ATGCCCAACCCCTGCAATGGAGGTAATGCAATTGTAAGGCAAATGTAAGTGTCCAAAGGTTACCGAGGG  
AGACCTCTGTTCAAAGCCTGTGCGAGCCTGGCTGTGGTCACATGGAACCTGCATGAACCCAAACAAATGCCA  
ATGTCAAGAAGGTTGCATGGAAGACACTGCAATAAAAGGTACGAAGGCCAGCCTCATACATGCCCTGAGGCCAGC  
AGGCCAGCTCAGGCAGCACAGCCTCACTAAAAAGGCCAGGAGCAGCGGGATCCACCTGAATCCAATT  
CATCTGGTGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTCATAGCCTTGTAAACTTTCACTGTGTT  
GAATGTTCAAATAATGTCATTACACTTAAGAAATCTGGCTGAATTGTTATTAGCTTCATTATAAATCACTGAGC  
TGATATTACTCTCCCTTAAGTTCTAAGTACGTCTGTAGCATGATGGTATAGATTCTGTTCACTGCT  
TTGGGACAGATTTATATTGTCATTGATCAGGTTAAATTTCACTGTGTTAGTTGGCAGATATTCTAAAT  
TACAATGCATTATGGTGTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAA  
GAATTTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCACTGAGATTGTTAGCTGAGATATTAGATGTTAC  
ATTTTAAAAAATTGCTCTAATTAAACTCTCAATACAATATTTGACCTTACCAATTCCAGAGATTCA  
GTATTAAAAAAAAAAATTACACTGTGGTAGTGGCATTAAACAATATAATATTCTAAACACAATGAAATAG  
GGAATATAATGTATGAACTTTGCATTGGCTGAAGCAATATAATATTGTAACAAAACACAGCTTACCT  
AATAAACATTTATACTGTTGTATGATAAAATAAGGTGCTGCTTAGTTGGAAAAA  
AAAAAAA

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**FIGURE 308**

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEEESLYLWIDAHQARVLIGFEEDILIVSEGKM  
APFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPLLGT  
VPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILOTPQNAIFFKTCQQAECPGGCRNG  
GFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCSTTCFN  
GGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKIGSKCKCSKGYQGDLCSPVCEPGCG  
AHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDPPESNYIW

**Important features:****Signal sequence:**

Amino acids 1-28

**N-glycosylation sites:**

Amino acids 88-92; 245-249

**Tyrosine kinase phosphorylation site:**

Amino acids 370-378

**N-myristoylation sites:**

Amino acids 184-190; 185-191; 189-195; 315-321

**ATP/GTP-binding site motif A (P-loop):**

Amino acids 285-293

**EGF-like domain cysteine pattern signatures:**

Amino acids 198-210; 230-242; 262-274; 294-306; 326-338

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**FIGURE 309**

CCACCGCGTCCGGTCTCGCTCGCTCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCGGG  
TTAGACTGGCGGGGGGAGGAGGCGGAGGAAAGGAAGCTGCATGCATGAGACCCACAGACT  
CTTGAAGCTGGATGCCCTCTGTGGATGAAAG**ATG**TATCATGGAATGAACCCGAGCAATGGAG  
ATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTGGCCG  
TGATCCTGTGGTTCACTGGCGTGTGCTCGGCCCTGCACAGCTCACGGCGGGTCGATG  
ACCTCAAGTGTGCTGACCCGGATTCCCAGAATGGCTTCAGGACCCAGCGGAGGGG  
TTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAGGGCGCTA  
CAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGATAATTCCA  
TCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATAACAAGACAT  
ATAGACATGGAGAGAAGCTAACATCACTGTGATGAAGGATTCAAGATCCGGTACCCGACC  
TACACAATATGGTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCCATCTGTCAG  
GCTGCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGCTCCAGACCTCCT  
TCCCGGTGGGACTGTGATCTCCTATGCTGCTTCCCAGATTAAACTGATGGGCTGCGT  
ATCTTGAGTGCTAACAAACCTATCTGGTGTCCAGCCACCCGGTGCCTGCTCTGGAAG  
CCCAAGTCTGTCCACTACCTCAATGGTAGTCACGGAGATTCTGCTGCCACCCGGCCCTT  
GTGAGCGCTACAACCACGGAACTGTGGTGGAGTTTACTGCGATCTGGCTACAGCCTCACCA  
GCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTCTTATCAAGTCTACTGCA  
TCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGACCACGTGGAAGATTGTGG  
CGTTCACGGCAACCAGTGTGCTGGTGCTGTCATCTGGCCAGGATGTTCCAGA  
CCAAGTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAGTCCAGCAGTGAACCTGACT  
TTGTGGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATGACGAAGCTGTGAGTGGCGGCT  
TGAGTGCCTTAGGCCCGGGTACATGGCTCTGTGGCCAGGGCTGCCCTACCGTGGACG  
ACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGACACAGGCCAGGGAGTCAGAAA  
CCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCAAAGTCTGTATTCAACCTCCAGGTGCC  
AAGAGAGCACCCACCTGCTCGGACAACCTGACATAATTGCCAGCACGGCAGAGGAGGTGG  
CATCCACCAGCCAGGCATCCATCATGCCACTGGGTGTTCTAAGAAACT**TGA**TTGATTA  
AAAAATTCCCAAAGTGTCTGAAGTGTCTTCAAATACATGTTGATCTGTGGAGTTGATTC  
CTTCCTCTCTGGTTAGACAAATGAAACAAAGCTGATCCTTAAATTGCTATGCTG  
ATAGAGTGGTGAGGGCTGAAAGCTGATCAAGTCTGTTCTTGACACAGACTGATTA  
AATTAAGNAAAAAA

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**FIGURE 310**

MYHGMNPSNGDFLEQQQQQQQPOSQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGIP  
ENGFRTPSGGVFFEGSVARFHQCQDGFKLKGATKRLCLKHFNGTLGWI PSDNSICVQEDCRIPO  
IEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLASSNG  
YVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLPPMVS  
HGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQTWPS  
ETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVDGVPVML  
PSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTTGPGESETCDSVGSSEL  
LQSLYSPPRCQESTHPASDNPDI IASTAEEVASTSPGIHHAHWVLFLRN

**Important features:****Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472**N-myristoylation site.**amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

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**FIGURE 311**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCTGAGCGCCGGTTGGATGGCCAGGTTGGAG  
CGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTGGACTAGGCCTGG  
AGGCCGCCGCGAGCCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAGGCT  
CGTGCCCACCCACCAAGTCCAGTGCCGACCAGTGGTTATGCGTGCCTCACCTGGCGCT  
GCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCCATGTA  
CCCAGAAAGGGCAATGCCAACGCCCTGGCCTCCCTGCCCTGCACCGGGCTCAGTGA  
GCTCTGGGAACTGACAAGAACTGCGCACTGCAGCCGCTGGCCTGCCTAGCAGGCGAGC  
TCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGCCACCCAGACT  
GTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAGGGATGCCA  
CAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCCACATCCTCTGCCGGAG  
GGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCCACATCCTCTGCCGGAG  
ACCAGTCTGGAAGCCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGCTCAGTGAAGCC  
TGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGGCCAGGAGCGCCTCCGCCACTGG  
GGTTACTGGTGGCCATGAAGGAGTCCTGCTGTCAGAACAGAACCTCGCTGCCCTTGAG  
GACAAGCACTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACAGGAGGAGAGCAGTGA  
TGCAGGATGGGTACCCGGGACACCAGCCCTCAGAGACCTGAGTTCTCTGCCACGTGGAACC  
TCGAACCCGAGCTCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCCTGGACACTCCCTATGGA  
GATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAGGGCTGCCAGGCAGC  
TCCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTGCCCGTCTGAGGGTGGCGA  
TTAAAGTTGCTTC

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**FIGURE 312**

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRT  
SGLCVPLTWRCDRDLDSDGSDEEECRIEPCTQKGQCPCPTGVSDCSGGTDKKLRN  
CSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVTLES  
VTSLRNATTMGPPTVTLSEVPVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLLLLSW  
LRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Important features:****Signal sequence:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 231-248

**N-glycosylation sites:**

Amino acids 126-130;195-199;213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation sites:**Amino acids 3-9;10-16;26-32;30-36;112-118;166-172;212-218;  
224-230;230-236;263-269**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 44-55

**Leucine zipper pattern:**

Amino acids 17-39

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**FIGURE 313**

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGCGGAGGCAGCAGGGCCAGCCTGGCCCCAGCCCACAC  
CTTCACCAGGGCCCAGGAGCCACCATGTGGCATGTCACTGGGCTACTGCTTGTGCTGCCGCTGGCTGGCAC  
TTGGCTCTGGTGCCCAGCAGGGCTGTGGCGCCGGAGCTAGCACCGGTCTGACCTGCGGGCATCGGGAC  
GCGGGAGGCCGGTACTGCCAGGAGCAGGACCTGTGCTGCCGCGCCGACGACTGTGCCCTGCCCTACCTG  
GGCGCCATCTGTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGTGCCCTGACTCTGGGACTTCTGC  
CTCGCGTGCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCTATCTATCCAGTCTGGAAACG  
TACTGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGTGCATGGATCCAGACATGATCAAAGC  
CATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACACAGCGCCTCTGGGCATGACCTGGGATGAGGGCAT  
TCGCTACCGCCTGGCACCATCCGCCATCTCCTCGGTCTGAACATGATGAAATTATACAGTGTGAACCC  
AGGGGAGGTGCTTCCCACAGCCTTCGAGGCCCTGTAGAAGTGGCCAACCTGATTCATGAGCCTCTGACCAAGG  
CAACTGTGAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTCTCAATCCATTCTGGGAC  
CATGACGCCCTGTCCGTGCCCCAGAACCTGCTGTCTTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGCG  
TCTCGATGGTGCCCTGGTGGTCTCGCGTCCGAGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGA  
ACGAGACGAGGCTGCCCTGCGGCCCCCTGTATGATGCACAGCGAGCCATGGTGGGGCAAGGCCAGGCCAC  
TGCCCACTGCCCAACAGCTATGTTAATAAACATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTCCAA  
CGACAAGGAGATCATGAGGAGCTGATGGAGAATGCCCTGTCAAGCCCTCATGGAGGTGCATGAGGACTTCTT  
CCTATACAAGGGAGGCATCTACAGCACGCCACGCCAGTGAGCCTGGGAGAGGAGCCTGCAAGGACGCTCAAAATACTGGACTGCC  
CCACTCAGTCAAGATCACAGGATGGGAGAGGAGCCTGCAAGGACGCTCAAATGAGTGCGCACATCGA  
CAACTCCTGGGCCCAGCCTGGCGAGAGGGCACTCCGCATCGTGCCGCCGTCAATGAGTGCACATCGA  
GAGCTTCGTGTGGCGTCTGGGCCGCTGGGATCCAGGTAAGGGCCGGAAAGAGGCCAATGGGCGGTGACCCAGCCTGCCGA  
CAGAGCCGGGCGCAGGCGGGGCCAGGGCGTAATCCCGCGGGTCCGCTGACGCAGCGCCCCGCCTGG  
AGCCGCGGGCAGGCGAGACTGGCGAGCCCCAGACCTCCAGTGGGACGGGCTGCCCTGGGAAGAG  
CACAGCTGCAGATCCAGGCCTCTGGGCCCCACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGCC  
CAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCGTTGCCAGGTTGGAG  
TGCAGTGGCCCATCAGGCTCACTGTAACCTCCGACTCCTGGGTTCAAGTGACCCCTCCACCTCAGCCTCTCAAG  
TAGCTGGACTACAGGTGCACCACCACACCTGGCTAATTTTGTATTGGTAAAGAGGGGGTCTCACTGTGT  
TGCCCAGGCTGGTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCCTGCCCTCCAAAGTGTGGGATTGCAGG  
CATGAGGCCACTGCACCCAGGCCGTATTCTTATTCTCAGATATTATTTCTTCAGTGTTAAAAAAA  
CCAAAGTATTGATAAAAAAAA

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**FIGURE 314**

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDCA  
LPYLGAIACYCDLFCNRTVSDCCPDFWDFFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNRCT  
CQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**Important features:****N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415**N-myristoylation site.**amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

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**FIGURE 315**

CGGACGCGTGGGCCCTGGTGGCCCAGCAAGATGGATCTACTGTGGATCCTGCCCTCCCTGT  
GGCTTCCTGCTTGGGGGCCTGCCTGCCTGAAGACCCAGGAACACCCCAGCTGCCAGGAC  
CCAGGGAACTGGAAGCCAGCAAAGTTGCCTCCTGCCAGTTGTCCGGAGCTCCAGGAAGTC  
CTGGGGAGAAGGGAGCCCCAGGTCCCTCAAGGGCCACCTGGACCACCAGGCAAGATGGGCCCA  
AGGGTGAGCCAGGCCAGAAACTGCCGGGAGCTGTTGAGCCAGGGGCCACCTTGAGCGGCT  
GGTACCATCTGTGCCTACCTGAGGGCAGGGCCCTCCAGTCTTGTGACATGGACACCGAGG  
GGGGCGGCTGGCTGGTGTTCAGAGGCCAGGATGGTTCTGTGGATTCTCCGCTTTGGT  
CCTCCTACAGAGCAGGTTTGGAACCAAGAGTCTGAATTCTGGCTGGAAATGAGAATTG  
ACCAGCTTACTCTCCAGGGTAACCTGGGAGCTGGGGTAGAGCTGGAAGACTTAATGGTAACC  
GTACTTCGCCACTATGCCACCTTCCGCCTCCTCGGTGAGGTAGACCACTACCAGCTGGCAC  
TGGGCAAGTTCTCAGAGGGCACTGCAGGGATTCCCTGAGCCTCCACAGTGGGAGGCCCTTA  
CCACCTATGACGCTGACCACGATTCAAGCAACAGCAACTGTGCAGTGATTGTCCACGGTGCCT  
GGTGGTATGCATCCTGTTACCGATCAAATCTCAATGGTCGCTATGCAGTGTCTGAGGCTGCCG  
CCCACAAATATGGCATTGACTGGCCTCAGGCCGTGGTGTGGCCACCCCTACCGCAGGGTTC  
GGATGATGCTTCGATAGGGACTCTGGCAGCCAGTGCCCTATCTCCTGTACAGCTCCGG  
ATCGTCAGCCACCTTGCCTTGCCAACCACCTCTGCTTGCCGTCCACATTAAAAATAAAAT  
CATTTAGGCCCTTC

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**FIGURE 316**

MDLLWILPSLWLLLLGGPACLKTQEHPSCPGPRELEASKVLLPSCPGAPGSPGEKGAPGPQG  
PPGPPGKMGPKGEPGPRNCRELLSQGATLSGWYHLCPEGRALPVFCDMTEGGGWLFQRRQ  
DGSVDFFRSWSSYRAGFGNQESEFWLGNENLHQTLQGNWELRVELEDFNGNRTFAHYATFRL  
LGEVDHYQLALGKFSEGTAGDSLISHSGRPFTTYDADHDSSNSNCAVIVHGAWWYASCYRSNL  
NGRYAVSEAAAHKYGIDWASGRGVGHPYRRVRMMLR

**Important features:****Signal peptide:**

Amino acids 1-16

**N-glycosylation site:**

Amino acids 178-182

**Glycosaminoglycan attachment site:**

Amino acids 272-276

**Tyrosine kinase phosphorylation site:**

Amino acids 188-197

**N-myristoylation sites:**

Amino acids 16-22;89-95;144-150;267-273

**Fibrinogen beta and gamma chains C-terminal domain signature:**

Amino acids 242-255

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**FIGURE 317**

CCCAAGCCAGCCGAGCCGCCAGAGCCGCGGGCGCGGGGGTGTGCAGGGCCAACCCCAGG**AT**  
**G**CTCCCTGCGCCTCCTGCCTACCCGGGTCTCTACTGCTCTGGCGCTGCTACTGTCCTT  
GGGATCAGCTCTCCTCAGGATTCTGAAGAGCCCGACAGCTACACGGAATGCACAGATGGCTA  
TGAGTGGGACCCAGACAGCCAGCAGTGCACAGAGTGTCTGACCATCCCTGAGGC  
CTGCAAGGGGAAATGAAGTGCATCAACCACATGGCGAGGGACCCCCGCCACAGTGCCTCCCGCTAACACCC  
TGCGTCATCAACGACCTACATGGCGAGGGACCCCCGCCACAGTGCCTCCCGCTAACACCC  
CAACCCCTGCCACCAGGCTATGAGCCGACGATCAGGACAGCTGTGTGGATGTGGACGAGTG  
TGCCCAGGCCCTGCACGACTGTCGCCAGCCAGGACTGCCATAACTTGCCTGGCTCCTATCA  
GTGCACCTGCCCTGATGGTTACCGCAAGATCAGGAGTGTGTGGACATAGACGAGTGCAG  
CTACCGCTACTGCCAGCACCGCTGCGTGAACCTGCCTGGCTCCCTCCGCTGCCAGTGCAGGCC  
GGGCTCCAGCTGGGCCTAACAAACCGCTCTGTGTTGATGTGAACGAGTGTGACATGGGGC  
CCCATGCGAGCAGCGCTGCTCAACTCCTATGGGACCTTCTGTGTCGCTGCCACCAGGCTA  
TGAGCTGCATGGGATGGCTTCTCCTGCAGTGTATTGATGAGTGTAGCTACTCCAGCTACCT  
CTGTCAGTACCGCTGCGTCAACGAGCCAGGCCCTTCTCTGCCACTGCCACAGGTTACCA  
GCTGCTGGCCACACGCCTCTGCCAAGACATTGATGAGTGTGAGTCTGGTGCACCGAGTGC  
CGAGGCCAAACCTGTGTCAACTTCCATGGGGCTACCGCTGCGTGGACACCAACCGCTGCGT  
GGAGCCTACATCCAGGTCTGTGAGAACCGCTGTCTCTGCCGCCCTCAACCCCTATGTC  
AGAGCAGCCTTCATCCATTGTGACCGCTACATGACCATCACCTCGGAGCGGAGCGTGC  
TGACGTGTTCCAGATCCAGGCACCTCGTCTACCCGGTGCCTACAATGCCTTCAGATCC  
TGCTGGAAAATCGCAGGGGGACTTTACATTAGGCAAATCAACAACTGTCAGGCCATGCTGGT  
CCTCGCCCGGCCGTGACGGGCCCCCGGAGTACGTGCTGGACCTGGAGATGGTCACCATGAA  
TTCCCTCATGAGCTACCGGGCAGCTGTACTGAGGCTCACCGTCTTGTAGGGCCTACAC  
CTTCT**G**AGGAGCAGGAGGGAGCCACCCCTCCCTGCAGCTACCCTAGCTGAGGAGCCTGTTGTGA  
GGGGCAGAATGAGAAAGGCAATAAAGGGAGAAAGAAAGTCTGGTGGCTGAGGTGGCGGGTC  
ACACTGCAGGAAGCCTCAGGCTGGGAGGGTGGCACTTGGGGGGCAGGCCAAGTTCACCTA  
AATGGGGGTCTCTATGTCAGGCCAGGGCCCCATTGACAGGAGCTGGAGCTCTGCAC  
CACGAGCTTCAGTCACCCCGAGAGGGAGGGAGGTAAACGAGGAGGGGGACTCCAGGCC  
CCAGAGATTGGACTGGCTGGCTGCAAGGGTCTAAGAAACTCCACTCTGGACAGCGCAG  
GAGGCCCTGGGTTCCATTCTAACTCTGCCTCAAACGTACATTGGATAAGCCCTAGTAGTT  
CCCTGGCCTGTTTCTATAAAACGAGGCAACTGGAAAAAAAAAAAAAA

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**FIGURE 318**

MLPCASCLPGSLLLWALLLGSASPQDSEEPDSYTECTDGYEWPDSQHCRDVNECLTIPE  
ACKGEMKCINHYGGYLCLPRSAAVINDLHGEGPPPVPPAQHPNPCPPGYEPDDQDSCVDVDE  
CAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYRCQHRCVNLPGSFRCQCE  
PGFQLGPNNRSCVDVNECDMGAPCEQRFCNSYGTFLCRCHQGYELHRDGFSCSDIDECSYSSY  
LCQYRCVNEPGRFSCHCPQGYQLLATRLCQDIDECESGAHQCSEAQTCVNFHGGYRCVDTNRC  
VEPYIQVSENRCLCPASNPLCREQPSSIVHRYMTITSERSVPADVFQIQATSVYPGAYNAFQI  
RAGNSQGDFYIRQINNVSAMVLARPVTGPREYVLDLEMVTMNSLMSYRASSVRLTVFGAYTF

**Important features:****Signal sequence:**

Amino acids 1-25

**N-glycosylation sites:**

Amino acids 198-202;394-398

**N-myristoylation sites:**Amino acids 76-82;145-151;182-188;222-228;290-296;305-311;  
371-377;381-387**Aspartic acid and asparagine hydroxylation sites:**

amino acids 140-152;177-189;217-229;258-270

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**FIGURE 319**

GCTGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTGCCTCCTC  
TCAAAGGTGCGTACCCAGCTGTGCCGACACCATGTACCTGCCCTGGCCACCTCCCCGATGC  
CCGCTGGGAGTACCCCTGGTCTGGATGGCTGTGGCTGCTGCCGGTATGTGCACGGCGCTG  
GGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCTGCCAGCCC  
GCAGGACCCGGTGGCCGGGGCCCTGTGCCTCTTGGCAGAGGACGACAGCAGCTGTGAGGT  
AACGGCCGCCTGTATCGGAAGGGGAGACCTCCAGCCCCACTGCAGCATCCGCTGCCGCTGC  
GAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATGTGCGGCTGCCAGCTGG  
TGCCCCCACCCCAGGAGGGTCGAGGTCTGGCAAGTGCCTGCCCTGAGTGGGTGTGCGGCC  
GGAGGGGACTGGGACCCAGCCCCCTCCAGCCAAGGACCCCAGTTCTGCCCTGTCT  
TCCCTGCCCTGGTGTCCCCCTGCCAGAATGGAGCACGCCCTGGGACCCCTGCTGACCACC  
TGTGGGCTGGGATGCCACCCGGGTCTCAACCAGAACCGTTCTGCCACTGGAGACCCAG  
CGCCGCCCTGTGCCCTGTCCAGGCCCTGCCACCCCTCAGGGTCGAGTCCACAAAACAGTGC  
**TTCTAG**AGGCCGGCTGGGAATGGGACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCC  
TGGGCCCTGGGCTGATGGAAGATGGTCCGTGCCAGGCCCTGGCTGCAGGCAACACTTAGC  
TTGGGTCCACCATGCAGAACACCAATTAAACACGCTGCCGGTCTGTCTGGATCCCGAGGTA  
TGGCAGAGGTGCAAGACCTAGTCCCCCTTCCTCTAACACTCACTGCCCTAGGAGGCTGGCAAGGT  
GTCCAGGGCTCTAGGCCACTCCCTGCCCTACACACACAGCCTATATCAAACATGCACACGG  
CGAGCTTCTCCGACTCCCCCTGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGC  
TGCAGCAGGTGCTGGCTGGACTGGCCTTTCTGGGGTAGGATGAAGAGAAGGCACACAG  
AGATTCTGGATCTCTGCTGCCCTTCTGGAGTTGTAAAATTGTTCTGAATACAAGCCTAT  
GCGTGA

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**FIGURE 320**

MRGTPKTHLLAFSLLCLLSKVRTQLCPTPCTCPWPPPRCPLGVPLVLDGCGCCRVCARRLGE  
CDQLHVCDAASQGLVCQPGAGPGGRGALCLLAEDDSSCEVNNGRLYREGETFQPHCSIRCRCEDG  
GFTCVPLCSEDVRLPSWDCPHPRRVEVLGKCCPEWVCGQGGGLGTQPLPAQGPQFSGLVSSL  
PGVPCPEWSTAWGPCSTTCGLGMATRVSNQNRCRLETQRRLCLSRPCPPSRGRSPQNSAF

**Important features:**

Signal sequence:

Amino acids 1-23

**N-myristoylation sites:**Amino acids 3-9; 49-55; 81-87; 85-91; 126-132; 164-170; 166-172;  
167-173; 183-189; 209-215**Insulin-like growth factor binding proteins signature:**

Amino acids 49-65

**von Willebrand C1 domain:**

Amino acids 107-124

**Thrombospondin 1 Homology Block:**

Amino acids 201-216

**IGF binding protein site:**

Amino acids 49-58

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### **FIGURE 321**

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**FIGURE 322**

MMGLSLASAVLLASLLSLHLGTATRGSDISKCCFQYSHKPLPWTWRSYEFTSNSCSQRAVI  
FTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-myristylation sites.**

amino acids 3-9, 26-32

**Amidation site.**

amino acids 68-72

**Small cytokines (intecrine/chemokine).**

amino acids 23-88

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**FIGURE 323**

ACCGAGCCGAGCGGACCGAAGGCAGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGGGCGTGAGGAGCA  
TGGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTCTGGCTCAGTGTCAAGGCTCGGCCA  
CGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCAGGACCGCCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAG  
TCCCCGAGGGCATCCCCACCGAGACGCGCTGCTGGACCTAGGAAGAACCGCATCAAAACGCTCAACCAGGACG  
AGTTGCCAGCTCCCGCACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGGCCGTGGAGCCGGCCT  
TCAACAAACCTCTCAACCTCCGACGCTGGCTCCGACGCCCTGAAGCTCATCCCGCTAGGCGTCTCA  
CTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCAGAACAAGATCGTTATCCTACTGGACTACATGTTCAAG  
ACCTGTACAACCTCAAGTCACTGGAGGTTGGCGACAATGACCTCGTACATCTCACCAGGCCCTCAGCGGCC  
TCAACAGCCTGGAGCAGCTGACCGTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCCGTGTCCCACCTGC  
ACGGCCTCATCGTCTGAGGCTCCGCACCTAACATCAATGCCATCCGGACTACTCCTCAAGAGGCTGTAC  
GACTCAAGGTCTGGAGATCTCCACTGGCCTACTTGGACACCATGACACCCAACACTGCCCTACGGCCTCAACC  
TGACGTCCTGTCCATCACACACTGCAATCTGACCGCTGCCCTACCTGGCGTCCGCCACCTAGTCTATCTCC  
GCTTCCTCAACCTCTCTACAACCCCATCAGCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGG  
AGATCCAGCTGGTGGCGGGCAGCTGGCGTGGAGGCCCTATGCCCTCCGCCCTCAACTACCTGCGCGTGC  
TCAATGTCTCTGGCAACCAAGCTGACCCACTGGAGGAATCAGTCTTCACTCGTGGGCAACCTGGAGACACTCA  
TCCGGACTCCAACCCGCTGGCTCGACTGCGCTCCGTGGGTGTTCCGGCGCCGTGGCGGCTCAACTTCA  
ACCGCAGCAGCCCACGTGCGCCACGCCAGGTTGTCCAGGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTAC  
TGCCCAACTACTTCACCTGCCGCCGCGCCGATCCGGACCGCAGGTTGTGGGCAACCTGGAGACACTCA  
ACACGGTGCAGTTGTGTGCCGGCCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACC  
TGGTCTAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGTACGCCAGGTAC  
AGGACAACGGCACGTACCTGTGCATCGCGCCAACGCCGGCAACGACTCCATGCCGCCACCTGCATGTGC  
GCAGCTACTGCCCGACTGGCCCATCAGCCAACAAGACCTTCGTTCTCATCTCCAACCAGCCGGGAGGGAG  
AGGCCAACAGCACCCGCCACTGTGCCCTTCCCTCGACATCAAGACCCCATCGCCACCCACCATGGCT  
TCATCTTTCCCTGGCGTGTCCCTCTGCCCTGGTGTGCTGTTCTCTGGAGCCGGCAAGGGCAACACAA  
AGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGACATCAGCTCGCCACGCCGGCAAGT  
TCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCCGGCGGCCGGCAGGGGAAGGGGCTGGT  
CGCCACCTGCTCACTCTCAGTCTCCACCTCCCTCCCTACACACGTTCTTTCTCCCTCCCGCC  
TCCGTCCCTGCTGCCCGCCAGCCCTCACCACTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGG  
GGACCCACCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCATAAT  
TCAATAAAAAGTTACGAACCTCTGTAACTTGGTTCAATAATTATGGATTTATGAAAACCTGAAATAA  
TAAAAGAGAAAAAAACTAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 324**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCFVAVPEGIPPTETRL  
LDLGKNRIKTLNQDEFASFPHLEELNÉNIVSAVEPGAFNNLFNLRLRSNRLKLIPLGVFTGLSNLTQDI  
SENKIVILLDYMFQDLYNLKSLEVGDNDLTVYISHRAFSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRH  
NINAIRDYSFKRLYRLKVEISHWPYLDTPNCYLGLNLTSLSIHCNLTAVPYLAVRHLVYLRFNLNSYNPIS  
TIEGSMILHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLLIDSNPLACDC  
RLLWVFRRRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQVFDVDEGHTVQFVCRADG  
DPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYLCIAANAGGNDSMPAHLHVRSYSPDWPHQD  
NKTFAFISNQPGEGEANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCVLVLLFLWSRGKGNTKHNEIEYVPR  
KSDAGISSADAPRKFNMKMI

**Important features:**

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345, 492-496,  
505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353, 607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143, 262-268, 320-326,  
344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

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**FIGURE 325**

CCACCGCGTCCGCCACCGGTCCGAGGGACAAGAGAGAAGAGACTGAAACAGGGAGAAGAG  
GCAGGAGAGGAGGGAGGTGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGAGG  
AGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGAAAGGAGAGAGGGAGGAGGAGGAG  
GAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTGGAGAGCTTAATGAAAAGAGAACGGAG  
AGGAGGTGTGGTTAGGAACCAAGAGGTAGCCCTGTGGCAGCAGAAGGCTGAGAGGAGTAGG  
AAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGAAAAGAGCAGAGGAAAGAGGAAAGAC  
ACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTGAAGGGCGGATCTCAGTCCTGGCTGCTT  
TGGCATTTGGGAACTGGACTCCCTGTGGGAGGAGAGGAAAGCTGGAAGTCCTGGAGGGAC  
AGGGTCCCAGAAGGAGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTGGCAGGGTCC  
CTCGGAGGCCTCTGGGATGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGCGCTGGTACTC  
TGGGCTGCACTGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGGACTGGTGGAGC  
TACAAGGATAATCTCCAGGGAAACTTCGTGCCAGGGCCTCTTCTGGGCCTGGTGAATGCA  
GGTGGAGTCTGTGCTGTGGGAAGCGGCAGAGCCCCGTGGATGGAGCTGAAGAGGTT  
CTTTATGACCCCTTCTGCCCTTACAGCCACCGACTCAGTGAACCTGCGCTGCTGACCCGAC  
TTGTACAACACCGGCCGACATGTCTCCTCCTGCCTGCACCCGACCTGTGGTCAATGTGTCT  
GGAGGTCCCCTCTTACAGCCACCGACTCAGTGAACCTGCGCTGCTGCTGAGGTGCAGCTCATT  
GGAGCCGGCTCGAACATCAGATCAACCACCAAGGGCTCTGCTGAGGTGCAGCTCATT  
TTCAACCAGGAACTCTACGGGAAATTCAAGCGCTGCCCTCCGCGGCCCAATGCCCTGGCATT  
CTCAGCCTCTTGCAACGTTGCCAGTACCTCTAACCACTCAGTCGCTCCCTAACCGC  
GACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTCTTCAAGACCTGAGCCTGGAG  
CTCCTGTTCCCTGAATCCTCGGCTTCATCACCTACAGGGCTCTCAGCACCCCGCCCTGC  
TCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAATATCACCTCCCTCAGATGCAC  
TCCCTGAGACTCCTGAGCCAGAACCTCCATCTCAGATCTTCCAGAGCCTCAGCGGTAAACAGC  
CGGCCCTGCAGCCCTGGCCCACAGGGCACTGAGGGCAACAGGGACCCCGGCACCCGAG  
AGGCCTGCCAGGGCCCCAACTACCGCCTGCATGTGGATGGTGTCCCCATGGTCGCTGAGAC  
TCCCTCGAGGATTGCACCCGCCGCTTAAGCCTCCCCACAAGGCAGGGAGTTACCCCT  
AAAACAAAGCTATTAAAGGGACAGAATACTTA

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**FIGURE 326**

MGAAARLSAPRALVLWAALGAAAHGAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCA  
VGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLY  
SHRLSELRLLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSLFVN  
VASTSNPFLSRLLNRDITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSETVTW  
ILIDRALNITSQMHSRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGP  
NYRLHVDGVPHGR

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 177-199

**N-glycosylation sites:**

Amino acids 118-122;170-174;260-264

**Eukaryotic-type carbonic anhydrases proteins:**

Amino acids 222-271;128-165;45-93

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**FIGURE 327**

GGACTAATCTGGGGAGCAGTTATTCCAGTATCACCCAGGGCAGGCCACACCAGGACTGTGTTGAAGGGTGT  
TTTTCTTTAAATGTAATACCTCTCATTTTCTTACACAGTGTCTGAGAACATTACATTAGATAA  
GTAGTACATGGTGGATAACTCTACTTTAGGAGGACTACTCTCTGACAGTCTAGACTGGTCTTACACT  
AAGACACCATGAAGGAGTATGTGCTCTATTATTCCCTGGCTTGCTCTGCCAACCCCTTCTTAGCCCTTCAC  
ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG  
ATGATGATGAGGACAACCTCTTTCCAACAAGAGGCCAGAACAGCCATTGATCTGTTCAA  
TGTGTCATTGGATGTCAGTGTCTTACCGAGTTGTCAGATTGCTCAGATTAGGTTGACCTCAGTCCCACCA  
ACATTCCATTGATACTCGAATGCTTGATCTTCAAAACAATAAAATTAGGAAATCAAAGAAAATGATTTAAAG  
GACTCACTCACTTATGGTCTGATCCTGAAACAACAAGCTAACGAAGATTACCCAAAAGCCTTCAACCA  
CAAAGAAGTGCAGGCTGTATCTGTCACAACTAACAGTGAATACCAACTTAATCTCCAAATCATTAG  
CAGAACTCAGAATTCTGAAATAAAAGTTAAGAAAATACAAAGCACATTCAAAGGAATGAATGCTTACACG  
TTTGGAAATGAGTGCAAACCCCTTGATAATAATGGATAGGCCAGGGCATTGAGGGGTGACGGTGTCC  
ATATCAGAATTGCAAGCAGTGTCTGTCACAACTAACAGTGAATACCAACTTTATTGGAGCTTCACTTAG  
ATTATAATAAAATTCAACAGTGGAACTTGAGGATTTAAACGATACAAAGAACTACAAAGGCTGGGCTAGGAA  
ACAACAAAATCACAGATATGAAAATGGAGTCTGCTAACATACCACTGAGAGAAAATACATTGAAAACA  
ATAAACTAAAAAAATCCCTTCAGGATTACAGAGTTGAAATACCTCAGATAATCTCCTTCAATTCAA  
TTGCAAGAGTGGAGTAAATGACTTCTGTCACAGTGCCAAAGATGAAGAAATCTTATACAGTGAATAAGTT  
TATTCAACAACCCGGTGAATACTGGAAATGCAACCTGCAACATTGTTGTGAGCAGAATGAGTGTTC  
AGCTTGGAACTTGGAAATGTAAATTAGTAATTGGTAATGTCATTAAATAAGATTCAAACCCAT  
TTGGAATACTGAACTCTTAAATGGTAGTTATATACAGCAAAATCTTCAAGTGGTAAGTCC  
ACTGACTTATTTATGACAAGAAATTCAACCGAATTGCAACACTTCAAGTGTGAGAGAAAACA  
AGCATCTATTGCAAGTTCTTTCGGTACAAATGATCTTACATAAAATCTCATGCTTGCACATTCTTCTCAT  
AACAAAAAGTAAGATATTGGTATTAAACACTTGTATCAAGCACATTAAAGAAACTGTACTGTAATGG  
AATGCTGACTTAGCAAAATTGCTCTTCATTGCTTGTAGAAAAACAGAATTAACAAAGACAGTAATGTGA  
AGAGTCATTACACTATTCTTATTGTTAGTAACCTGGTAGTACTGTAATATTAAATCATCTTAAAGTATGA  
TTTGATATAATCTTATTGAAATTACCTTACATGCTTAGAGGCCGTCTTATGTTAAAACATAATTCTTAAA  
TAAAGCCTCAGTAAATGTCATTACCAACTGATAATGCTACTCATAGAGCTGGTTGGGCTATAGCATAT  
GCTTTTTTTTAAATTATTACCTGATTTAAAATCTGTAAAAACGTGTAGTGTCTTCAAAATCTGTAAC  
CGCATTAAATGATCCGCTATTATAAGCTTTAATAGCATGAAATTGTTAGGCTATATAACATTGCCACTCAA  
CTCTAAGGAATATTGGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGACACTAACAAATTCTACACC  
AAATTGCTCTTCAAAACGTATGGACTGGATAACTCTGAGAAACACATCTAGTATAACTGAATAAGCAGAGCAT  
CAAATTAAACAGACAGAAACCGAAAGCTCTATATAATGCTCAGAGTTCTTATGATTCTTATTGGCATTCAA  
CATATGAAAATCAGAAAACAGGGAAATTTCATTAAAAATATTGGTTGAAAT

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**FIGURE 328**

MKEYVLLLFLALCSAKPFESPShIALKNMMLKDMEDTDDDDDDDDDDDDDEDSLFPTRPRSHFFPFDLFPMCPFGCQCYSRVVHCS\_DLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQKDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHDYNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI\_PRVREIHLENNKLKKIPSGLPELKYLQIIFLHSNSIARGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSVQLGNFGM

**Important features:****Signal sequence.**

amino acids 1-15

**N-glycosylation site.**

amino acids 281-285

**N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

**Leucine zipper pattern.**

amino acids 154-176

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**FIGURE 329**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGCA  
TCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGACAAGAACCTGTGT  
TTGCCCTCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATACTGGTGTGTT  
CAGCATGCGCTTGTGGACCCCAGTGGCGCTTGACCTCGCTGGCGTACTGCCTGCACCAGCG  
GCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGCCAGTGTCCGGTCGACCAGCAGCCTGCT  
GAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGCTCGGAGTCCTCTCAAGCCGCTCCC  
GCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTCAGTTGA  
TTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCTCAATACCA  
TGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATGCAGCAAAT  
GTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTCAAC  
CTTCAACCCACAGGAGGTCTTATTGCTTCCACTAACATTTCGGAATCTGGAGTCCACCCG  
TTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGCCATCATCCACACTGATGA  
AGCAGATTTCAGAAGTCTTGTATCCAACTACCAAAAGCTGCTGGAGGCCTGAGGAGAAC  
AGGCCGGAGGCAGACTGCCCTTACAGCCAGGAATCTCAGAGGATTGAAAAAGGTGAAGGA  
CAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTTCATCCTCTGGACAAACGTGGCTGC  
CGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTGACGGATGATCGAAC  
GAGAGCTGTGGACACATCCTGTACATACTGCCCAAGGAAGACAGGGAAAGTCTTCAGATGGC  
AGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGCCATGGACTCTGCCACTGC  
CCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATGTGACCTCATACCGCTCTT  
AATGACCCCTGGGATTTGACCACAAATGCCACCGTTGCTGTTGACCTGACCATGGAAC  
TTACCACGACCTGGAATCTAAGGAGTGGTTGTCAGCTCTATTACACGGGAAGGAGCAGGT  
GCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGTTCTGAAATGCCATGTCAGTTA  
TACCTTAAGCCCAGAAAATACCATGCACCTGCTCTCAAACACTCAGGTGATGGAAGTTGGAAA  
TGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATTTAAAATAAGTGCCTTATACAATG

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**FIGURE 330**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGARSPLKPLPLEEQVE  
WNPQLLEVPPQTQFDYTVTNLAGGPKPSPYDSQYHETTLKGGMFAGQLTKVGMQQMFALGERLRKNYVEDIPFL  
SPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRTASLQ  
PGISEDLKKVKDRMGIDSSDKVDFEFFILLDNVAAEQAHLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA  
VGPFLHILESNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPFAVDLTMELYQHLESKEWFVQ  
LYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Important features:****Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

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**FIGURE 331**

CGAGGGCTTTCCGGCTCCGGAATGGCACATGTGGAATCCCAGTCTGTTGGCTACAACATTTCCTTC  
AACAAAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGTTCTCTGCTGGAGAAGAAAGGGCTGAGGCAG  
AGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTGCCTCTGTGGATAACAGACCATGAGAAAGTGAAGAGAT  
GCAGCGGAGTGAGGTGATGGAAGTCTAAAATAGGAAGGAATTTGTGCAATATCAGACTCTGGGAGCAGTTGA  
CCTGGAGAGCCTGGGGAGGGCCTGCCTAACAGCTTCAAAAACAGGAGCGACTTCACTGGGCTGGGATAAG  
ACGTGCCGTAGGATAGGAAGACTGGGTTAGTCCTAACATTGACTGGCTGGGTAACTTCAACAGCCT  
TTAACCTCTCTGGAGATGAAACGATGGCTAACGGGCCAGAAATAGAGATGCTTGTAAAATAAAATTAA  
AAAAAGCAAGTATTTATAGCATAAAAGGCTAGAGACCAAAATAGATAACAGGATCCCTGAACATTCTAACAGG  
GAGAAAGTATGTTAAAATAGAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACC  
CTGGGTCAAGGCCAGCCTCTTGCTCTCCGGAAATTATTTGGTCTGACCCTGCTGTGTTTGAGAA  
TCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCCCTCACCGCCGCCCCCTC  
AGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGGACAGCCGCTCTGGTCTCTCAGTGGTC  
TGGGTGCTGCTGGCCCCCCCAGCAGCCGCATGCCAGTCTGAGCACCTCCACTCTGAGAATCGTACTGGACC  
TTCAACCACTTGACCGTCCACCAAGGGACGGGGCGCTATGTGGGGCCATCAACCGGTCTATAAGCTGACA  
GGCAACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAACAGGACAACAGTCTCGTTACCGCCCCCTCATC  
GTGCAGCCCTGCAGCGAAGTGTCAACCCACCAACATGTCAACAAAGCTGCTCATCATTGACTACTCTGAGAAC  
CGCCTGCTGGCTGTGGAGCCTTACCAAGGGCTGAGCTGCTGGATGGAGCAGGATTACTCCGACCTGTCC  
GAGCCATCCCACAAGAAGGAGCAACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGC  
TCTGAGGGTGAAGCTTCTCATCGGACGGCTGTGGATGGAGCAGGATTACTCCGACCTGTCC  
AGCCGGAAGCTGCCAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCAGTGTCTCC  
CTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGTACATCTACATCTACGGCTTGCTAGT  
GGGGCTTGTCTACTTCTCATGTCCAGCCAGACCCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCT  
TTCTACACCTCAGCATCGTGGCTCTGCAAGGATGACCCCAAGTCCACTCATCGTGTCCCTGCCCTCGGC  
TGCACCCGGGCCGGGTGGAATACCGCCTCTGCAAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCAG  
GCCTCAATATCACCAGCCAGGACGATGTACTTGTGCAAGGCTGAGGCTCAACTCCAGTGGAGGGCTGACCC  
CCCGATGACTCTGCCCTGTGTGCCCTCCATCCGGCCATCAACTTGAGATCAAGGAGCGCCTGCAGTCC  
TACCAAGGGGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGAAGGAGCTCAACTCCAGTGGAGGGCTGACCC  
ATCGATGATAACTCTGTGGACTGGACATCAACCAAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCC  
TACACCACAGCAGGGACCGCATGACCTCTGTCCTACGTTACAACGGCTACAGCGTGGTTTGAGGG  
ACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTCAGATGCTCAATGCCATTACCTCAGCAA  
GAGTCCCTTGGAGGTAGCTATTGGTGGAGATTAACTATAGGCAACTTATTTCTGGGAACAAAGGTGA  
AATGGGGAGGTAAGAAGGGTTAATTGTGACTTAGCTAGCTACTCCCTCAGCCATCAGTCATTGGGTAT  
GTAAGGAATGCAAGCGTATTCAATATTCCAAACTTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAA

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**FIGURE 332**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWPR  
ALEVDSRSVVLSVVWVLIAPPAAGMPQFSTFHSENRDWTFNHLTGHQGTGAVYVGAINRVYK  
LTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLACGSLYQG  
VCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDYFPTL  
SSRKLPDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFLTVQPE  
TPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKPGDSLQ  
AFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGNLELNWLL  
GKDQCTKAPVPIDDNFCGLDINQPLGGSTPVVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGT  
KSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Important features:****Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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**FIGURE 333**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAGG  
CCCCCCCAGAGCCCTACCACGCTGGCGCCCCAGAGCCCACACC**ATG**CCGGGCACCTACGC  
TCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGAT  
GCGGGACTTCCCCTCGTGGACGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTACCA  
GAAAGGGCTACAGGATGTTAACCTGCGCAATTCAAGCTACGCCAGACCAGCCTGGACAGGCT  
TAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCG  
GGATGCCCTGCGCCTCACCCCTGGAGCAGATTGACCTCATAGCCGCATGTGTGCCTCCTATT  
TGAGCTGGAGCTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGCCCTGCCCTCAT  
CGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTTACATGCT  
GGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGAGCTCGCTAA  
GGCGTCCACTCCTCTACAAACAACATCAGCGGCTGACTGACTTGGTGAGAAGGTGGTGGC  
AGAAATGAACCGCCTGGCATGATGGTAGACTTATCCATGTCTCAGATGCTGTGGCACGGCG  
GGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCACTCGCTGCCGGGGTGTGCAA  
CAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTCGTGAT  
GGTGTCTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGA  
TCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGATTGGTGGAGATTATGA  
TGGGGCGGCAAATTCCCTCAGGGCTGGAAGACGTGTCCACATACCCGGCTGATAGAGGA  
GTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCG  
GGTCTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTGGAGGACAA  
GTTCCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACA  
GAGTCTGACTTCAGGCCAGGAACACTCACTGAGATTCCATACTGGACAGCCAAGTTACCAGC  
CAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAGTCCTGCAGTTGTGGCCACCTT  
CCCAGTCCTATTCTGTGGCTCT**TGAT**GACCCAGTTAGTCCTGCCAGATGTCACTGTAGCAAGC  
CACAGACACCCACAAAGTCCCTGTTGTGCAGGCACAAATATTCTGAAATAATGTTT  
GGACATAG

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**FIGURE 334**

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYQQTSLDRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIIRRMCASYSELELVTSAKALNDTQKLA CLIGVEGGHSLDNSLSILRTFYMLGVRYLTLLHTCNPWAESSAKGVHSFYNNISGLTDFGEKVVAEMNRLGMMVDSLHVSDA VARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQLKKNGGVVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLEDVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQEVKQEE NKWQSPLEDKFPDEQLSSSCHSDL RLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPV LILWL

**Important features:****N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

**N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

**Renal dipeptidase active site.**

amino acids 134-157

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**FIGURE 335**

CCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCAG  
AGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCTCCTGCTGCT  
GCTGCCCTACCTGGTGGTCGCCCTGGCTATCATAGGCCATGGTTCTGCCCAAAGA  
CCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCCAGAA  
GACTGTTCCCTCCAGATTAGAGTGGAAAGAAACTGGGTCGGAGTGTCTCCTTGCTACTATCA  
ACAGACTCTCAAGGTGATTTAAAATCGAGCTGAGATGATAGATTCATAATCCGGATCAA  
AAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTCCCCATCTGAGCAAGG  
CCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCCATCATG  
TGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGACAAAGAAGG  
GAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAAATCCCAGACT  
TGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAACTCTGCAATTAA  
TAATGTTCCAAACTGGACACTGGAGAATATTCCCTGTGAAGCCCGCAATTCTGTTGGATATCG  
CAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCATCATGCAGCCGT  
AGTAGTTGTGGCCTAGTGATTCGTTGTGGCCTGGTGTATGCTATGCTCAGAGGAAAGG  
CTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAG  
TGAAAATGTGCAGTGGCTACGCCTGTAATCCAGCACTTGGAAAGGCCGGCGGGCGGATC  
ACGAGGTCAAGGAGTTCAGACCAGTCTGCCAATATGGTAAACCCATCTACTAAAATAC  
AAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTGGAGACAGGAGAATC  
ACTTGAAACCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGG  
TAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATAAAATAACTGGTTTACCT  
TGTAGAATTCTTACAATAATAGCTTGATATT

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**FIGURE 336**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLEW  
KKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEEDTV  
TLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGLRLLENPRLGSQSTNSS  
YTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAVVVVALVIS  
VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

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**FIGURE 337**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCCAGCCTCGG  
CACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGGCAA  
TGATTTCCCTCCCGGGCCCTGGTGACCAAATTGCTGCGGTTTTGTTCTGGGCTGAGTG  
CCCTCGCGCCCCCCTCGCGGCCAGCTGCAACTGCACCTGCCAACCGGTTGCAGGC  
TGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGTGTTCATCCC  
AGCCATGGGAGGTGCCCTTGTGATGTTCTCAAACAGAAAAGGAGGATCAGGTGT  
TGT CCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCCATGCC  
CCCGAACCTGTCCCTGCGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCACAGCT  
CCGTGAATGTGCAAGACAAACAAGCAAATCTAGGGCCACAGCATCAAACCTAGAACTCA  
ATGTAUTGGTCCCTCCAGCTCCATCCTGCCGTCTCCAGGGTGTGCCCATGTGGGCAA  
ACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGTGTCCAATACCAGTGGGATCG  
AGCTTCCATCCTCCAGACTTCTTGACCAAGCATTAGATGTCATCCGTGGTCTTAAGCC  
TCACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCAGGCCACAATGAGGTGGCA  
CTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGCAGTGGTGTGGAG  
CTGTTGTGGTACCCCTGGTTGGACTGGGTTGCTGGCTGGCTGGCCTCTGTACCAACCG  
GGGGCAAGGCCCTGGAGGAGCCAGCAATGATCAAGGAGGATGCCATTGCTCCCCGGACCC  
TGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCCTTCCTCTGTACCTCC  
CACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTCATTGACCCCCACGCCAGTC  
TCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGATGGGCCACCCCAACCAA  
TATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTGAGCCGATGGGTGCTGTGCCTGTGA  
TGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGACCCCCACCACTCATTGGCTAAAG  
GATTGGGTCTCTCCTTATAAGGGTCACCTCTAGCACAGAGGCCCTGAGTCATGGAAAG  
AGTCACACTCTGACCCCTTAGTACTCTGCCACCTCTTACTGTGGAAAACCATCTCA  
GTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGAAGTGGATCTGAAATTGGAGGAGC  
CTCCACCCACCCCTGACTCCCTTATGAGGCCAGCTGCTGAAATTAGCTACTCACCAAGAGT  
GAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGCCCTTGATCTGTACCCACCCCTAT  
CTAACACCACCCCTGGCTCCACTCCAGCTCCCTGTATTGATATAACCTGTCAGGCTGGCTT  
GTTAGGTTTACTGGGCAGAGGATAGGAACTCTTATTAAAACATGAAATATGTGTT  
GTTTCATTGCAAATTAAAGATACTAATGTTGTATGAAAAA

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**FIGURE 338**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSSS  
QPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNILSRLEGLQEKDGPYSC  
SVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTILSCQSPRSKPAVQYQWDR  
QLPSFQTFFAPALDVRGSLSLTNLSSSMAGVYVCKAHNEVGTACNCNTLEVSTGPGAAVVAG  
AVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIAPIRTLWPWPKSSDTISKNGTLSSVTS  
ARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVPV  
MVPAQSQAGSLV

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristylation site.**amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

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**FIGURE 339**

GCGAGAACCTTGACCGCACAACACTACGGGACGATTCTGATTGATTTGGCGTTTCGATCCACCCCTCT  
CCCTTCTCATGGGACTTTGGGGACAAAGCGTCCCACCGCCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGCCA  
GGACAGCGTCGGGAACCAGACCATGGCTCTGGACCCCAAGATCCTTAAGTTCGTCGTCTTCATCGTCGGTT  
TGCTGCCGTCGGGTTGACTCTGCCACCATCCCCCGCAGGACGAAGTTCCCCAGCAGACAGTGGCCCCACAGC  
AACAGAGGCCAGCCAAAGGAGGAGTGTCCAGCAGATCTCATAGATCAGAATAACTGGAGCCTGTAACC  
CGTGCACAGAGGGTGGATTGACCATGGCTTCCAAACAATTGGCTCTTGCCTGCTATGTACAGTTGAAAT  
CAGGTCAAACAAATAAAGTTCTGTACACAGGACAGAGACCCGTGTCAGTGTGAAAAGGAAGCTCCAGG  
ATAAAAACCTCCCTGAGATGTGCCGAGCTGAGAACAGGGTGTCCCAGAGGGATGGTCAAGGTCAAGTAAATTGTA  
CGCCCCGGACTGACATCAAGTGCACAAATGAATCAGTGCAGTTCACTGGGAAACCCAGCAGCGGAGGAGA  
CAAGTGCACACCACCTGGGGATGCTGCCCTCCCTATCACTACCTTATCATCATAGTGGTTTAGTCATCATT  
TAGCTGTGGTTGTGGTTGGCTTCATGTCGGAAGAAATTCAATTCTACCTCAAAAGGCATCTGCTCAGGTGG  
GAGGAGGCCCCAACCTGTGACAGACTGCTTCCGGCGGCGTCTAGTCCTTCACGAGGTTCTGGGGCGGAGG  
ACAATGCCCGAACAGAGACCTGAGTAACAGATACTTGAGCAGGACCCAGGTCTGAGCAGGAAATCCAAGGT  
AGGAGCTGGCAGAGCTAACAGGTGTGACTAGACTCCCGAGGAGGCTGCTGGTCAAGCAGCTGGTGGAAACAGGAG  
CTGAAGGGTGTGAGGAGGAGGCTGCTGGTCAAGTGAAGTGCAGTGCAGTGCACATCAGCACCTGCTGG  
ATGCCCTCGCAACACTGGAAGAAGGACATGCAAAGGAAACAATTCAAGGACCAACTGGTGGGCTCGAAAAGCTCT  
TTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCGTGAAAGAAATCTTCAGGAAACCAGAGCTCCCT  
CATTTACCTTTCTCTACAAAGGGAAAGCAGCCTGGAAGAAACAGTCAGTACTTGACCCATGCCCAACAAAC  
CTACTATCCAATATGGGCAGCTTACCAATGTCCTAGAACTTTGTTAACGCACTGGAGTAATTTTATGAAAT  
ACTGCGTGTGATAACCAAACGGGAGAAATTATATCAGATTCTGGCTGCATAGTATACGATGTGATTAAAG  
GTCGTTTAAAGGCCACATGCGGTGGCTCATGCGTGAATCCAGCACTTGAAGGCTGAGGGTGGATTGCTT  
GAGCTCGGGAGTTGAGACAGCCATCAACACAGTGAACACTTCATCAATTAAAAGAAAAAAAGTGGTT  
TAGGATGTCATTCTTGCAAGTCTTCATCATGAGACAAGTCTTTCTGCTTCTATATTGCAAGCTCCATCT  
CTACTGGTGTGTCATTAATGACATCTAACATACAGATGCCACAGCCACAATGCTTGCCTTATAGTTTTA  
ACTTTAGAACGGGATTATCTGTTATTACCTGATTTCAGTTGGATATTTCAGTTAATGATGAGATTATC  
AAGACGTAGCCCTATGCTAAGTCATGAGCATATGGACTTACGAGGGTTCGACTTAGAGTTTGAGCTTAAAGATA  
GGATTATTGGGGCTTACCCACCTTAATTAGAGAAACATTATATTGCTTACTACTGAGGCTGTACATCTCTT  
TTCCGATTTTGTATAATGATGAAACATGGAAAATCTAGGAAATGCACTTATAGGCTGTTACATGGGTTG  
CCTGGATAACAGCAGCTGCAAGTCAAAATGACTAAAAATATAACTAGTGCAGGGAGGAAATCTCCCTCTGTTGG  
AGGCACTTAAGTCATCCAGTTCTCCCTGCGCCCTGAGACTGGACCAAGGGTTGATGGCTGGCAGCTCTCA  
AGGGCGAGCTGTCTTACTTGTAAATTAGAGGTATATAGCCATATTATTTATAAAATATTATTTATT  
ATTTATAAGTAGATGTTACATATGCCAGGATTGAAAGAGCCTGGTATCTTGGGAAGCCATGTGCTGGTT  
GTCGTGCTGGGACAGTCAGGGACTGCATCTCGACTTGTCCACAGCAGATGAGGACAGTGAGAATTAGTTAG  
ATCCGAGACTGCGAAGAGACTTCTTCAAGCGCATTACAGTTGAAACGTTAGTGAATCTTGAGCCTCATTGGG  
CTCAGGGCAGACGGCTGTTATCTGCCCCGGCATCTGCATGGCATCAAGAGGGAGACTGGACGGTGTGCTGG  
AATGGTGTGAAATGGTGCAGGACTCAGGGATGGGGCTCTCGCTTGTGACTGAACTGAGTCCCT  
GGGATGCCATTAGGGCAGAGATTCCTGAGCTGCGTTAGGTACAGATTCCCTGTTGAGGAGCTGGCCCT  
CTGTAACGATCTGACTCATCTCAGAGATATCAATTAAACACTGTCAGAACCGGATCTAAATGGCTGACACA  
TTTGTCTTGTGTCAGTTCCATTATTTATAAAACCTCAGTAATCAGTTAGCTTCTAGCTTCTTCAGCAAACCT  
TCTCCACAGTAGCCCAGTCGTGGTAGGATAAAATTACGGATATAGTCATTCTAGGGTTTCAGTCTTCCATCTC  
AAGGCATTGTTGCTTGTGCTGGGACTGGTTGGCTGGACAAAGTTAGAAGTGCACATTCAG  
ATTGTTGTGCTCCATGGAGTTTAGGAGGGATGGCCTTCCGGTCTTCGCACTTCATCTCTCCACTTCATC  
TGGCGTCCCACACCTGTCCCCTGCACTTCTGGATGACACAGGGTGTGCTGCCCTCTAGTCTTGCCTTGCTG  
GGCCTTCTGTGCAAGGAGACTTGGTCTAAAGCTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTGTCCCT  
AGAGGCCCTCTGAGAGATGCATCTAGACTACCAGCCTTACAGTGTAAAGCTTATTCTTTAACATAAGCTC  
CTGACAACATGAAATTGTTGGGTTTTGGCGTTGGTGTGTTAGGTTAGGTTGCTTATACCCGGGCAAAT  
AGCACATAACACCTGGTTATATGAAATACTCATATGTTATGACCAAAATAATGAAACCTCATRTTAAAA  
AAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 340**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQDEVPQQTVAPQQQR  
RSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNLLPSCLLCTVKSGQTNKSSCTTRDTVCQCEKGSFQDKN  
SPEMCRTCRTGCPRGMVKVSNCPRSDIKCKNESASSTGKTPAAEETVTIILGMLASPYHYLIIIVVLVIIILAV  
VVVGFSCRKKFISYLIKICGGGGGPERVHRLFRRRSCPSRVPGaednarneTLSNRYLQPTQVSEQEIQQQEL  
AELTGVTVESPEEPQRLLEQAEAGCQRRRLVPVNDAADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYE  
EDEAGSATSC

**Important features:**

**Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276, 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139

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**FIGURE 341**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCGGTCTGACAGCCACTCCAGAGG  
CCATGCTCGTTCTGCCAGATTGGCTTCAGCTCCTGTTAATTCTGGCTTGCCAGG  
CAGTCCAATTCAGAAATATGCTTCTCCAATTCTGGCTTAGATAAGGCCCTCACCCC  
AGAAGTTCCAACCTGTGCCTTATATCTGAAGAAAATTTCAGGATCGCGAGGCAGCAGCGA  
CCACTGGGTCTCCGAGACTTATGCTACGTAAAGGAGCTGGCGTCCGCGGGAAATGTACTTC  
GCTTCTCCAGACCAAGGTTCTTCTTACCAAAGAAAATTCCAAGCTCCTCCTGCC  
TGCAGAAGCTCCTCTACTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACATTGCC  
AGCTGGGCCTGGACTTGGGCCAATTCTACTATAACCTGGGACCAGAGCTGGAACTGGCTC  
TGTTCTGGTTCAGGAGCCTCATGTGTGGGCCAGACCACCCCTAACCCAGTAAAATGTTG  
TGTTGCCGTCAGTCCCATGCCACAAGGTGCTGTTCACTCAACCTGCTGGATGTAGCTAAGG  
ATTGGAATGACAACCCCCGGAAAATTCGGTTATTCGGAGATAGGTCAAAGAAGATA  
GAGACTCAGGGGTGAATTTCAGCCTGAAGACACCTGTGCCAGACTAAAGATGCTCCCTCATG  
CTTCCCTGCTGGTGGTGACTCTCAACCTGATCAGTGCCACCCTCTCGGAAAAGGAGAGCAG  
CCATCCCTGTCCCCAAGCTTCTGTAAGAACCTCTGCCACCGTCACCAGCTATTCAACT  
TCCGGACCTGGTTGGCACAAGTGGATCATTGCCACCCAGGGTTCATGGCAAATTACTGCC  
ATGGAGAGTGTCCCTCTCACTGACCACTCTCAACAGCTCAATTATGCTTCATGCAAG  
CCCTGATGCATGCCGTTGACCCAGAGATCCCCAGGCTGTGTATCCCCACCAAGCTGTCTC  
CCATTCCATGCTCTACCAGGACAATAATGACAATGTCACTACGACATTATGAAGACATGG  
TAGTCGATGAATGTGGGTGGGTAGGATGTCAGAAATGGGAATAGAAGGAGTGTCTTAGGG  
TAAATTTAATAAAACTACCTATCTGGTTATGACCACTTAGATCGAAATGTC

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**FIGURE 342**

MLRFLPDLA  
FSFLLILALGQAVQFQEYVFLQLGLDKAPS  
PQKFQPVPYILKKIFQDREAAAT  
TGVSRLCYVKELGVGNVLRF  
LPLDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQ  
LGDLGPNSYYNLGPELELALFLVQE  
PHVGQTPKPGKMFVLRSPWPQGA  
VFNLLDVAKD  
WNDNPRKNFGLFLEILVKEDRD  
SGVNQPEDTCARLRC  
SLHASLLVVTLNP  
DQCHPSRKRAA  
IPV  
PKLSCKNLCHRQLF  
INFRDLGWHK  
WIIAPKGFMANYCH  
GECPFSLTISLN  
SSNYAFM  
QA  
LMHAVDPEIPQAVCI  
PTKLSP  
ISMLYQDN  
NDNVILRH  
YEDMV  
VDEC  
GCG

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 112-116, 306-310

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

**N-myristoylation site.**

amino acids 77-83

**TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364

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**FIGURE 343**

CCACACGGTCCGGCCTTCCTCTGGACTTTGCATTCCATTCTTCAATTGACAAACTGACTTTTTATTC  
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCTTCTCCCCTGACATTGGCATTGCTTAGTGGTGTGGGAGGGAGACCAACGTGG  
GCTCAGTGCTGCTTGCACTTATCGCTAGGTACATCGAAGTCTTGCACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCTGGCGGCCCTGCTCTGCTGATAGTTGCTGCTCTGCTTACTTCAAAATACACAAC  
GCGCTAAAGCTGCAAAGGAACCTGAAGCTGGCTGAAAAATCACAAACCCAGACAAGGTGTGGTGGCCAAG  
AACAGCCAGGCCAAACCAATTGCCACGGAGCTTGTCTGCCCTGCAGTGTGAAGGATATAGAATGTGTGCC  
AGTTTGATTCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
GCAGAGGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAAGGACAG  
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGGAGAGAAACCCACTGTGGGAATGCTGATAAAACCAAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGCGTCTTAAGGCTGCCAGGCCCTGCAAAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTCTGTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGAAAT  
GCAAGCTGCACAGTCAGTCTAGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTAAGTAAAACATTAAGCTTGTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG  
CAAGTCTGAGTAAAACGACTATGTCCTGTATTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT  
GACTCAGCAAGAATCAGGAAACTGTCCTTGCTCTACTACTTCTCTCTTAACATCTCTATTCCTAACTGTT  
GGCGTTACCTGGATACCTTGGAAAGGATCTTCAACGGCCCAATTACCCAAAGGGCATCTGAGCTGGCTTAT  
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTCAAAGGATTTCTAGAAATAGAC  
AAACAGTGCACATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATGGACAGTCTGT  
GGCGTGTGACTCCACCTCGAATCGTCATCAAACCTCTGACTGTGTTGCTACAGATTATGCCAATTCT  
TACCGGGGATTTCTGCTCTACACCTCAATTATGCGAAAACATCAACACTACATCTTAACTTGCTCT  
GACAGGATGAGAGTTATAAGCAAATCTTACCTAGGGCTTTAACTCTAATGGAATAACTGCAACTAAA  
GACCCAACTTGCAGGCCAAATTATCAAATGTTGGAAATTCTGCTCTTCAATGGATGGTACAATCAGA  
AAGGTTAGAAGATCAGTCACATTACTACACCAATATAATCACCCTTCTGCATCTCAACTCTGAGTGTACCC  
CGTCAGAAACAACCTCAGATTATGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA  
GAAGATGATGTAATACAAAGTCACACTGGGAAATATAACACAGCATGGCTTTTGAAATCCAATTCA  
TTTGAAAAGACTTACTGTAATCACCATTATGTTGATTTGAACCAAACCTTTTGTTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTGGTGGTGTCTTCTGATACCTGTAAGGCTCTCCACCTGACTTGCATCTCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCAGGATGAAACTTGTGAAAGGTGATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTAATGCCCTTAAATTCTGAGAAAGTATGAGCTCTGTTGATCTGAGTGTAAAGTTGATATGTGAT  
AGCAGTGACCAACAGTCTGCTGCAATCAAGGTTGCTCAGAAGCAAACAGAGACATTCTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAAGGATTTCAAGCAT  
GAAACACATGCGGAAGAAACTCCAAACCGCCTTCAACAGTGTGCACTGTTCTCATGGTTCTAGCTCTG  
AATGTGGTACTGTAGCGACAATCACAGTGAGGCAATTGTAATCAACGGGAGACTACAAATACCAAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCCTAACGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTGAAATAATGAGGAAGGGCCTGAAAGTGAACACAGGCCTGCATGTA

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**FIGURE 344**

MELVRRLMPLTLIISCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTIE  
RPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLTFQ  
IVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQVEKD  
YKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCRVTPTFESSSNSTVVLDY  
NSYRGFSASYTSIYAENINTTSLTCSSDRMVIISKSYLEAFNSNGNNLQLKDPTCRPKLSNV  
VEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIVKCEMGHNSTVEIIYI  
TEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPNLVVFLDT  
CRASPTSDFASTPYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSVYLQCKVLICD  
SSDHQSRCNQGCCRSKRDISSYWKWTDIIGPIRLKRDRSASGNSGFQHETHAEEETPNQPFN  
SVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Important features:****Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423**Casein kinase II phosphorylation site.**amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 345**

TGGGGGCCCCCAGGCTCGCGGTGGAGCGAAGCAGCATGGCAGTCGGTGCAGCTGGCCCTGGCGGTGCTCTC  
 GCCCTGCTGTCAAGGTCTGGAGCTCTGGGTGTTGCAACTGAAGCTGCAGGAGTTCGTCAACAAGAAGGGGCT  
 GCTGGGAACCGCAATTGCTGCCGGGGGGCGGGGGCCACCGCCGTGCGCCTGCGGACCTTCTTCCGCGTGTG  
 CCTCAAGCACTACCAGGCCAGCGTGTCCCCCGAGCGGGGGCGCCACTCGCGTTCAAGCAACCCATCCGCTTCCCCTCG  
 CGTCGACTCCTTCAGTCTGCCGACGGGGGGCGCCACTCGCGTTCAAGCAACCCATCCGCTTCCCCTCG  
 CTTCACCTGGCCGGCACCTCTCTGATTATTGAAGCTCTCACACAGATTCTCTGATGACCTCGAACAGA  
 AAACCCAGAAAGACTCATCAGCCGCTGGCACCCAGAGGACCTGACCGTGGCGAGGAATGGTCCAGGACCT  
 GCACAGCAGCGGGCGACGGACCTCAAGTACTCTACCGCTTCGTGTGACGAACACTACTACCGAGAGGGCTG  
 CTCCGTTTCTGCCGTCCCCGGAGATGCGCTTCCGCACTTCACCTGTGGGGAGCGTGGGGAGAAACTGTGCAA  
 CCCTGGCTGAAAGGGCCCTACTGCACAGAGCGATCTGCGCTGGATGTGATGAGCAGCATGGATTGTGA  
 CAAACAGGGGAATGCAAGTGAGGTGGCTGGCAGGGGGGTACTGTGACGAGTGTATCCGCTATCCAGGCTG  
 TCTCCATGGCACCTGCCAGCAGCCCTGGCAGTGCACACTGCAAGGAGGCTGGGGGGCCTTCTGCAACCCAGGA  
 CCTGAACTACTGCAACACACCATAAGCCCTGCAAGAATGGAGCCACCTGCAACACAGGGGAGGGAGCTACAC  
 TTGCTTGTGCCGGCTGGTACACAGGTGCCACCTGCGAGCTGGGGATTGACGAGTGTGACCCCCAGGCTTGTAA  
 GAACGGAGGGAGCTGACGGATCTGAGAACAGCTACTCTGTACCTGCCACCCGGCTTCTACGGCAAATCTG  
 TGAATTGAGTGCCATGACCTGTGCCAGGCCCTGCTTAACGGGGGCTGGTCTCAGACAGCCCCGATGGAGG  
 GTACAGCTGCCGTGCCGGCTACTCCGGCTTCAACTGTGAGAAGAAAATTGACTACTGCACTCTCACC  
 CTGTTCAATGGTCCAAGTGTGGACCTCGGTGATGCCCTACCTGTGCGCTGCCAGGCCGCTTCTCGGGAG  
 GCACTGTGACGACAACGTGGACGACTGCCCTCTCCCGTGCAGGAGGGGACCTGCCGGGATGGCGTGA  
 CGACTTCTCTGCCACCTGCCGCTGGCTACACGGGAGGAACATGCACTGCCCCCTGAGCAGGTGCGAGCACGC  
 ACCCTGCCACAATGGGGCACCTGCCACAGAGGGGCCACCGTATGTGCGAGTGTGCCCCGAGGCTACGGGG  
 TCCCAACTGCCAGTCCCTGCTCCCCGAGCTGCCCTGGGGCCAGCGGTGGTGGACCTCACTGAGAAGCTAGAGGG  
 CCAGGGGGGCCATCCCTGGGTGGCGTGTGCGCCGGGTATCCTGTCTCATGCTGTGCTGGGCTGTGC  
 CGCTGTGGTGGCTCGTCCGGCTGAGGCTGCAAGAACCGGCCCCAGCCGACCCCTGCCGGGGAGACGGA  
 GACCATGAAACAACCTGCCAACCTGCCAGCGTGAAGAGGACATCTCAGTCAGCATCATCGGGGCCACGCAGATA  
 GAACACCAACAAGAAGCGGACTTCCACGGGACCACAGCGCCACAAGAATGGCTTCAAGGGCCGCTACCCAGC  
 GGTGGACTATAACCTCGTGCAGGACCTCAAGGGTGACGACACCGCCGTCAGGGACCGCACAAGCAAGCGTACAC  
 CAAGTGCCAGCCCCAGGGCTCTCAGGGAGGGAGAACGGGACCCGACCACACTCAGGGGTGGAGAAGCATCTGA  
 AAGAAAAAGGCCGACTCGGGCTGTTCAACTTAAAGACACCAAGTACCAAGTCGGTGTACGTATATCCGAGGA  
 GAAGGATGAGTGCCTCATAGCACTGAGGTGTAAGGATGGCAAGACTCCGTTCTCTTAAATA  
 AGTAAAATTCCAAGGATATATGCCCAACGAAATGCTGAGAGGAGGGAGGCTCTGACTGCTGAGAA  
 ACCGAGTTCAAGCCGAGCAGGTTCTCCCTCTGAGGTCTCGACGCCGTCAGGCCGACAGCTGTGCGGGCCGGCC  
 TGCGGCACTGCCCTCGTGCAGCTGCCGTTGCACTATGGACACTTGTCTTAAAGAGAATATATTTAAATGGGT  
 GAACTGAATTACGCATAAGAACGATGCACTGCCGTAGTGATATTTGGATTCTTATGAGCCAGCTTTCTGTA  
 ATTAGAAACACAAACACTGCCTTATTGCTTTTGATACGAAGATGTGCTTCTAGATGGAAAAGATGTGT  
 GTTATTTTTGGATTGTAAGGATATTTTCTGATGATATCTGTAAGGCTTGACTATTGTGATGTTGCTTCTTAA  
 TAATTTAAATTTGGTAAATATGTACAAGGCACCTCGGGCTATGTGACTATATTGTTGATATAAATGTAT  
 TTATGGAATATTGTGCAAATGTATTGAGTTTTACTGTTTGTAAATGAAGAAAATCCTTTTAAATATT  
 TTCCAAAATAATTATGAATGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAA

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**FIGURE 346**

MGSRCALALAVLSALLCQVWSSGVFELKLQEfvNKGLLGNRNCRGAGPPPACRTFFRVC  
LKHYQASVSPEPPCTYGSAVTPVLGDSFSLPDGGGADSAFSNPIRFPGFTWPGBTFSLLIEA  
LHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRDLKYSYRFVCDEHYYGEGCS  
VFCRPRDDAFGHFTCGERGEKVCNPWGKPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR  
YCDECIRYPGCLHGTCQQWPQCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQGSYTCS  
CRPGYTGATCELGIDECDPSPCKNGSCTDLENSYSCTCPPGFYKICELSAMTCADGPCFNG  
GRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFSGRHCD  
DNVDCASSPCANGGTCRDGVNDFSCTCPGPYTRNCSAPVSRCEHAPCHNGATCHERGRYV  
CECARGYGGPNCQFLPELPPGPAVVDLTEKLEGQGGPFPPWAVCAGVILVLMLLLGAAVVV  
CVRLRLQKHRRPADPCRGETETMNNLANCQREKDISVSIIGATQIKNTNKKADFHDHSADKN  
GFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSGEEKGPTTLRGGEASERKPD  
SGCSTS KDTKYQSVYVISEEKDECVIATEV

**Important features:****Signal sequence:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 546-566

**N-glycosylation site:**

Amino acids 477-481

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 660-664

**Tyrosine kinase phosphorylation sites:**

Amino acids 176-185;252-261

**N-myristoylation sites:**Amino acids 2-8;37-43;40-46;98-104;99-105;262-268;281-287;  
282-288;301-307;310-316;328-334;340-344;378-384;387-393;512-518;  
676-682;683-689;695-701**Aspartic acid and asparagine hydroxylation sites:**

Amino acids 343-355;420-432;458-470

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 552-563

**EGF-like domain cysteine pattern signature:**Amino acids 243-255;274-286;314-326;352-364;391-403;429-441;  
467-479;505-517

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**FIGURE 347**

CCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAACA  
TCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCCAGCCAG  
GGAGCCGGCCGGGAAGCGCG**AT**GGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTGT  
TCGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGGACAT  
CTGATGAAACAGTGGTGGCTGGCACCGTGCTCAAGTGCCAAGTGAAAGATCACGAGG  
ACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGAGAGCCC  
TCGAGATAATCGAATTCACTGGTACCTCTACGCCAACGAGCTCAGCATCAGCATCAGCA  
ATGTGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGTGCGAAGT  
CCAAGTCCCTCGTCACTGTCTAGGAATTCCACAGAACGCCATCATCACTGGTTATAATCTT  
CATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAGCCTGCAGCCC  
GGCTCACCTGGAGAAAGGTGACCAAGAACTCCACGGAGAACCAACCGCATACAGGAAGATC  
CCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCGGGAGGATGATG  
GGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTC  
AACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCCCTCCCCATCCTCGT  
AGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGAATCCAGTCCCCAGCAGTACCTAT  
GGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTCCCTT  
TCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGCAGCTACA  
AGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCCTCCCTCCAGCACCTACC  
ACGCCATCATCGTGGATCGTGGCTTCATTGCTTCCCTGCTCATCATGCTCATCTTCC  
TTGGCCACTACTGATCCGGCACAAAGGAACCTACCTGACACATGAGGAAAAGGCTCCGACG  
ATGCTCCAGACCGGGACACGGCATCATCAATGCGAGAAGGGGGCAGTCAGGAGGGACGACA  
AGAAGGAATATTCATCT**A**GGCGCTGCCACTTCCTGCGCCCCCAGGGGCCCTGTGGGG  
ACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCGCCCTCCGCTT  
GCTCCCCAGCCCACCCACCCCTGTACAGAATGTCGTTGGTGCAGGGTTACTCGGT  
TTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGGTTGCCCTCAGCCCTTCCGTGGCTT  
CTCTGCATTTGGTTATTATTATTTGTAACAATCCAAATCAAATCTGTCTCCAGGCTGGA  
GAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAACAAACAAAAACA

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**FIGURE 348**

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQWS  
NPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLTV  
LGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFT  
VSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQKLLL  
HCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMSYKAYYTLN  
VNDPSPVPSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIHKGTYLTHEAKGSDDAPDADT  
AIINAEGGQSGGDDKKEYFI

**Important features:****Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site:**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristylation site.**amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 349**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGCACATGGAGGACAGCAGCAAAG  
AGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTACCATACGCCCTCAGGACGTTCCCTCTA  
GCTGGAGTCTGGACTTCACAGAACCCCCTACCCAGTCATTTGATTGCTGTTATTTTTCTTTCTT  
TTTCCCACCACTTGTATTTATTCCTGACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGG  
CTTTTCTCTGAAGTCTGGCTATCATTCCCTGGGCTACTCACAGGTGTCACACTCCTGGCCTGCCCTA  
GTGTGTGCCGCTGCCAGAGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTGCCTTGGGATCCGG  
AGGGCGTAACCGTACTCACCTCCACAACAACAAATTAAATGCTGGATTCTGCAGAACTGCACAATGTAC  
AGTCGGTGCACACGGTCTACCTGTATGGCAACCAACTGGACGAATTCCCATGAACTTCCCAAGAATGTCAGAG  
TTCTCCATTGCAAGGAAAACAATATTCAAGACCATTACGGGCTGCTTGCCTGGCAGCTTGAAGCTTGAAGAGC  
TGCACCTGGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGAGGCTATTAGCCTCAAAT  
TGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTCTGTGGACTTGCAAGAGCTGAGAGTGG  
ATGAAAATCGAATTGCTGTCTATCCGACATGGCCTTCCAGAACTCTCACAGGCTGGAGCGTCTTATTGGACG  
GGAACCTCCTGACCAACAAGGGTATGCCGAGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATTG  
TACGTAATTGCTGCCCACCCCTCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACC  
AGATAAACACATTCCCTTGACAGCCTCTCAAATCTGCTAACGCTGGATATATCCAACAAACCAAC  
TGCAGGATGCTGACTCAAGGGTTTGATAATCTCTCCAACCTGAAGCAGCTACTGCTCGGATAACCCCTGGT  
TTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAAATATATCCCTCATCTCTCACGTCGGGGTTCA  
TGTGCCAAGGTCTGAACAAGTCCGGGGATGGCGTCAGGGAAATTAAATATGAATCTTGTCTGTCCACCA  
CGACCCCCGGCCTGCCCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCCTCTA  
TTCCAAACCCTAGCAGAAGCTACACGCCCTCAAACCTTACACATCGAAACTTCCACGATTCTGACTGGGATG  
GCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATCCATTGTGAATGATACTCCATT  
AAGTCAGCTGGCTCTCTCTTCAACGGTATGGCATACAAACTCACATGGGTGAAATGGGCCACAGTTAGTAG  
GGGCATCGTTCAAGGAGCGCATAGTCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCA  
CCTATCGGATTGTTAGTGCACACTGGATGCTTTAACTACCGCGCGTAGAAGACACCATTGTTCAAGAGCCA  
CCACCCATGCCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGTCCACAGCATGG  
GCTCCCCCTTCTGCTGGCGGGCTTGTACGGGGCGCGGTGATATTGTGCTGGTGGTCTTGCTCAGCGCTTTT  
GCTGGCATATGCACAAAAAGGGCGCTACACCTCCCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATT  
ATTGCGAGGCAGGCACCAAGAAGGACAACCTCCATCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCCTAA  
ATAACGATCAACTCTTAAAGGAGATTCAAGACTGCAGCCCATTACACCCAAATGGGGCATTAAATTACACAG  
ACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCACACTGGAGCACTGCCATACGTGACAGC  
CAGAGGCCAGCGTTATCAAGGCGACAATTAGACTCTTGAGAACACACTCGTGTGCACTAAAGACACCGCAG  
ATTACATTGATAAAATGTTACACAGATGCATTGTGCAATTGAATACTCTGTAATTATACGGTGTACTATATAA  
TGGGATTAAAAAGTGTATCTTTCTATTCAAGTTAAATTACAAACAGTTGTAACTCTTGCTTTTAA  
TCTT

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**FIGURE 350**

MGLQTTKWPSPHGAFFLKSWLIIISLGLYSQVSILLACPSVCRCDRNFVYCNERSLTSVPLGIPE  
GTVVLVLYHNNQINNAGFPAELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTISR  
AALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSSVPVGLPVDLQELRVDE  
NRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPDLPGT  
HLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLNSNLKQLTARNNPWFCD  
CSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMAVRELMNNLLSCPTTPGLPLFTPAPSTAS  
PTTQPPTLSIPNPSRSYTPPTPTTSLPLTIPDWDRGRERVTPPISERIQLSIHFVNNTSIVQSW  
LSLFTVMAYKLTWVKMGMHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPPLDAFNYRAV  
EDTICSEATTHASYLNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVLLSVFCWHMH  
KKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNNDQLLGDFRLQPIYTP  
NGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Important features:****Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

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**FIGURE 351**

AGCCGACGCTGCTCAAGCTGCAACTCTGTGCAGTTGGCAGTTCTTCCGTTCCCTCTGTTGGGGCA  
 TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC  
 GAGGGCGGGCGTGACCCCTCGCTGGAGTTGTGCCGGCCCGAGCGCGCCGGCTGGGAGCTTCGGGTAGA  
 GACCTAGGCCGCTGGACC CGATGAGCGCCGAGCCTCCGTGCCGCCGCCGGTTGGGAGCTGTGCTGTG  
 GCGGTGCTGGGGCGCCTGGCCGCTGCCAGCGGGCTGCCGGGGAACTCGGGCAGCCCTGGGGTAGCCGCC  
 GAGCGCCCATGCCCACTACCTGCCGCTGCCCTGGGGACCTGCTGGACTGCACTGTAAGCGCTAGCGCTT  
 CCCGAGCCACCTTCAAAGCCTCGAGAACTGAAACTGAACAACAATGAATTGGAGACCATTCAAATCTGGACCA  
 GTCTCGGCAAATATTACACTTCTCTTGGCTGGAAACAGGATTGGTAAATACTCCCTGAACATCTGAAAGAG  
 TTTCAGTCCCTGAAACATTGGACCTTACGCAACAAATTTCAGAGCTCAAACACTGCAATTCCAGCCCTACAG  
 CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGAACTGGTATTGACAATTGGCAACACA  
 CTCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTAAACTGCCAACACTGCAA  
 CATCTCGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCAAGGCCCTGGTCTGAAGTCT  
 CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGAAATTG  
 CAGCTGGACCATACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGCAGGAACCTCAT  
 CTCAGGAAAATGCCCACAGGATCAGCGCTGATGCCCTGGAGTCTGCCAGAGCTCAGTGAGCTGGACCTA  
 ACTTCAATCACTTATCAAGTTAGATGATTCAGCTAACGCTTCTGGCTTAAGCTTAAACTACACTGCAACATTGG  
 AACAAACAGAGTCAGCTACATTGCTGATTGCTCTTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC  
 AATGAAATTTCCTGGACTATTGAAAGACATGAATGGTCTTCTGGCTTGACAACACTGAGGGACTGATACTC  
 CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT  
 GACAACGCAATCATGCTTTACAAGGCAATGCAATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA  
 TCAAGCCTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGTGGCGGAAACAAACTTCAAGGCTTGTG  
 AATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAAGCATTGGTGTGTTAGGCCAGATGGCTTGTG  
 GATGATTTCCTAACCCCCAGATCACGGTTCAGCCAGAAACACAGTGGCAATAAAAGGTTCAATTGAGTTTC  
 ATCTGCTCAGCTGCAGCAGCTGATTCCCAATGACTTTGCTTGGAAAAAGACAATGAACACTGCACTGATGAT  
 GCTGAAATGGAAAATTATGCACACCTCGGGCCAAGTGGCGAGGTGATGGAGTATACCACCATCCTTGGCTG  
 CGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAACTCAATTGGTCTCATCTACTGTC  
 AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCATCCGAGCTGGGGC  
 ATGGCACGCTTGGAGTGTGCTGCTGGGGACCCAGCCAGATAGCTGGCAGAAGGGATGGGGCACAGAC  
 TTCCCACTGCAAGGGAGAGACCATGCTGATGCTGAGTGGGGCAACTGTGGGTGCTGATCATAGCCGGTTG  
 GAGGACATTGGGTATACAGCTCACAGCTGAGGAAACTGTAACCAAGGGAAACAGCCGTCTACAGTGC  
 CTAGAACACCATATTGGCGCACTGTTGGACGAAGCTGTAACCAAGGGAAACAGCCGTCTACAGTGC  
 ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACCTGGACCAAGATGATAGCCATTGGTAAACGGAGAGGCAC  
 TTTTTGCACTGGAGGAACTCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGTGATGCTGGAAATACACATGTGAG  
 ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCAACCTGCACTCCCT  
 CAGATGAGACCCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGGTTG  
 GTGGTGGGACGTCACTCGTGGGGTGTGATCATATACACACACAAGGGAGGAATGAAGATGCACTGAGCAT  
 AACACAGATGAGACCAACTTGCACAGATATTCTAGTATTGTCATCTCAGGGAAACGTTAGCTGACAGGCAG  
 GATGGGTACGTGCTTCAAGAAAGTGGAGCCACCCAGGTTGTCACATCTCAGGGTGTGATTTTCTTACCA  
 CAACATGACACTACTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTTGGAAAGCTGCCACAGATCTGTT  
 CTTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGCTCAGATCTTGAACAA  
 TATCATACAGGTTGCACTGCTGCCAGAACAGTTTAAATGGACCAACTATGAGCCCAGTTACATAAAAGAAAAG  
 GAGTGTACCCATGTCTCATCTTCAAGAAAGATCTGCCAGGGACCTTCAGTAATATATGTTGGCTTACAT  
 GTGAGGAAGCTTAAACACTAGTTACTCTCACAAATGAAGGACCTGGATGAAAATCTGTCTAAACAAGTCC  
 TCTTAGATTAGTCAAAATCCAGAGCCAGCGTGGTGCCTCGAGTAATTCTTCACTGGGACCTTGGAAAA  
 GCTCTCAGGAGACCTCACCTAGATGCTTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTAT  
 TTGAAAGCTCATTCTCCCCCAGACTGGACTCTGGGTGAGGAAAGATGGGAAAGAAAGGACAGATTTCAAGGAA  
 GAAAATCACATTGACCTTAAACAGACTTAGAAAACAGACTCAGGACTCCTTCAAGTCTTATGACTTGGAC  
 ACATAGACTGAATGAGACCAAGGAAAAGCTAACATACTACCTCAAGTGAACCTTATTAAAGAGAGAGAAT  
 CTTATGTTTTAAATGGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGATGAACCAAATTAC  
 AAAAAGTTATGAAAATTTTATACGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTTAATTG  
 TTTTATGCAAAAAGTATCTACGTAATTATGATATAATCATGATTATTTATGTATTTTATAATGCCAGA  
 TTCTTTTATGGAAAATGAGTTACTAAAGCATTTAAATAACCTGCCCTGTACCATTTTAAATAGAAGT  
 ACTTCATTATATTGCACTTATTTAATAAAATGTCATTGAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 352**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAAERPCPTTCRCLGDLDCSRKRLARLPEPLPSW  
 VARLDLSHNRLSFIKASSMSHLQLSREVKLNNNELETIPNLGPVSAINTLLSLAGNRIVEILPEHLKEFQSLETL  
 DLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVTKLNRRNISAIPPKMFKLPOQLQHLELNRN  
 KIKNVDGLTFQGLGALKSLKMQRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLMLQELHLSQNAIR  
 RISPDWEFCQKLSELDLTFNHLSDLSSFLGLSLLNTLHIGNNRVSYIADCARGLSSLKTLDLKNNEISWTI  
 EDMNGAFSGLDKLRLILQGNRIRSITKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMKKLQQLHNTSSLLCDC  
 QLKWLWPQVAENNFSFVNASCAPQLLKGRSIFAVSPDGVCDDFPKPQITVQPETQSAIKGSNLSFICSAASS  
 SDSPMTFAWKDNELLHDAEMENYAHLRAGGEVMEYTTILRLREVEFASEGKYGCVISNHFGSSYSVKAAKLTVN  
 MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPOIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYS  
 CTAQNSAGSISANATLTLETSPSLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSPVVTERHFFAAGNQ  
 LLIIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSQMUTAPSLODDGWATVGVVIIAVVCCVVGTSLV  
 WVIIYHTRRNEDCSITNTDETNLPADIPSYLSQGTIADRQDGYSSESAGSHHQFVTSSGAGFFLPQHDSSGT  
 CHIDONSSEADVEATDLCFLCPFLGSTGPMYLKGNVYGSDFPETYHTGCSPDPTVLMHYEPsyIKKKCYPCH  
 PSEESCRSFSNISWPSHVRKLNNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHL  
 DAYSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
 1073-1077, 1079-1083, 1081-1085**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939**Leucine zipper pattern.**

amino acids 58-80, 65-87

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**FIGURE 353**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCCTGGCTCGACATTGG  
ACCACTAAATGAACCTGAATTGTCTGTGGCAGCAGGATGGTCGCTGTTACTTGTGATGAGATCGGGATGA  
ATTGCTCGTTAAAAATGCTGTTGGATTCTGTTGCTGGAGACGCTCTTGTGTTGCCGCTGGAAACGTTAC  
AGGGGACGTTGCAAAGAGAAGATCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAA  
GGGCTTCACAAGTCTGCAGCGTTCACTGCCCGACTTCCAGTTTACCATTTATTCATGGCAATTCCCT  
CACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGTTAGTTGCACATGGAAAACAATGGCTGCA  
TGAAATCGTCCGGGGCTTCTGGGCTGCAGCTGGTAAAAGGCTGCACATCAACAACAAGATCAAGTC  
TTTCGAAAGCAGACTTTCTGGGCTGGACATCTGGAATATCTCAGGCTGATTTAATTATTACGAGATAT  
AGACCCGGGGCCTCCAGGACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCCTACC  
TGCCAACGTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCCCTATGA  
GGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTGGACTGCACCTGTGATCT  
GCTCCCTGAAAGAATGGCTGGAAACATTCCAAGAATGCCCTGATCGGCCAGTGGCTGCGAAGCCCCAC  
CAGACTCGAGGGTAAAGACCTCAATGAAACCACCGAACAGGACTTGTGTCCTTGAAAACCGAGTGGATTCTAG  
TCTCCGGGCCCTGCCAAGAAGAGACCTTGCTCCAAACCGAGGTACAAAGATCCCAGGCAACTGGCAGATCAAATCAG  
ACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCCCTAGCTAACAGTTACCCCTGCCCTGGGCTG  
CAGCTGGGACACATCCCAGGGTGGGTTAAAGATGAACTGCAACACAGGAACGTGAGCAGCTGGCTGATTT  
GAAGCCCAAGCTCTAACGTGCAGGAGCTTCTACGAGATAACAAGATCCACAGCATCCGAAATCGCACTT  
TGTGGATTACAAGAACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAA  
GAACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCGGGAGAAATTGGGG  
GCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTACCCAGCTCATCCTCCGGGACTTCAATGCCAT  
GCCCAAACCTGAGGATCCTCATTCTCAACAAACACCTGCTGAGGTCCCTGCTGACGTGTCGCTGGGCTC  
GCTCTCTAAACTCAGCCTGCACAACAATTACTCATGTACCTCCGGTGGCAGGGTGTGGACCTGTTAACCTC  
CATCATCCAGATAGACCTCACGAAACCCCTGGAGTGCTCCTGCACAATTGTGCCCTTCAAGCAGTGGCAGA  
ACGCTTGGGTTCCGAAGTGTGAGCGACCTCAAGTGTGAGACGCCGGTAACCTTCTTAGAAAGGATTCT  
GCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCTGCCACGTTAACCTGCACAGTAAAAAA  
CAGCACTGGGTTGGCGAGACCGGGACGCACTCCAACCTCACCTAGACACCAGCAGGGTGTCCATCTGGTGT  
GGTCCCAGGACTGCTGCTGGTGTGTCACCTCCGCTTACCGTGGCATGCTCGTTATCTGAGGAA  
CCGAAAGGGTCCAAGAGACGAGATGCCAACCTCCCGCTCCGAGATTAATTCCCTACAGACAGTCTGTGACTC  
TTCCCTACTGGCACAATGGGCTTACAACGAGATGGGCCCACAGAGTGTATGACTGTGGCTCTACTCGCTCTC  
**AGACTTAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAGGGATA**CATCCCTCCCCACCGCAGGCACCCGGG  
GGCTGGAGGGCGTGTACCCAAATCCCCGCGCCATCAGCTGGATGGCATAAGTAGATAAAACTGTGAGCTC  
GCACAACCGAAAGGGCTGACCCCTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGA  
GCGCAGCCAGCTCGCTTTGCTGAGAGCCCCCTTGACAGAAAGCCAGCACGACCCCTGCTGGAAGAACTGACA  
GTGCCCTGCCCTGCCCGGGCCTGTGGGTTGGATGCCCGGTTCTATACATATACATATATCCACATC  
TATATAGAGAGATAGATATCTATTTCCCTGTGGATTAGCCCGTGTGGCTCCCTGTTGGCTACGCAGGGAT  
GGGCAGTTGCACGAAGGCATGAATGTATTGTAATAAGTAACCTTGACTTCTGAC

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**FIGURE 354**

MLLWILLLETSLCFAAGNVTDVCKEKEKICSCNEIEGDLHVDCEKKGFTSLQRFTA  
P TSQFYHL  
FLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQTF  
LGLDDLEYLQADFNLRLIDPGAFQDILNKLEVILNDNLISTLPANVFQYVPITHLDLRGNRL  
KTL PYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQGKDL  
NETTEQDLCPLKNRVDSSLAPPAAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGTKIPGNW  
QIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCCNRNVSSLADLKPKLSNVQ  
ELFLRDNIHSIRKSHFVDYKNLILDLGNNNIATVENNTFKNLLDLRWLYMDSNYLDTLSRE  
KFAGLQNLEYLNVEYNNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSLSKLSLHNN  
YFMYLPVAGVLDQLTSIIQIDLHGPNPWECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRK  
DFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVLVPGLLL  
SAFTVVGMLVFILENRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHS  
LSD

**Important features:****Signal sequence:**  
amino acids 1-15**Transmembrane domain:**  
amino acids 618-638**N-glycosylation site.**  
amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 122-126, 646-650**Casein kinase II phosphorylation site.**  
amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697**N-myristoylation site.**  
amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 337-348

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**FIGURE 355**

AGTCGACTGCGTCCCCGTACCCGGCGCACGGTGTCTGACCCCCAGAATAACTCAGGGCTGCACCGGGCTG  
GCAGCGCTCCGCACACATTCTGTCGGGCCATAAGGAAACTGTTGGCGCTGGGCCGCGGGGGATTCTGG  
CAGTTGGGGGGTCCGTCGGAGCGAGGGCGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAG  
GGCGGTGACCGCGCTCCAGACACAGCTCTGCGCCTCGAGCGGGACAGATCCAAGTGGAGCAGCTCTGCGTGC  
GGGGCCTCAGAGAATGAGGCCGGCTTCGCCCTGTGCCCTCTGGCAGGCCTCTGGCCCAGGGCGGGCG  
CGAACACCCCCACTGCGGACCGTGTGGCTGCTCGGCCCTGGGGCCTGCTACAGCCTGCACCACGCTACCATGAA  
GCGGCAGCGGCCAGGGCCTGCATCCTGCGAGGTGGGGCCTCAGCACCGTGCCTGCAGGCCGAGCTGCG  
CGCTGTGCTCGCCTCTGCGGGAGGCCAGGGCCGGAGGGGCTCAAAGACCTGCTGTTCTGGCTGCCTCCGACCCGG  
GGAGCGCAGGCCTCCCACTGCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCCTGGCTGTCCTCCGACCCGG  
CGGTCTCGAAAGCAGACCGTGCAGTGGGTGGAGGAGCCCCAACGCTCTGCACCGCGAGATGCGCGGTACT  
CCAGGCCACCGTGGGTGAGGCCAGGGCTGGAGAGATGCGATGCCACCTGCGGCCAACGGTACCTGTG  
CAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCCGGGCCCTAACTTGAGCTATCGCGGCCCT  
CCAGCTGCACAGCGCCGCTCTGGACTTCAGTCACCTGGGACCGAGGTGAGTGCCTGCGCCGGACAGCTCC  
GATCTCAGTTACTTGCATCGCGAACGAAATCGCGCTCGCTGGACAAACTCTCGGGCAGTGTGTTGTCCTG  
CCCCGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCTAACTGCCAGACGACTGGGAGGCTTGCGCTG  
CGAATGTCTACGGCTCGAGCTGGGAAGGACGGCGCTCTGTGACCAGTGGGAAGGACAGCCGACCC  
TGGGGGACGGGGTGCACCAGCGCCGCCACTGCAACCAGCCCCGTGCCAGAGAACATGGCAAAT  
CAGGGTCACGAGAACGCTGGAGAGACACCACCTGTCCTGAACAAGACAATTCAAGTAACATCTATTCC  
TGGAGAT  
TCCCTCGATGGGATCACAGAGCACCGATGTCACCCCTCAAATGTCCTCAAGCCGAGTC  
AAAGGCCACTATCAC  
CCCACATCAGGGAGCGTATTCAAGTTAAATTCTACGACTCCCTGCAACTCCTCAGGCTTCA  
GACTCCTCCTG  
TGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTGTGTTGGTGA  
CTTGACCATGACAGTACTGGGCTTGT  
CAAGCTCTGCTTCAAGAAAGCCCCCTTCCCAGCCAAGGAAGGAGTCA  
TGGGCCCCGGGCCCTGGAGAGTGA  
TCCTGAGCCGCTGCTTGGCTCCAGTTCTGCACATTGCA  
AAACACAATGGGGTGAAGTGGGACTGTGATCT  
GCCGGACAGAGCAGAGGGTGCCTTGTGGAGTCCCTCTGGCT  
TAGTGTGATGCAAGGGAAACAGGGGACA  
TGGGCACTCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAAC  
TTACTTGTA  
ACTGACAA  
TTCTGCAAGAAATCCCCCTCCTCAAATCCCTTACTCCACTGAGGAGCT  
AAATCAGAACACTGCACACTCCTTC  
CCTGATGATAGAGGAAGTGGAGTGCCTT  
TAGGATGGTGA  
ACTGGGGACCGGGTAGTGTGCTGGGAGAGATATT  
TTCTTATGTTATTGGAGAATTGGAGAAGTGTGATTGA  
ACTTTCAAGACATTGAA  
ACAAATAGAACACAATAT  
AATTTACATTAAAAAAATTTCTACCAAAATGGAAAGGAAATGTT  
CTATGTTGTCAGGCTAGGAGTATATTGG  
TTCGAAATCCCAGGGAAAAAAATAAAAAATAAAAAATAAAGGATTGTTGAT

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**FIGURE 356**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGA  
VRAGAELRAVLALLRAGPGPGGGSKLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLES  
TLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGASN  
LSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPGRYLR  
AGKCAELPNCLDDLGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATATSPVP  
QRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITPSGSVIS  
KFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPRKESMGPP  
GLES DPEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Important features:**

**Signal sequence:**  
amino acids 1-16.

**Transmembrane domain:**  
amino acids 399-418

**N-glycosylation site.**  
amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**  
amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**  
amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**  
amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**  
amino acids 262-274

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**FIGURE 357**

CCCATCTCAAGCTGATCTGGCACCTCTCATGCTCTGCTCTTCACACCAGACCTACATTCCATTGGAAAGA  
AGACTAAAATGGTTTCCAATGTGGACACTGAAGAGACAATTCTTACATAATCCTAATTCC  
AAACTCTGGGCTAGATGGTTCTAAAACCTGCCCCGTGATGTCACCTGGATGTCAGAACACCACGAAACCTCACCC  
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCTGGAGGTATCCCACGAACACCACGAAACCTCACCC  
ACCATTAAACCACATACCAGACATCTCCCAGCGCTTACAGACTGGACCATCTGGTAGAGATCGATTTCAGA  
TGCAACTGTGACCTATTCCACTGGGTCAAAAACACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAC  
TTTAGTGGACTCACTTAAATCCCTTACCTGGATGAAACAGCTACTAGAGATACCGCAGGGCTCCCG  
CCTAGCTTACAGCTCTCAGCCTGAGGCAACAAACATCTTCCATCAGAAAAGAGAACTAACAGAACTGGC  
AACATAGAAAATCTACTGGGCAAAACTGTTATTATCAGAAATCTTCCATCAGAAAAGAGAACTAACAGAACTGGC  
CTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTCGTTGTTAAATGCCCATTTCTGTGCC  
TGTAAAAATAATTCTCCCACAGATCCCTGAAATGTTGATGCGCTGACAGAAATTAAAGTTTACGTCTA  
CACAGTAACCTCTCAGCATGTGCCCAAGATGGTTAAGAACATCAACAACTCCAGGAACGGATCTGTCC  
CAAAACTCTGGCAAAAGAAATGGGATGCTAAATTCTGCATTCTCCCGACGCTCATCCAATTGGATCTG  
TCTTCATTTGAACTCAGGTATCTGCATCTGAATCTACAAACATGATTGCAAAAATCCAAGAAGATGTTAAAC  
CTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTCGTTGTTAAATGCCCATTTCTGTGCC  
TGTAAAAATAATTCTCCCACAGATCCCTGAAATGTTGATGCGCTGACAGAAATTAAAGTTTACGTCTA  
CACAGTAACCTCTCAGCATGTGCCCAAGATGGTTAAGAACATCAACAACTCCAGGAACGGATCTGTCC  
CAAAACTCTGGCAAAAGAAATGGGATGCTAAATTCTGCATTCTCCCGACGCTCATCCAATTGGATCTG  
TCTTCATTTGAACTCAGGTATCTGCATCTGAATCTACAAACATGATTGCAAAAATCCAAGAAGATGCTTAAAC  
AACTTGAAAGTCTGTGACTAACTTATAAAATTGCTAACCTCAGCATGTTAAACAAATTAAAAGA  
CTGAAAGTCATAGATCTTCAGTGAATAAAATCACCTCAGGAGATTCAAGTGAAGTGGCTCTGCTCAAAT  
GCCAGAACTCTGTAGAAAGTTATGAACCCCAGGTCTGGAACAATTACATTATTCAGATATGATAACTATGCA  
AGGAGTTGCAAGGTTCAAAACAAAGAGGCTCTTCATGCTGTTAATGAAAGCTGCTACAAGTATGGCAGACC  
TTGAGATCTAAGTAAAAAGATGTTATTTTGCAAGTCTGCTGATTTCAGCATTTCTTCAGCATTCAAAATGCC  
AACTGTCAGGAAATCTCATTAGCCAAACTCTTAAGGAGCTGAATTCCAACCTTCTGAGAGCTGAGATATTG  
GACTTCTCCAACAGGCTTGTACTCCATTCAACAGCATTGAAAGAGCTCAGAAACTGGAAGTTCTGGAT  
ATAAGCAAAATAGCCATTATTTCAATCAGAGGAATTACTCATATGCTAAACTTACCAAGAACCTAAAGGTT  
CTGCAGAAAATGATGATGACGACAATGACATCTTCCACCGAGCAGGACCATGGAGAGTGGTACTCTTAGA  
ACTCTGGAATTCAAGAGGAATCACTTAGATGTTTATGGAGAGAAGGTGATAACAGAACTTACAATTATTCAAG  
AACTGCTAAATTAGAGGAATTAGACATCTAAAAATTCCCTAAGTTCTGCTCTGGAGTTTTGATGGT  
ATGCCCTCAAATCTAAAGAATCTCTTGGCAAAATGGGCTCAAATCTTCAAGTGGAGAGAAACCTCAAGTGT  
CTAAAGAACCTGGAAACTTGGGACTCAGCCACAAACCAACTGACCACTGTGCTGAGAGATTACCAAGATGCTTC  
AGAACCTCAAGAACATCTGATCTTAAGAATAATCAAAATCAGGAGTCTGACGAAGTATTTCTACAAGATGCTTC  
CAGTTGGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGCC  
AACAACTGAAAGATGTTGCTTTCATATACTGGTTCTGACCTGTGATGCTGTTGAGAGATTTCTGGGAT  
GTTAACCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTTGGGCCAGGAGCACACAAGGGC  
CAAAGTGTGATCTCCCTGGATCTGACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTCCATA  
TCTGTATCTCTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTCTGGGATGTTGAGAGATTACCAAGG  
TTCTGTAAAGGCAAGATAAAGGGTATCAGCTGCTAAATACCCAGACTGTGCTATGATGCTTTATTGTTGAT  
GACACTAAAGAACCCAGCTGTGACCGAGTGGGTTGGCTGAGCTGGTGGCCAAACTGGAAGACCAAGAGAGAAA  
CATTAAATTGTCAGGAAAGGGACTGGTACCGGGCAGCCAGTTCTGGAAAACCTTCCAGAGCATA  
CAGCTTAGAAAAGACAGTGTGTTGATGACAGACAAGTATGCAAAGACTGAAAATTAAAGATAGCATTTC  
TTGTCCCATTAGAGGCTCATGGATGAAAAGTTGATGTTGATTATCTTGATATTCTTGAGAAGCCCTTCAAGAAG  
TCCAAGTCCCTCCAGCTCCGAAAAGGCTGTGGAGTTCTGCTTGTGAGTGGCCAACAAACCGCAAGCTCAC  
CCATACTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCTATAGTCAGGTGTTCAAGGAA  
ACGGTAGCCTTTGC  
AAACACAACACTGCCTAGTTACCAAGGAGAGGCC  
GGC

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**FIGURE 358**

MVFPMWTLKRQILILFNIIILISKLLGARWFPTLPCDVTLDPKHNHIVDCTDKHLTEIPGGI  
PTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFSGL  
TYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLQNCYYRNPC  
YVSYSIEKDAFLNLTKVLKSLKDNNVTAVPTVLPSTLTLYLYNNMIAKIQEDDFNNLNQLQ  
ILDLSGNCPRCYNAPFPCAPCKNNSPLOIPVNADALTELKVRLHSNSLQHVPPRWFKNINK  
LQELDLSONFLAKEIGDAKFLHFLPSLIQLDSFNFELQVYRASMNLSQLSSLKSLKILRIR  
GYVFKEKSFNLSPLHNLQNLEVLDLGTNFKIANLSMFQFKRLKVIDLSVNKISPSGDSSE  
VGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKGQTLDLSKNS  
IFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNRNLDDLLHSTAFEELHK  
LEVLDISSLNSHYFQSEGITHMLNFTKNLKVLQKLMNDNDISSLRTMESESRLTLEFRGNH  
LDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWK  
KLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSS  
NKIQMIQKTSFPENVLNNLKMLLHHNRFLCTCDAVWFVWWVNHTEVТИPYLATDVTCVPG  
HKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQ  
RLISPDCCYDAFIVYDTKDPAVTEWLAELVAKLEDPREKHFNLCLEERDWLPGPVLENLSQ  
SIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLEKPFQSKFLQLRKRLC  
GSSVLEWPTNPQAHPYFWQCLKNALATDNHVAYSQVFETV

**Important features:****Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

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**FIGURE 359**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTAC  
TGCTGGTGGCCACCACAGCCCCGTGGAGCCCTCACAGATGAGGAGAACGTTGATGGTGG  
AGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGCCCTCAGACATGCTGCACATGAGAT  
GGGACGAGGAGCTGGCCGCCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCCACAACA  
AGGAGCGCGGGCGCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGTGCCGC  
TGGCCATGGAGGAAGTGGCACCAACGAGCTGAGCACTACAACCTCAGGCCGCCACCTGCAGCC  
CAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCAAGACAGAGAGGATCGGCTGTG  
GTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACTGGTGTGCA  
ACTATGAGCCTCGGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTCCGTGCTCCC  
AATGTCCTCTGCTACCAC TGCAAGAACTCCCTCTGTGAACCCATCGGAAGCCCGGAAGATG  
CTCAGGATTGCTTACCTGGTAACTGAGGCCCATCTCCGGCGACTGAAGCATCAGACT  
CTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCTGGTAACAGAGG  
TCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCCCAACTCCTTAG  
CAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAACAACGTGAGGTCCCTT  
CCATTTGGCAGCTCACAGCCTGCCCTCTGGATGAGGAGCCAGTTACCTCCCAAATCGA  
CCCATGTTCCCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACAAAAGTGCCCTCTAGGA  
GCCAGAGAACTCTGGACCCCAAGATGTCCTGACAGGGCAAGGGAACTCCTACCCATG  
CCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTGAGGTCTTGGCCTCAGTT  
TTCCAGGCCAGGACAAGCCAGGTGAGCTGAGGCCACACTGGACCACACGGGGCACACCTCCT  
CCAAGTCCCTGCCAATTCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGCGTGC  
TGGCTCTGCAGTCGTCCTGCCAGGTGCAGAGGCCCTGACAAGCCTAGCGTTGTGTCAGGGC  
TGAACTCGGCCCTGGTCATGTGTGGGCCCTCTGGACTACTGCTCCTGCCCTCTGG  
TGTTGGCTGGAATCTCTTGAATGGATACCAACTCAAAGGGTAAGAGGTCAGCTGTCCCTCTG  
TCATCTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATACTTCTGGTTAAGGCCCTCCGAA  
GGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCCATCTGGAGGCACAAGGCCTGGCTG  
GCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACGGGGCCACACCTCTCCTGCCCTCCC  
TCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCTCACTGCCCTACCTGGCCTGGGCTGTCT  
GCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGAGCTGGGATGGGATTCCTAGGG  
CAGATGAAGGACAAGCCCCACTGGAGTGGGTTCTTGAGTGGGGAGGCAGGGACGAGGGAA  
GGAAAGTAACCTGACTCTCCAATAAAACCTGTCCAACCTGTGAAA

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**FIGURE 360**

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEEL  
AAFAKAYARQCVWGHNKERRRGENLFAITDEGMVPLAMEEWHHEREHYNLSAATCSPGQMC  
GHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPyQEGTPCSQCPSG  
YHCKNSLCEPIGSPEADAQDLPYLVTAEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSL  
ATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPI  
PKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQD  
KPGELQATLDHTGHTSSKSLPNFPNTSATAÑATGGRALALQSSLPGAEGPDKPSVVSGLNSGP  
GHVWGPLLGLLLPPLVLAGIF

**Important features:****Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

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**FIGURE 361**

GAATAGTTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAACTGG  
GGTGACGGCAGGGCAGGGGGCGCTGGCCGGGAGAAGCGGGGGCTGGAGCACCAACT  
GGAGGGTCCGGAGTAGCGAGCAGCCCCGAAGGAGGCCATCGGGAGCCGGAGGGGGACTGCG  
AGAGGACCCCAGCGTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCTCCGGCT  
CCTGGGCCTGGCGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGCCCGG  
GCACCCCGGCCTCCAGGCACGCCGGCCACCATGGCAGCCAGGGCTTGCCGGCCGCATGG  
CCGCGACGGCCCGACGGCGCGCCGGCTCCGGAGAGAAAGCGAGGGCGAGGCCGG  
ACTGCCGGGACCTCGAGGGGACCCCGGGCGAGGAGAGGCCGGACCCGCCGGGACCGG  
GCCTGCCGGGAGTGCTCGGTGCCCTCGCATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCG  
GGTGCCTCCGCGTCTGACGCACCCCTGCCCTCGACCAGCGTGTGGTAACGAGCAGGGACA  
TTACGACGCCGTACCGCAAGTTCACCTGCCAGGTGCCCTGGGTCTACTACTTCGCCGTC  
TGCCACCGTCTACCGGCCAGCCTGCAGTTGATCTGGTAAGAATGGCAATTGCCTC  
TTTCTCCAGTTTCGGGGGTGGCCAAGCCAGCCTCGCTCTGGGGGGGCCATGGTGAG  
GCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTGC  
CAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCCGACTGGCACAGCT  
AGTCTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGA  
GGCTGACAACAGGTATCCAGGAGGGCTGGCCCCCTGGAATTGTGAATGACTAGGGAGG  
TGGGGTAGAGCACTCTCCGCTGCTGGCAAGGAATGGAACAGTGGCTGTGCGATCA  
GGTCTGGCAGCATGGGCAGTGGCTGGATTCTGCCAAGACCAGAGGAGTGTGCTGTGG  
CAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGTGCTCTTCC  
CTCTGCTCTGGATCCTCCCCACCCCTCGCTCCTGGGCCGGCTTTCTCAGAGAT  
CACTCAATAAACCTAAGAACCCCTATAAAAAAAAAAAAAAAA

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**FIGURE 362**

MRPLLVLLLLGLAAGSPLLDDNKIPSLCPGHGPLPGTPGHHGSQGLPGRDGRDGRDGAPGAPG  
EKGEGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFD  
RVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA  
SLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

**Important features:****Signal sequence.**

amino acids 1-15

**N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

**Cell attachment sequence.**

amino acids 77-80

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**FIGURE 363**

GGAGAGCGGAGCGAAGCTGGATAACAGGGACCG**TG**ATGTGGCGACCATCAGTTCTGCTGCT  
TCTGTTGCTACTGAGGCACGGGCCAGGGAAAGCCATCCCCAGACGCAGGCCCTCATGGCCA  
GGGGAGGGTGCACCAGGCCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAACCT  
CCAGTACGACCATGAGGCTTCCTGGGACGGGAAGTGGCAAGGAATTGACCCAACTCACCCC  
AGAGGAAAGCCAGGCCGCTCTGGGGCGGATCGTGACCGCATGGACCGCGCGGGGACGGCGA  
CGGCTGGGTGTCGCTGGCCGAGCTTCGCGCTGGATCGCGCACACCGCAGCAGGGCACATACG  
GGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGCGTGTGGTTGGGA  
GGAGCTGCGAACGCCACCTATGCCACTACGCCCGGTGAAGAATTTCATGACGTGGAGGA  
TGCAGAGACCTACAAAAGATGCTGGCTGGGACGAGCGCTGGGAGGAGTCCGGTGGCCGACCAGGA  
TGGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCCTCA  
CATGCCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAAGATGGCTATGT  
CCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGAGGCCGGCGTG  
GGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGGATGGCACCTGGA  
TGGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCCTGGTGGAAAGCCAA  
CCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAAAGCGGAAATCCTGGG  
TAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCAGGACCTGACCCGGCACCA  
CGATGAGCTG**TG**AGCACCGCGCACCTGCCACAGCCTCAGAGGCCGACAATGACCGGAGGAG  
GGGCCGCTGTGGCTGGCCCTCCCTGTCCAGGCCCGCAGGAGGCAGATGCAGTCCCAGGC  
ATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTCTGTCCTGTACACCCCCA  
ACCCCCAGGGAGGGCTGTCAAGTCCCAGAGGATAAGCAATACCTATTCTGACTGAGTCTCC  
CAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTAAGAACCGCCCCAACCCCTCCAG  
CTCCAAATCTGAGCCTCCACACATAGACTGAAACTCCCTGGCCCCAGCCCTCCTGCCTG  
GCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAAAAGCCAGCGCCGGACCTTGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 364**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGRE  
VAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDTYD  
TDRDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATREELT  
AFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQFRDF  
RDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFVGSQAT  
NYGEDLTRHHDEL

**Important features:****Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

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**FIGURE 365**

GTCTGTTCCCAGGAGTCCTCGCGGCTGGTGTCAAGTGGCCTGATCGCG**ATGGGACAAAG**  
GCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGGCA  
TTGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCTGTG  
AAGTTGTCCGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCAAGGA  
GACACCACAGACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGGTGACC  
TTCTGCCAACCTGGTATCACCTCAAGTCGTGACACGGGAAGACACTGGGACATACACTTGT  
ATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGTGTGCTG  
CCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATGGAACCGGGCAGTGTGCTG  
ACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGATGGGATAGTG  
ATGCCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTTCTATGTCCTGAATCCACA  
ACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTGTGATACTGGAGAACAGCTGTGAGGCA  
CGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAAT  
GTGGGGGTATCGTGGCAGCGTCCTGTAACCTGATTCTCTGGGAATCTGGTTTTGGC  
ATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGACTTCGAGTAAGAAG  
GTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAGACACTCGTCATTCTG  
GTG**TGA**GCTGGTCGGCTACCGCCTATCATCTGATTGCTTACTCAGGTGCTACCGGACT  
CTGGCCCTGATGCTGTAGTTCACAGGATGCCTTATTGCTTCTACACCCACAGGGCCC  
CCTACTTCTCGGATGTTAATAATGTCAGCTATGTGCCCATCCTCTCATGCCCTC  
CCTCCCTTCTACCCTGCTGAGTGGCCTGGAACCTGTTAAAGTGTATTCCCCATTCT  
TTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCCTCTAAGTAGACAGCAAAAA  
TGGCGGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGCTGGCAGGGATCTTGAATAGG  
TATCTTGAGCTGGTTCTGGCTCTTCTGTCTCCATGGGAAGTGCCTACTGGGATCCCTGCCCCTGTC  
GCGGGAAATTAGAGGCTAGAGCGGCTGAAATGGTGTGATGACACTGGGGCTTCCAT  
CTCTGGGGCCCACCTCTCTGTCTCCATGGGAAGTGCCTACTGGGATCCCTGCCCCTGTC  
CTCCTGAATACAAGCTGACTGACATTGACTGTGTGAAAATGGGAGCTTGTGAGG  
GAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAGGATTAAAACCGCTGCTCTAAAGAAA  
AGAAAACGGAGGCTGGCGCAGTGGCTCACGCCGTAAATCCAGAGGCTGAGGCAGGCGGAT  
CACCTGAGGTCGGGAGTTGGGATCAGCCTGACCAACATGGAGAACCCACTGGAAATACAA  
AGTTAGCCAGGCATGGTGGTCATGCCTGTAGTCCCAGCTGCTCAGGAGCCTGGCAACAAAGAG  
CAAAACTCCAGCTAAAAAAAAAAAAAA

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**FIGURE 366**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEWK  
FDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKVKL  
IVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNSSYV  
LNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNNGVIVAAVLVTLILLGI  
LVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

**Important features:****Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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**FIGURE 367**

GGGGAGAGGAATTGACCATGTAAGGAGACTTTGGTGGCTGTTGGTGCCTGCAAAATG  
AAGGATCGAGGACGCAGCTTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTTGAGGCCCTGGATCTAACACAATGTGTATATGTGACACAGGGAGCATTCAAGAATGAAA  
TAAACCAAGAGTAGACCCGCGGGGGTGGTGTCTGACATAAAATAATCTAAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAAGGATGATGGAAATGAGAACCGAGGATTCAAAAGAAAAGTATGTTCATTTTCTC  
TATAAAGGAGAAAGTGGCAAGGAGATATTGGAAATGAAAAGTTGGGCTTTTAGTAAGTAAAGAAACT  
GGTGTGGTGTCTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAAACAGCAGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATGACGGATAATTGCAAGTTGGATTTCATCAACCTCCTTTTTAAAT  
TTTATTCTTTGGTATCAAGATCATGCTTTCTCTTCAACCACCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGCTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGC  
GCTGGCTTCAACTCTGTGGCTGGCTGGTCTGGCAGACCTGGCTCAGACCTGGCCCTCTGTGTGCTCCTGCAGCAA  
CCAGTTCAAGGTAAGGTGATTGTGGTGGAAAACCTCGTGGAGGTTCCGGATGGCATCTCCACCAACACGGCT  
GCTGAACCTCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGCTTCAATGGTCTGGCGAACCTAACACTCTGGA  
ACTCTTGACAATCGCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT  
GGCAAACACCCCATGAAAGCATCCCTTATGCTTTAACAGAAATTCTCTTTGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTCATACATCTCAGAACGGTGCCTTGAAGGTCTGCAACTTGAGGTATTGAAACCTTGC  
CATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCATCAGGCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATAACAGTCCCAGAT  
TCAAGTGAACGGAATGCCTTGACAACCTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTGATCATCTAGAGCGGATACATTACATCACAACCCCTGGAACTG  
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGTG  
TAACACTCTCCAACTCAAAGGGAGGTACATTGGAGAGCTCGACCGAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGGCCCTGCAAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGCCCTCACATC  
CCTGACATCTGTATCTGGATTACTCCAATGGAACAGTCATGACACATGGGCTGACAAAGTGGGAGTAGCTGT  
GCTCAGTGTGGTACGTAAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGGTAA  
TTCCGTTGGAAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCAACTACTCTTTCTTACTTTT  
AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACGGACCAAGATAACAAATGGGGCTCCACTCC  
AGTGGTCACTGGAGACCACCAATGTGACCCACCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTT  
CACCATCCCAGTGAATGATATAAACAGTGGGATCCAGGAATTGATGAGGTATGAAGACTACCAAAATCATCAT  
TGGGTGTTGTGGCATCACACTCATGGCTCAGTGTGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTATTAATGTGGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCCCTGCCTGCTATCGAGCATGAGCACCTAAACTCATATAACTCATACAAATCTCC  
CAACCACACAACAGTTAACACAATAAATTCAATACACAGTTCACTGCACTGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGACAAGAGACTCAAACTTAAAACATTACAGGTTACAAAAACAAACAAATCAAAAAACAA  
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAACAA  
AAAAGAAAAGAAATTATTATTAAACAGACACAAAA

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**FIGURE 368**

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLVVAGLVRQAQTCPSVCSCSNQFSKVICVRKNLREVPDGIS  
TNTRLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPNGAFVYLSKL  
KEWLWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNRLYLNLCNLREIPNLTPLIKLDELD  
LSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIERNADNLQSLVETNLAHNNLTLLPHDLFTPPLHHLERIHLHH  
NPWNCCNDILWLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAELKC  
RASTSLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVGNTTASATLNVTAATTTP  
FSYFSTVTVETMEPSQDEARTTDNNVGPTPVWDETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKT  
TKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLHYNS  
YKSPFNHTTVNTINSTIHSVHEPLLIRMNSKDNVQETQI

**Important features:****Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438, 442-446,  
488-492, 606-610**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243, 391-397,  
422-428, 433-439, 531-537

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**FIGURE 369**

CAAAACTTGGTCCGGAGAGCGCCAGCTTGACTTGAAATGGAAGGAGCCCAGGCCGGAGCAGCTGAGAC  
 TGGGGAGCGCGTCGGCTGTGGGCCACTGGTGTGAACCGGGAGAGGCCCTGGTGGTCCCTATCCCTCTTATATA  
 GAAACCTTCCACACTGGAAAGGCAGCGGAGGGCTATGGTAGCAAGGAGGCCGCTGATCTGCAG  
 GCGCACAGCATTGGAGTTACAGATTTACAGATACCAATGGAAAGGGAGGGAGGAACAGCAGCTGCTGGT  
 TCCATCAGCCCTGGGCCAGGGCATCTGACTCGGCACCCCTGCAGGCCACCATGGCCAGAGCCGGGTGCTGC  
 TGCTCTGCTGTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGGCTGAGGGCCCCAGGGATTGGCCGAA  
 GTGGGCCACAGCTGAGGCCGAAGAGAACGAATTGGAGGGAGGCCGTGCTGGTAGCTGAGGCCCTGAGG  
 AGCCGGCTGGGCCAGCGGGTCAGTGCCTGGAGACTGTGCTGTTCCCAGGAGGGCTGTTGACTGTG  
 GCGTAGCTGGCTGAGTCTGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACACCAGC  
 TGGAAAAGATCTACCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAACAAACCAGCCTGA  
 CTTCCCAGGGCTCCAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
 TGACCTGGCACCCGCTCTGCCAACGCCCTGATCAGTGTGGACTTGTGCAACTATCTACCAAGATCT  
 ATGGGCTCACCTTGCCAGAGCAAACCTGAGGTGTGTAACCTGACAACAAACAGCTGGAGACGCCGGG  
 TGCGGACAACATGTTCAACGGCTCAGCAACGTCGAGGTCTCATCTGTCCAGCAACCTCTGCGCCACGTGC  
 CCAAGCACCTGCCCTGCCCTGACAAGCTGCACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGG  
 TCAGCGAGCTGAGCAGCTGCCAGCTGAGCTACCTGCAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA  
 CCTTCTGGAGGCTCTCCAGCTGGAGTACCTGGATCTGTCAGCAACACCTGTCTGGTCTGGAGCTGGCTGC  
 CGCGAGCCTGGTGTGTCAGTGGAGAACGCCATCCGGAGGGCTGGAGCGATCTGGCTTCCAGGCTTCCAGGG  
 GCAGCCTGGAGTACCTGCTGTCAGCAACGCAACCAGCTGCCAGGGCATCCACCCACTGGCTTCCAGGG  
 TCAAGCGGTTGCACCGGTGCACCTGTACAACAAACCGCTGAGCTGGCTGGAGGGCATGGCTCAGCTGCGTGAGCTGACTCA  
 GCACCCCTCATGATCTGCAACACCAGATCACAGGATTGGCCGAGAACACTTGCACCCACTTCTGGAGG  
 AGCTCAACCTCAGTACAACCGCATCACAGGCCACAGGTGACCGCAGCCTTCCGCAAGCTGCCCTGCTGC  
 GCTCGCTGGACCTGTGGCAACCGCTGCACACGCTGCCACCTGGCTGCCCGAAATGTCATGTGCTGAAGG  
 TCAAGCGCAATGAGCTGGCTGGCACCGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGACTCA  
 CCAGCAACCGACTGCCAGGCCAGGGCTGGGGCCATCTGCAAGCTGCTGGAGAC  
 TCGCCGGGAATCAGCTCACAGAGCATCCCCGAGGGGCTCCCCGAGTCAGTGTACCTGAGAACAAACA  
 AGATTAGTGCCTGGCCCAATGCCCTGACTCCACGCCAACCTCAAGGGGATTTCTCAGGTTAACAAAGC  
 TGGCTGTGGCTCCGTGGAGCTGCTTCCGGAGGTGAAGCAGCTGCAGGTCTGGACATTGAAGGCAACT  
 TAGAGTTGGTGAACATTCCAAGGACCGTGGCGCTTGGGAAGGAAAGGAGGAGGAGGAAGGAGGAGGAGG  
 AGGAAGAGGAAACAAGATGTCACAAGGTGATGCAAGATGTGACCTAGGATGATGGACCGCCGACTCTTCTGC  
 AGCACACGGCTGTGCTGTGAGCCCCACTCTGCCGTGCTCACACAGACACACCAGCTGCACACATGAGGCA  
 TCCCACATGACACGGCTGACACAGCTCATATCCCCACCCCTCCACGGCGTGTCCCACGGCAGACACATGC  
 ACACACATCACACCCCAAACACCCAGCTCAGGCCACACACAACTACCTCCAAACACCCAGTCTGTACAC  
 CCCCACACTCCGCTGCCACGCCCTGTGAATCATGCAAGGGAGGGCTGCCCTGGCACACACAGGCCACCC  
 TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACACATGCAAGGTGATGCGGA  
 CAGCCCTCCAAAGCTATGCCACAGACAGCTTGGCCAGGCCAGAACATGCCATAGCAGCTGCCGTCTGCC  
 GTCCCATCTGTCGTTCCCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCTGCCACCCCT  
 GGAACCTCACAAAGCTGGCTTTATCCCTTCCATCTATGGGAAGGAGGCCCTCAGGACTGCTGGCTGGCC  
 TGGCCCAACCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
 CAGGCAGCTTCTCAATGGCAAGGCCAGTGGAGGAGGATGGAGGAGGCCCTGGTGTGCTGGGCTTGGGG  
 CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGAACCCAGCTGCACCTAGGAGACACCTT  
 GTTCTTCAGGCCTGTGGGGAGTTCCGGGTGCTTATTTTATTCTTCTAAGGAAAAAAATGATAAA  
 CTCAAAGCTGATTTCTGTTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

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**FIGURE 370**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRLVLLLPPQLHLGPVLAVRAPGFGRSG  
GHSLSPEENEFAAEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLPEH  
TNHLSLQNNQLEKIYPEELSRLHRLETLNQNNRLTSRGLPEKAFFEHTNLNYLYLANNKTL  
APRFLPNALISVDFAANYLTAKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNVEVLI  
LSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDNETFWK  
LSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSNQLREQG  
IHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYFEEELNLS  
YNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAARGALAGMA  
QLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYLQNNKISAVP  
ANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKEE  
EEEEEEEEETR

**Important features:****Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554**Leucine zipper pattern.**amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

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### **FIGURE 371**

CACTTTCTCCCTCTTCTTACTTTCGAGAAACCGCGCTCCGCTCTGGTCGAGAGACCTCGGAGACCGCG  
CCGGGGAGACGGAGGTGCTGTTGGTGGGGGACCTGTGCTCGTACCGCCCCCACCCTCTTCTGAC  
TGCCGTCTCCGGAAGACCTTTCCCCTGCTCTGTTCTTACCGAGTCTGTGATCGCCCCGGACCTGGCG  
GAGGAGGCTTGGCCGGAGATGCTTAGGGCGGCCGGAGGAGCAGGCCGGAGGACGGAGGGCCGG  
GAAGATGGCTCTCCGGACAGGACTCTTGTGCTGGCTACTGCTCTGCTCTTGCCTTGTGCTCTGGCT  
GAGTCGCTGTCGGGGCATGTCAGGGGGAACAGCAGGACTGGGGAGGGACTGAGGAGCTGCCGTCCCTCGGACCA  
TGCCGAGGGCTGAAGAACACATGAAAATACAGGCCAGTCAGGACAGGGCTCCCTGCTTCCCCTGCTT  
GCGCTGTGACCCGGTACCTCATGTACCCGGCACCGCCGTCCCCAGATCAACATCACTATCTTGAAGG  
GGAGAAGGGTGAACCGGGAGATCGAGGCTCCAAGGAAATATGCAAAACAGGCTCAGCAGGGCCAGGGCCA  
CACTGGACCCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGAGCGGTGCAAGAGCCACTACGCCGCTTTC  
GGTGGGCCGAAGAACCCATGCACAGCAACCACTACTACCAAGCGGTGATCTCGACACGGAGTCTGTAACCT  
CTACGACCACTTCAACATGTTACCGGCAAGTCTACTGCTACGTGCCGCTCTACTCTTCAACGCTCAACGT  
GCACACCTGGAAACCGAAGGAGACCTACCTGCACATCATGAAGAACGAGGAGGGTGTGATCTTGTGCGCA  
GGTGGGCCAGCCGACCATCATGCAAAAGGAGCCGTGAGCTGGAGCTGCCGAGAGCAGGAGGGTGTG  
CCTCTACAGGGCGAACGTGAGAACGCCATCTCAGCAGGGAGCTGGACACCTACATCACCTCAGTGGCTACCT  
GGTCAAGCACGCCACCGAGCCTAGCTGGCCGCCACCTCTTCTCGCCACCTCCACCCCTGCGTGTG  
TGACCCCACCGCTCTTCCCGATCCCTGGACTCCGACTCCCTGGCTTGGCATTCAGTGAGACGCCCTGCAACAC  
ACAGAAAGCCAAAGCGATCGGTGCTCCAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAG  
GGCggggcaccgcgagaaccccttgggacccctccggcgccccctctgcacacatctcaagtgacccgcacgg  
cgagacgggggtggccgcggggcgtcccccagggtggccaccgcggctccaggcttggaaaatttaggcaatt  
CTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAGAAAAGGGTTGTTTTGTCTTCCAGGAC  
CCTGTGCTCCCAAAGAGAGGGCTTTCTAGTTGAGACTCTGCTTAAGAGAATCCAAGTAAAGCTCTGG  
GTCAGGGAGGGGCCGGGGCAGGAAACTACCTCTGGCTTAATTCTTTAAGGCCACGTAGGAACCTTCTGAGGG  
ATAGGTGGACCCCTGACATCCCTGTCGGCTTGCCCAAGGGCTGCTGTTCTGAGTCACAGCTGCGAGGTGA  
TGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGGGACAGCTGAGCCCCCTGCCTTGGCTCAGGTTGGTAGAA  
GCAGCCGAAGGGCTCTGACAGTGGCAGGGACCCCTGGTCCCCAGGCGTGCAGATGTTCTATGAGGGCAG  
AGCTCTTGTGATCATCCATGTGTTGCTCTGCTCCACCCCTGTGCCACCCAGAGGCCCTGGGGTGTCTCCATG  
CTGCCACCTGGCATGGCTTCTGTCGGCCCTCCACAAAATCAGGCCAGAGGCCCTGGGGCTTGGCT  
CTGTTTTATAAAACACCTCAAGCAGCACTGCACTGGCTGATCCAGACCCCTCTGCCCTCATCCAGGCTCTGACCA  
TGTGTTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCTCATCCAGGCTCTGACCA  
GTAGCCTGAGAGGGGTTTCTAGGCTTCAGAGCAGGGAGAGCTGGAAGGGCTAGAAAGCTCCGCTGTCT  
GTTTCTCAGGCTCTGTGAGCCTCAGTCCTGAGACCAGAGTCAGAGGAAAGTACACGTCCTAACCGTGTCA  
GGATTCACTCTCAGGAGCTGGTGGCAGGAGAGGCAATAGCCCTGTCAGGACAGCTGGAGCAGG  
TTGCGGTGTCACCGGTGCTCTGCCCTGCCCATGCCCCAGAGCTCTGATCTCCAGGAAACCCCATAGGCC  
TCTCCACCTACCCCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGGCCCCAAACCCCGTGCCTCTC  
TCTCCCTCCCCCATCCCCCATGTTGTTGACTAATCTGCTTCTCTGTCGGGCTGGCTGCCGGATCTGGGG  
TCCCTAAGTCCCTCTTTAAAGAACCTCTGCGGTCAAGACTCTGAAGCGAGITGCTGTGGCGTGCCTGG  
CAGAGCGCCACACTCGCTGCTTAAGCTCCCCAGCTTTCAGAAAACATTAAACTCAGAATTGTTCAA

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**FIGURE 372**

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRPS  
QDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGHTG  
PKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFYCYV  
PGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWVRLYK  
GERENAIIFSEELDTYITFSGYLVKHATEP

**Important features:****Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

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**FIGURE 373**

CGGAGTGGTGC~~GG~~CAACGTGAGAGGAACCCGTGCGCGCTGC~~G~~CTTCCTGTCCCCAAGCCG  
TTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGGAA  
GCATTTC~~T~~GTGCTTGATCACTATGCTAGGACACATTAGGATTGGT~~C~~ATGGAAATAGAATGC  
ACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTGAAAATTCAGAGG  
ATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACCAAAG  
ATGTGAGTCTTGGGCTGCAGTAAGGAGACTTGGACAAACACTGTGACAAAGCAGAGTTCT  
TCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATGTGGTTAA  
TGATGAGAAAAGCTACAAATACGCC~~TT~~GATAAGTATAGAGACCAATACAAC~~T~~GGT~~T~~CTTCC  
TTGCACGCC~~CC~~ACTACGTTGCTATCATTGAAAACCTAAAGTATTTGTAAAAAAGGATC  
CATCACAGC~~CC~~TTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAA~~T~~ATGTGGT~~A~~TGG  
AAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCTCAATATCCCAG  
AAAAGTGT~~C~~CTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAACAGCTAGCAGTT  
GCCTGAAATATGCTGGAGTATTGCAAGAAATGCAGAAGATGCTGATGGAAAAGATGTATTAA  
ATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCCCAACCAGGTAGTAG  
AAGGCTGTTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAAATCAGATGCATGTGA  
TGATGTATGGGTATACCGCCTAGGCATTGGCATATTTC~~A~~ATGATGCATTGGTTCT  
TACCTCAAATGGT~~C~~TGACAATGACTGAGAAGTGGTAGAAAAGCGTGAATATGATCTTGT~~A~~  
TAGGACGTGTGTTGTCATTATTGTTAGTAGTA~~A~~CTACATCCAATACAGCTGATGTTCTT  
TTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAAGTCAGTAGTACATTAA  
TGAGGGTGGTTTTCTTAAACACATGAACATTGTAATGTGTTGGAAAGAAGTGT~~TT~~TA  
AGAATAATAATTGCAAATAAACTATTAATAAAATTATATGTGATAAAATTCTAAATTATGA  
ACATTAGAAATCTG~~GGG~~CACATATTGCTGATTGGTAAAAAATT~~T~~TAACAGGT~~TT~~TA  
GCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATTGTGATTAAAGTAAAAC~~TT~~TAG  
CTGTGTGTTCC~~TT~~TACTCTAATACTGATTATGTTCTAAGCCTCCCCAAGTT~~CC~~ATGGAT  
TTGCCTCTCAAATGTACAAC~~A~~AGCAACTAAAGAAAATTAAAGTGAAGTGTAAAAAT

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**FIGURE 374**

MLSESSSFLKGVMGLSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILV  
KPKDVLWAAVKETWTKHCDKAFFSSENKVVFESINMDTNDMWLMRKAYKYAFDKYRDQYNWFFLARPTTFAI  
IENLKYLKKDPSQPFYLGHТИKSGDLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAV  
CLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFG  
HIFNDALVFLPPNGSDND

**Important features:**

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389, 399-403,  
409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550, 558-564,  
651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

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**FIGURE 375**

TTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTGCACAAGCTGAGAGCAACACAAT  
CTATCAGGAAAGAAAGAAAGAAAAACCGAACCTGACAAAAAAGAAGAAAAGAAGAAGAAA  
AAAAATCATGAAAACCATCCAGCAAAATGCACAATTCTATCTCTGGCAATCTCACGGG  
GCTGGCTGCTGTCTCTCCAAGGAGTGCCCAGCAGCGGAGATGCCACCTCCCCAA  
AGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAA  
CCGGGTCAACCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGACAAGTG  
GTGCCTGGATCCTCGCGTGGCTTCTGAGCAACACCCAAACGCACTACAGCATCGAGATCCA  
GAACGTGGATGTGTATGACGGAGGGCCCTACACCTGCTCGGTGCAAGACAGACAACCACCCAA  
GACCTCTAGGGTCCACCTCATTGTCAAGTATCTCCAAAATTGTAGAGATTCTTCAGATAT  
CTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACCAGAGCCTAC  
GGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTGTGAGTGAAGACGAATACTTGGA  
AATTCAAGGCATCACCCGGGAGCAGTCAGGGACTACGAGTGCAGTGCCTCAAATGACGTGGC  
CGCGCCCGTGGTACGGAGAGTAAAGGTCAACCGTGAACATCCACCATACATTCAAGGCCAA  
GGGTACAGGTGTCCCCGTGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCC  
AGCAGAAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAAGT  
GGAAAACAGACCTTCCTCTCAAAACTCATCTTCAATGTCTGAACATGACTATGGAA  
CTACACTTGCCTGGCCTCCAACAAGCTGGCCACACCAATGCCAGCATCATGCTATTGGTCC  
AGGCGCCGTACGGAGGTGAGCAACGGCACGTGAGGGCAGGCTGCGTCTGGCTGCTGCC  
TCTTCTGGTCTTGCACCTGCTCTCAAATTTCAGATGTGAGTGCCTTCCACCCGGAAAG  
GCTGCCGCCACCACCAACACAGCAATGGCAACACCGACAGCAACCAATCAGATA  
TATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAAATTGAGGGAGGGGAACAAA  
GAATACTTGGGGGAAAGAGTTTAAAAAAGAAATTGAAATTGCCCTGCAAGATATTAGG  
TACAATGGAGTTTCTTCCAAACGGGAAGAACACACAGCACACCCGGCTGGACCCACTGCA  
AGCTGCATCGTGCACCTCTTGGTGCAGTGTGGCAAGGGCTAGCCTCTGCCACAGA  
GTGCCCGACGTGGAACATTCTGGAGCTGGCCATCCAAATTCAATCAGTCCATAGAGACGAA  
CAGAATGAGACCTTCCGGCCAAGCGTGGCGTGGGGACTTGGTAGACTGTGCCACCAACG  
GCGTGTGTTGAAACGTGAAATAAAAGAGCAAAAAAAA

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**FIGURE 376**

MKTIQPKMHNSISWAIFTGLAALCFFQGVPVRSQDATFPKAMDNVTVRQGESATLRCTIDNRV  
TRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVDVYDEGPYTCVQTDNHPKTS  
RVHLIVQVSPKIVEISSLISINEGNNISLTCIATGRPEPTVTWRHISPKAvgFVSEDEYLEIQ  
GITREQSGDYECASNDVAAPVVRRVKVTVNYPPISEAKGTGVPVGQKGTIQCCEASAVPSAE  
FQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNYTCVASNLGHTNASIMLFGPGA  
VSEVSNGETSRRAGCVWLLPLLVHLLLKF

**Important features:**

**Signal peptide:**

amino acids 1-28

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**FIGURE 377**

CTTCTTGAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGAA  
ATGTGGCTCAAGGTCTTCACAACTTCCCTTGCACAGGTGCTGCTCGGGCTGAAG  
GTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTCCAC  
TATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCACACA  
ATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACCAACAC  
AAGTTACCATGATGCCACCCAATGCATCTGTCTTATCAACCCACTGCAGTCCCTGATGAA  
GGCAATTACATCGTGAAGGTCAACATTCAAGGGAAATGGAACACTCTATCTGCCAGTCAGAAGATA  
CAAGTCACGGTTGATGATCCTGTACAAAAGCCAGTGGTGCAGATTCACTCCTCCCTGGGGCT  
GTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAAGGGGCACTCGGCTAGCTTAC  
CAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTCTCCCCAAAAC  
AATACCCCTCATATTGCTCAGTAACCAAGGAAGACATTGGGAAATTACAGCTGCCCTGGTGAGG  
AACCTGTCACTGAAATGGAAAGTGAATCATTATGCCCATCATATATTATGGACCTTATGGA  
CTTCAAGTGAATTCTGATAAAAGGGCTAAAGTAGGGGAAGTGTACTGTTGACCTTGGAGAG  
GCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACTCCTGGATTAGGAGG  
ACTGACAATACTACATATCATTAAAGCATGGGCTCGCTTAGAAGTTGCATCTGAGAAAGTA  
GCCAGAAGACAATGGACTATGTGCTGTGCTACAACAAACATAACCGGCAGGCAAGATGAA  
ACTCATTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTGCTGCACAGAAAGGAAAATCA  
TTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATTATATCCATGTGTCTTCTC  
TTCCTATGGAAAAAAATATCAACCCCTACAAAGTTATAAAACAGAAACTAGAAGGCAGGCCAGAA  
ACAGAAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATGCTCTGGATGACTTCGGAAATA  
TATGAATTGTTGCTTTCCAGATGTTCTGGTGTGTTCCAGGATTCCAAGCAGGTCTGTTCCA  
GCCTCTGATTGTATGGGCAAGATTGCACTACAGTGTATGAAGTTATTCAAGCACATC  
CCTGCCAGCAGCAAGACCATCCAGAGTGAACTTCACTGGCTAACAGTACATTGAGTGAA  
ATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGTATATTAAATCTGGAATCAGTGAAGA  
AACCAGGACCAACACCTCTACTCATTATTCTTACATGCAGAAATAGAGGATTATGCAAA  
TTGAACTGCAGGTTTCAGCATATACACAATGTCTTGCAACAGAAAAACATGTTGGGAA  
ATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGGGGAGAACGAAAGTGAAGGGTTTCT  
CATAAGTTGTTATGAAATATCTCTACAAACCTCAATTAGTTCTACTCTACACTTCACTATC  
ATCAACACTGAGACTATCCTGCTCACCTCAAAATGTGGAAACTTACATTGTCATTGTTTC  
AGCAGACTTGTATTAAATTATTAGTGTAAAGAATGCTAAATTATGTTCAATT  
ATTTCaaaATTCTATCTGTTATTGACAACAAAGTAATAAGGATGGTTGTCAACAAAACA  
AAACTATGCCTCTCTTTTCAATCACCAGTAGTATTGAGAAGACTTGTGAACACTT  
AAGGAAATGACTATTAAAGTCTTATTGTTATTCAAGGAAAGATGGATTCAAATAAATT  
ATTCTGTTTGCTTTAAAAAAAAAA

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**FIGURE 378**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIWLFERPHTMPKYLLGSVNKS  
VVPDLEYQHKFTMMPNASSLNLINPLQFPDEGNYIVKVNIQGNGTLSASQKIQVTVDDPVTKPVVQIHPPSGAVEY  
VGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPII  
YYGPYGLQVNSDKGLKVGEVFTVDLGEAIFDCSADSHPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMD  
YVCCAYNNITGRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKKLEG  
RPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTVYEVIQHIPAQQQDHPE

**Important features:****Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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**FIGURE 379**

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTCACTTCACATGGGCACAA  
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTATATTATGTTAAATCACTGTTTTGTT  
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACCTCTCCAGAAGCAAGC  
GCACATGCGTTCCAAAATAAGAGCAAATCGCTCTAACACAGGAAAAGACCTGAAGCTTAA  
TTAAGGGGTTACATCCAACCCCAGAGCGCTTTGTGGGCACTGATTGCTCCAGCTTCTGCGTC  
ACTGCGCGAGGGAAAGAGGGAAAGAGGATCCAGGCAGTACATGTATAGACACAAAAACAGCTG  
GAGATTGGGCTTAAATACCCACCAAGCTCCAAAAGAAGAGACCCAAGTCCCCAAAACATTGAT  
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA  
GATGCCATTGTCCCCCGGCCTCTGCTGCTGCTCTCCGGGCCACGGCACCGCTGCCCT  
GCCCTGGAGGGTGGCCCCACCGGCCAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAG  
GAAAAGCAGCCTCCTGACTTCCCTGCTTGGTGGTTGAGTGGACCTCCAGGCCAGTGCCGG  
GCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCAGGAAGGCGCACCCCCCAGCA  
ATCCCGCGCGCCGGACAGAATGCCCTGCAGGAACCTCTGGAAGACCTTCTCCTCCTGCAA  
**ATAG**

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**FIGURE 380**

MYRHKNWRRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLS  
GATATAALPLEGGPTGRDSEHMQEAAAGIRKSSLTFLAWWFEWTSQASAGPLIGEEAREVARR  
QEGAPPQQSARRDRMPCRNFFWKTFSCK

**Important features:****Transmembrane domain:**

amino acids 51-69

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

**N-myristylation sites.**

amino acids 64-70, 75-81, 90-96

**Amidation site.**

amino acids 33-37

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**FIGURE 381**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGGGGCCGGCTGCGGCCCGGCC  
GCGCCGCCAACCCCCAACCCCAGGCCGCCCCCTAGCCCCCGCCCGGGCCCGGCCGCC  
CCGCGCCCAGGTGAGCGCTCCGCCCCCGCGAGGCCCCGCCGGCCGCCGCCGCC  
CGGCCGGCGGGGGAAACCGGGCGGATCCTCGCGGTCAAACCACCTGATCCCATAAAACATT  
ATCCTCCGGCGCCCGCTGCGAGCGCCCCGCCAGTCGCGCCGCCGCCCTGCCCTG  
TGCCTGCGCCCTGCGCACCCCGGGCCAGGCCAGCCAGAGCCGGGGAGCGGAGCG  
CGCCGAGCCTCGTCCCAGGGCCGGGGCCGGGCCGTAGCGGCGGCCCTGGATGCGGAC  
CCGGCCGCGGGAGACGGCGCCGCCAAACGACTTTAGTCCCCGACGGCCCCGCCA  
ACCCCTACG**AT**GAAGAGGGCGTCCGCTGGAGGGAGCCGGTGTGGCATGGTGCTGTGGCTG  
CAGGCCCTGGCAGGTGGCAGCCCCATGCCAGGTGCTGCTATGCTACAATGAGCCAAGGTG  
ACGACAAGCTGCCCTCAGCAGGGCCTGCAGGCTGTGCCCTGGCATCCCTGCTGCCAGCCAG  
CGCATCTCCTGCACGGCAACCGCATCTGCATGTGCCAGCTGCCAGCTCCGTGCC  
AACCTCACCATCTGTGGCTGACTCGAATGTCTGGCCGAATTGATGCGGCTGCCCTCACT  
GGCCTGGCCCTCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCC  
GCCACATTCCACGGCTGGGCCCTACACACGGCTGCACCTGGACCGCTGCCCTGCAGGAG  
CTGGGCCGGGCTGTTCCGGCCTGGCTGCCCTGCAGTACCTCACCTGCAGGACAACGCG  
CTGCAGGCACTGCCGTGATGACACCTTCCCGCACCTGGCAACCTCACACACCTTCTGCAC  
GGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCCTCCGTGGCTGCACAGCCTGACCGTCTC  
CTACTGCACCAGAACCGCGTGGCCCATGTCACCCGCATGCCCTCCGTGACCTGGCC  
ATGACACTCTATCTGTTGCCAACATCTACCGCCTGCCACTGAGGCCCTGGCCCCCTG  
CGTGCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGACTGCCGGGACGCC  
CTCTGGGCCTGGCTGCAGAAGTTCCCGGCTCCCTCCGAGGTGCCCTGCAGCCTCCGCAA  
CGCCTGGCTGGCGTGACCTCAAACGCCCTAGCTGCCATGACCTGCAGGGCTGCC  
ACCGGCCCTTACCATCCCACCTGGACGGCAGGGCACCGATGAGGAGCCGCTGGGCTTCCC  
AAGTGCTGCCAGGCAGATGCCGTGACAAGGCCACTGACTGGAGCCTGGAAGACCAGCTCG  
GCAGGCAATGCGCTGAAGGGACCGTGCCGCCGGTGACAGCCCGCCGGCAACGGCTCTGGC  
CCACGGCACATCAATGACTCACCTTGGACTCTGCCCTGGCTCTGCTGAGCCCCGCTCACT  
GCAGTGCGGCCGAGGGCTCCGAGCCACCAGGGTCCCCACCTGGGCCCTGCCGGAGGCC  
GGCTGTCACGCAAGAACCGCACCGCAGGCCACTGCCGTCTGGGCCAGGCAGGCCGG  
GGCAGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTCACCTGCAGCCTCACCCCC  
CTGGGCCTGGCGCTGGTGCTGGACAGTGCTGGCCCTGCT**TG**ACCCCCAGGGACACAAGA  
GCGTGCAGCAGGCCAGGTGTGTAACATACGGGTCTCTCCACGCCAAGCCAGCCGG  
GCCGCCGACCCGTGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCCCTGCCGCC  
CCCACATCTCCACCCCATCATGTTACAGGGTTGCCGGCAGCGTTGTTCCAGAACGCC  
CCACCCAGATGCCGTATATAGAGATATGCAATTATTTACTTGTGTAAAAATATCGGACGA  
CGTGAATAAGAGCTTTCTTAAAAAA

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**FIGURE 382**

MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPGIPAASQRIF  
LHGNRISHVPAASFACRNLTILWLHSNVLARIDAAAFTGLALLEQLDLSDNAQLRSVDPATF  
HGLGRLHTLHLDRCGLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNR  
ISSVPERAFRGLHSIDLRLHQNRVAHVPHAFRDLGRMLTYLFANNLSALPTEALAPRLAL  
QYLRILNDNPWVCDCRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCAVATGP  
YHPIWTGRATDEEPLGLPKCCQPDAAKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH  
INDSPFGTLPGSAEPLTAVRPEGSEPPGFPTSGPRRPGCSRKNRTRSHCRLGQAGSGGGGT  
GDSEGSGALPSLTCSTPLGLALVLWTVLGPC

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

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**FIGURE 383**

TTCGTGACCCCTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTCTAAGAAGGGGGAGTCCTGAACCTTGCTG  
AAGCCCTTGTCCGTAAGCCTGAACACTACGTTCTTAAATCTATGAAGTCGAGGGACCTTCGCTGCTTTGTAGGG  
ACTTCTTCTTGTCTCAGCAACATGAGGCTTTCTTGTGGAACGCCGCTTGACTCTGTTCGTCACTCTTGA  
TTGGGGCTTGTCTGACCCAGAAGTGAAGAAATTGAAGTTCTCCAGAAGCCATTCACTGCCATCGCAAGACCA  
AAGGAGGGGAGTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCTTATTCACCCACTCACA  
AACATAACAATGGTCAGCCCATTGGTTACCCGGCATCCTGGAGGCTCTCAAAGGTTGGGACCAGGGCTGA  
AAGGAATGTGTGAGAGAGAGAAGCTCATCATTCTCCTGCTCTGGCTATGAAAAGAAGGAAAAGGTA  
AAATTCCCCAGAAAGTACACTGATATTAAATTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAAT  
CATTCCAAGAAATGGATCTTAATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTAAAGAAGGAGT  
TTGAAAAACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTGGTGGAGGATATTTGATAAAGAAGATG  
AAGACAAAGATGGTTATATCTCCAGAGAATTACATATAAACACGATGAGTTATAGAGATACATCTACCCCT  
TTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTAAAGAACATTTATTTTATACAATGTTCTTCT  
TGCTTTGTTTTTATTTTATATTTCTGACTCCTATTAAAGAACCCCTTAGGTTCTAAGTACCCATT  
CTTCTGATAAGTTATTGGAGAAAAGCTAATTGGTCTTGAATAGAACACTCTGGACAATTTCACCTTC  
ACAGATATGAAGCTTGTCTTACTTCTCACTTATAAAATTAAATGTTGCAACTGGAAATATACCACGACATGA  
GACCAGGTTATAGCACAAATTAGCACCCCTATATTCTGCTTCCCTCTATTCTCAAGTTAGAGGTCAACATT  
GAAAAGCCTTTGCAATAGCCCAGGCTGCTATTTCATGTTATAATGAAATAGTTATGTGTAACGGCTCTG  
AGTCTGCTTGAGGACCAGAGGAAATGGTGTGACCTGACTGTTAATGGCTACTGCTTACTAAGGAGAT  
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCCTGAATCCCAGCACTTGGG  
GGCTGAGGCCGGCGGATCACCTGAGGTTGGAGTTGAGACCGACAGCCTGACCAACACGGAGAAACCCATCTC  
TAAAAATACAAAGTAGCCCGCGTGGTGTGCTGCTGTAATCCCAGCTACCCAGGAAGGCTGAGGCCAGAA  
TCACCTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAGATCACCTNCAGCCTGGACACTCTGCTCGAAAAAGAA  
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTGG  
CTCCTAGTGTGATTGGTGCCTATTGATAAAATAGGACAAATCATTATGTGAGTTCTTGTAAATAAAATGTA  
TCAATATGTTAGATGAGGTAGAAAGTTATATTATTCATTTACTTCTTAAGGCTAGCGGAATATCCTT  
CCTGGTTCTTAATGGTAGTCTATAGTATATTACTACAATAAACATTGATCATAGATAAAAGTAGTAAACCA  
GTCTACATTTCCTCATCTGCTCATCAAAACTGAAGTTAGCTGGGTGTGGCTCATGCCCTGTAATCCCAG  
CACTTGGGGGCCAAGGAGGGTGGACTTGAAGGAGTCAGGAGTTCAAGACCAAGCAGCCTGGCAACATGGTAAACCT  
TGTCTCTACTAAAATACAAAATTAGCCAGGCCGTTGGTCACACTGAGATCAGGAGTTCAAGACCAAGCAGCCTGG  
GACAGGAGATTGCTTAACCCGGAGGCCGAGGTTGCAGTGAGCAAGATTGTGCCACTGCACCCAGCCTGG  
TGACAGAGCAAGACTCCATCTCAAAAAAAAAAGAAGCAGACCTACAGCAGTACTATTGAATAAAACTA  
TCCTGGATT

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**FIGURE 384**

MRLFLWNAVLTLFVTSLIGALIPEPEVKIEVLQKPFICHRKTKGGDMLVHYEGYLEKDGSF  
HSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPESTLI  
FNIDDLLEIRNGPRSSESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHDALVEDIED.  
KEDEDKDGFISAREFTYKHDEL

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

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**FIGURE 385**

CTCCCACGGTGTCCAGCGCCCAGA**ATG**CGGCTCTGGTCTGCTATGGGTTGCCGTGCTGCTC  
CCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAATCAGCGGGTTCGAAGGGGACACTGTGTCC  
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG  
ATCCTCTCTCGCTGCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAATGAAG  
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCGCTATTGTGACCTGTGGAACCTC  
ACCTGCAAGACGCTGGGGAGTACTGGTGTGGGTGAAAAAACGGGCCCCGATGAGTCTTA  
CTGATCTCTCTGTTCGTCTTCCAGGACCTGCTGTCTCCCTCCCTCTCCACCTCCAG  
CCTCTGGCTACAACACGCCGTGAGCCAAGGCAAAGCTCAGCAAACCCAGCCCCCAGGATTG  
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC  
CCTCCATTGCCAGGGACTTCCAGTACGGGACAGAAAGGACTCTCAGTACACAGGAACCTCT  
CCTCACCCAGCGACCTCTCCCTGCAGGGAGCTCCGCCCTCCAGTGCAGCTGGACTCCACC  
TCAGCAGAGGACACCAGTCCAGCTCAGCAGTGGCAGCTAAGCCCAGGGTGTCCATCCG  
ATGGTCCGCATACTGGCCCCAGTCTGGTGTGAGCCTCTGTGAGCCGAGCAGTGAAGCAGTATGGCTGG  
GCCTCTGAGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG  
AACGAGAAGTTCTGGCTCTACGCTTGACTGGGAGGAAAAGGAAGGCCCTTCCAGGCCCT  
GAGGGGAGCTGATCTGATGCCCTCCACACATCTGAGGAGGAGCTGGGCTCTCGAAG  
TTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGG  
TGGATCAGCACCGATTCCGAAAGCTTCCACCTCAGCCTCAGAGTCCAGCTGCCGGACTCC  
AGGGCTCTCCCCACCCCTCCAGGCTCTCTGTGATGTTCCAGCCTGACCTAGACGCTTT  
GTCAGCCCTGGAGGCCAGAGCGGTGGCCTTGCTCTCCGGCTGGAGACTGGGACATCCCTGAT  
AGGTTCACATCCCTGGCAGAGTACCAAGGCTGCTGACCTCAGCAGGGCAGACAAGGCTCAG  
TGGATCTGGTCTGAGTTCAATCTGCCAGGAACCTCTGGCCTCATGCCAGTGTGGACCC  
GCCTCCCTCCACTCCAGACCCCACCTGTCTTCCCTGGCGTCTCAGACTAGTCCA  
CGGTCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCTGGGGTGAGACTGGGATTCTGGCTT  
CTCTTGAACCACCTGCATCCAGCCCTCAGGAAGCCTGTGAAAAACGTGATTCTGGCCCA  
CCAAGACCCACCAAAACATCTCTGGCTTGGTGCAGGACTCTGAATTCTAACATGCCAGT  
GACTGTCGCACTGAGTTGAGGGCAGTGGCCTGATGAACGTCACACCCCTCAGCTTAG  
AGTCTGCATTGGGCTGTGACGTCTCCACCTGCCCAATAGATCTGCTCTGTGACACCA  
GATCCACGTGGGACTCCCTGAGGCCTGCTAAGTCCAGGCCCTGGTCAGGTGACGTGACAT  
TGCAGGATAAGCCCAGGACCCGACAGAAGTGGTGCCTTNCCATTGCCCCCTGGNCCA  
TGCCTCTTGCCTTGGAAAAAAATGATGAAGAAAACCTTGCTCCTTCCCTGTCTGGAAAGGG  
TTACTTGCCTATGGGTTCTGGTGGCTAGAGAGAAAAGTAGAAAACAGAGTGCACGTAGGT  
CTAACACAGAGGAGAGTAGGAACAGGGCGATACTGAAGGTGACTCCGAGTCCAGCCCCCTG  
GAGAAGGGTGGGGTGGTAAAGTAGCACAACACTATTTTTCTTCCATTATT  
ATTGTTTTAAGACAGAATCTCGTGTGCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCA  
AACTCCGCCTGGGTTCAAGTGATTCTCTGCCCTAGCCCTCCGAGTAGCTGGGATTACAG  
GCACGCACCACCAACCTGGCTAATTTGTACTTTAGTAGAGATGGGGTTCACCATGTTG  
GCCAGGGCTGGTCTGAACCTGACCTCAAATGAGCCTCCCTGCTCAGTCTCCAAATTGCCG  
GGATTACAGGCATGAGCCACTGTGTCTGCCCTATTCTTTAAAAAGTGAATTAAGAGTTG  
TTCAGTATGAAAACCTGGAAAGATGGAGGAGAAAAGAAAAGGAAGAAAAAAATGTCACCCA  
TAGTCTCACCAGAGACTATCATTATTCGTTGTACTCCTCCACTCTTCTTC  
ACATAATTGCCGGTGTCTTTACAGAGCAATTATCTGTATATACAACCTTGTATCCTGC  
CTTTCCACCTTATCGTCCATCACTTATTCCAGCACTCTGTGTTTACAGACCTTTT  
ATAAATAAAATGTTCATCAGCTGCATAAAAAAAAAAAAAAA

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**FIGURE 386**

MRLLVLLWGCLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCG  
TIYAEEEGQETMKGRVSIRDSRQEELSLIVTLWNLTLDAGEYWCGVEKRGPDSSLISLVFP  
GPCCPPSPSPTFQPLATTRLQPKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ  
YGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSaedTSPALSSGSSKPRVSIPMVRILAPV  
LVLLSLLSAAGLIAFCSHLLWRKEAQQATEQRNEKFWSRLTAEEKEAPSQAPEGDVISMP  
PLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

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**FIGURE 387**

GCGCCGGGAGCCCATCTGCCCGCAGGGCACGGGGCGGGGCGGTCCGCCGGCACATG  
GCTGCAGCCACCTCGCGCGACCCCGAGGCGCGCCAGCTCGCCGAGGTCCGTGGAGG  
CGCCCCGGCGCCCCGGAGCCAAGCAGCACTGAGCGGGGAAGCGCCCGTCCGGGATCGGG  
**ATGT**CCCTCCTCTCTCTGCTAGTTCTACTATGTTGAACTTGGGACTCACACT  
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGCCCTGCCACCATCAACTGGGCTCCA  
GAAAAAGACACTCTGGATATTGAATGGCTGCTACCGATAATGAAGGGAACCAAAAGTGGT  
ATCACTTACTCCAGTCGTATGTCATAAATTAACCTGACTGAGGAACAGAACGGCCAGTGGC  
TTGCTTCAAATTCTGGCAGGAGATGCCCTTGCAAGATTGAACCTCTGAAGCCCAGTGAT  
GAGGGCCGGTACACCTGTAAGGTTAAGAATTCAAGGGCGTACGTGTGGAGGCCATGTCATTTA  
AAAGTCTTAGTGAGACCATCCAAGGCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAACAGT  
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCATTGTGATTACTGGCAGCGA  
ATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCCTCCAAATCTAGGATTGACTACAACCAC  
CCTGGACGAGTTCTGCTGAGAATCTTACCATGTCCTACTCTGGACTGTACAGTGACAGCA  
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGGCGAGTAACGTACAGTATGTACAAAGCATC  
GGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGGCCCTGCTGATTTCTTGGT  
TGGCTGCTAATCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGAGAGACCTAATGAAATT  
CGAGAAGATGCTGAAGCTCCAAAGGCCGTCTGTGAAACCCAGCTCCTCTCAGGCTCT  
CGGAGCTCACGCTCTGGTTCTTCCACTCGTCCACAGCAAATAGTGCCTCACGCAGCCAG  
CGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCACCCAGGCATACAGCTAGT  
GGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATGCTAATCTGACCAAAGCAGAA  
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTCCAAACGGCT**TGA**ATTACAATGGAC  
TTGACTCCCACGCTTTCTAGGAGTCAGGGCTTTGGACTCTCTCGTCAATTGGAGCTCAAGT  
CACCAAGCCACACAACCAGATGAGAGGTCTAAGTAGCAGTGAGCATTGCACGGAACAGATT  
CAGATGAGCATTCTTATAACATACAAACAGAAAAGGATGTAAGCTGATTCATCTGTA  
AAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGGAAAGCAGGGAGTCCAAATCTATTGT  
TGACCAAGGACCTGTGGTGAGAAGGTTGGGAAAGGTGAGGTGAATATACTAAACTTTAAT  
GTGGATATTGTATCAGTGCTTGATTCAACATTTCAGAGGAAATGGATGCTTTGT  
AAATTTCTATGCAATTCTGCAAACCTATTGGATTATTAGTTATTCAAGACAGTCAAGCAGAAC  
CCACAGCCTTATTACACCTGTCTACACCATGACTGAGCTAACCAACTCTAAGAAACTCCAAA  
AAAGGAAACATGTGCTCTATTCTGACTTAACCTCATTGTCAAAAGGTTGGATTAATT  
TCAAGGGGAGTTGAAATAGGGAGATGGAGAAGAGTGAATGAGTTCTCCACTCTATACTA  
ATCTCACTATTGTATTGAGCCAAAATAACTATGAAAGGAGACAAAATTGTGACAAAGGA  
TTGTGAAGAGCTTCCATCTCATGATGTTATGAGGATTGTGACAAACATTAGAAATATATA  
ATGGAGCAATTGTGGATTCCCTCAAATCAGATGCCCTCAAGGACTTCTGCTAGATATT  
CTGGAAGGAGAAAATACAACATGTCATTATCACAGTCCTAGAAAAGAATTCTTAGAGAAA  
AAGGGATCTAGGAATGCTGAAAGATTACCAACATACCATTAGTCTCTTCTGAGAAA  
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTCTTA  
ATATGTCAAGGAAGGTAGCCGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG  
GTTGCAGTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGTGACAGAGCGGGACTCCGTCTC

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**FIGURE 388**

MSLLLLLLSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLTDNEGNQKV  
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL  
KVLVRPSKPCELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH  
PGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRTVQYVQSIGMVAGAVTGIVAGALLIFLLV  
WLLIRRKDKEYEEEERPNEIREDAEAPKARLVKPSSSSGSRSSRGSSSTRSTANSASRSQ  
RTLSTDAAAPQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPSQSRAFQTV

**Important features:**

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

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## **FIGURE 389**

GGGGCACCTGGAAG**ATG**CGCCCATTGGCTGGTGCCTGCTCAAGGTGGTTCGTGGTCTCG  
CCTCCTGTGTGCCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCTGT  
CCAGTGCTGCCTATAGCATCCGCAGCAGCTGGGAGAGGCCCTGCCTCAAAGCTCCAGTCCCCA  
AAAGGCAAAATGTGACCCTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA  
GGGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGGAGAAC  
AGCTGGAAATGTGCCAGAGGAATAAACATTGCCATTGCAACTATGTAAGTGGAAATGTGA  
CAGCAACACGATTTTGATATGTATGAAGGCATAACTCTGGACCGATGACAAGTTATTG  
AGAGTGCTGCTCCAAATCCCTGCTCTCATGGTACCTATGACGACGGAAGCACAAGACTGA  
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAAGTAAAGAAATCAGGAACATGAAATTCA  
GGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACTCCCTCCGAAATTAGAGAGAAA  
AGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGAGATCCAGATAG  
AAGGCTGCATACCCAAAGAACGAAG**TGA**CACTGCAGGGCCTGAGTAAATGTGTTCTGTATA  
AACAAATGCAGCTGGAAATCGCTCAAGAATCTTATTTCTAAATCCAACAGCCCATATTGAT  
GAGTATTTGGGTTTGTGAAACCAATGAACATTGCTAGTTGTATCAAATCTGGTACGCA  
GTATTTATACCAAGTATTTATGTAAGATGTCAATTAGCAGGAAACTAAAATGAATGG  
AAATTCTAAAAAAAAAA

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**FIGURE 390**

MRPLAGGLLKVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC  
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC  
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRSSWV  
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAAEIQIEGCIPKERS

**Important features:****Signal sequence.**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125

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**FIGURE 391**

GGGGGCTTCTGGGTTGGCTGCTGGAACACCTGCCTCAAGGACCGGCCCTGGAGGGTCGCCGGAAAGGG  
 AGGGAAAGGAAGGGCGGGGCCGGCCCCCTGCGCCGCCCTGCGCCTCTGCCGCCCCCTGTCCGCCCGGCC  
 AGCCCAGCCCAGCCCCGCGGGCGGTACACGCGCAGGCCAGCGCCGCCAAGCGCGCCGCTCTG  
 CTGTGCCCTGCGCCCTGCCCCCGCCAGCTCTGCCGCGCAGGCCAGCGCCGCCAAGCGCGCCGCTCTG  
 GCCCTGGCGCGGGCGGAGCAGGATGCCCCGCCGGGACCGTACCCCAAGCGCTGGCCCTGGTGCTCTGG  
 AGTGACCCCTGGCCGGGTCGGAGGCCAGGGCGCAGCCCTCGAGGACCGTGAATTACGGGAGAGATCTGGAG  
 CGGGAGCCCTACTACGCGCCGGAGCCAGGCCAGGGCCACAAGGCCAAGAAAGCTCCAAGAGGGA  
 GGAGTGGAGCGGCCGGCCAGGAGCCAGGCCAGGGCCACAAGGCCAAGAAAGCTCCAAGAGGGA  
 GAAGTGGCTCGGAGCGGCCGGCCACCCACCAGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTGAGAA  
 GGCTGCAACGATGATCACAGTGTCCGTGGCCGTGAAGATGTCAGAGAGAGTTGCCACCTTGGTCTGG  
 AACCTAAAAATCACAGACTCCAGCTCATGCCCTCACGGTGAAGCGCTATGCCCTGGGGCACATCGAGGGAG  
 ACTCAACATCCAGGGGGCATTAATGAAAATGATTTTATGACGGAGCGTGTGCGGGAGAAATGACCTCCA  
 GCAGTGGATTGAAGTGGATGCTGGCGCTGACCAGATTCACTGGTGTCACTCACTCAAGGGAGGAACCTCTG  
 GCTGAGTGACTGGTGACATCTATAAGGTATGGTGAGCAATGACAGCCACAGCTGGTCACTGTTAAGAATGG  
 ATCTGGAGACATGATTTGAGGAACAGTGAGAAGGGAGATCCCTGTTCTCAATGAGTACCCGTCCCCATGGT  
 GGGCCGCTACATCGCATAAACCTCATGGCTCTGGTTGATAATGGGAGCATCTGATGAGAATGGAGATCTGG  
 CTGCCCCTGCGAGCTTAATTAATTATCACCGCCGAACGAGATGACCACCACTGATGACCTGGATTAA  
 GCACCAAAATTATAAGGAATGCCCGTGTGAGAAAGTGTGAATGAAATGTGCTCCAATATCACCAGAATTAA  
 CAACATTGAAAAAGCCACCAGGGCTGAGCTGTGAGGAGATCTAGATCACCCTGGGAGCATGAAGT  
 CGGTGAGCCCGAGTTCCACTACATCGGGGCCACGGCAATGAGGTGCTGGGGAGCTGCTGCTGCT  
 GGTGCAAGTTCTGTGTGTCAGGAGTACTTGGCCCGAATGCGCGATCGTCCACCTGGTGGAGGAGACCGGGATTCA  
 CGTCCCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCTACGAAGGGGCTGGAGCTGGAGGCTGGCCCT  
 GGGACGCTGGACCCACGATGGATTGACATCAACAACAACTTCTGATTTAACACCGTGTCTGGAGGAGA  
 GGATGACAGAAATGCCCCAGGAAGTCCCAACTACTATATTGCAATCCCTGAGTGGTTCTGCGGAAATGC  
 CACGGTGGCTGCCAGACAGCAGTCACTGGCTGGTGGCTACGGTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGG  
 GGGCGGGAGCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
 CCCCGATGACCACGTGTTCCGCTGGCTGGCTACTCCATGCTCCACACCCGCTCATGACAGACGCCCGGAG  
 GAGGGTGTGCCACACGGAGGACTTCCAGAAGGGAGGGACTGTCAATGGGCTCTGGCACACCGTGGCTGG  
 AAGTGTGACAGATTTCAGCTACCCCATACAAACTGCTCGAACTGTTCACTACGGTGGCTGTGATAAAATACCC  
 ACATGAGAGCCAGCTGGCGAGGAGTGGGAGATAACCGGAATCTCTGATGTTGTCATGGAGCAGGTTCATCG  
 TGGCTTAAAGGTTGTGAGGAGATTACATGGAAAAGGAATCCCAAACGCCATTATCTCGTAGAAGGCATTAA  
 CCATGACATCCGAACGCCAACGATGGGATTACTGGCCTCTGAACCTGGAGAGTATGTGGTACAGCAAA  
 GGCGAAGGTTTCACTGCATCCACCAAGAACACTGTATGGTGGCTATGACATGGGGCCACAAGGTGTGACTTCAC  
 ACTTAGCAAAACCAACATGCCAGGATCGAGAGATCATGGAGAAGTGGGAAGCAGCCGTCAGCCTGCCAGC  
 CAGGGCTGAAGCTGGGGGGCGGAAGAGACGACAGCTGGGTTGACCCCTGGGCTTGGAGACTCGTCTGG  
 ACCCATGCAAAATTAAACCAACCTGGTAGACTGCTCATAGTGGACTCACTACTGTGTTTCTCTGAAATTCAAG  
 AAGTGGCTGGAGAGGGGTGATTGTGAGGCAAGGTGCCCCAAAGGGAGGCTGGAGGCTGAGGCTGTTTCTTT  
 CTTGTTCCCATTATCCAATAACTGGAGAGCAGCAGAGAAAAGCTGATGGGAGTGGAGAGAAACTCAGCAAG  
 CCAACCTGGGAATCAGAGAGAGAGGAGAGGAGGGGGAGGCTGTCCGTTAGAGCCTCTGGCTGCAAGAAAAGG  
 ATTCTGGCTTCCCTGTTGCGTGGCAGCAAGGGTTCACGTGCAATTGCAATTGCAAGCTAAATTGCAAG  
 CATTCCCCAGCTGGCTGTCCCCAATGTTACCATTTGAGATGCTCCACGGCTCTAAGAGAATCCACCCCTCTC  
 TGGCCCTGGGACATTGCAAGCTGCTACAAATAATTCTGTTGTTCAACAAAGGAGTGTGTTGAGAAAAGGAGAGAGGGCTGA  
 TCAGTGAGCCTTGTGATCTGTTAGTCTCTTTCAACAAAGGAGTGTGTTGAGAAAAGGAGAGAGAGGGCTGA  
 GATCATTCAAGGAGTTGGGAGCAAGCATGGAGCTTCTGACAAATTCTGGTCCATAAAACAACCCCCAAA  
 GTCCCTGCTGATCCAGTAGGCCCTGGAGGTTCCCAGGTAGGGAGAGGCCAGAGCTGCCAGCCTTCTGAAAGGGCCA  
 GAAAATTAGCCTGGGATCTCTCTTTACCTGCTAGGACTGGAAAGAGGCCAGAGCTGGGAGGCTGAAGCCCTC  
 TCTCTGCTTGAGGTATTGCCCCCTGTGGAATGAGTGCTCATGGGTTGGCTCATATGAGCCTGGGAGTTATT  
 TTGATATGAGATGCCAGATCTCCAGATTAGGCTAAATGAAACACTCTTAGGATTATCTGTGGAGCAT  
 CAGTTGGAGAATTATTGAAATTCTGCAAGAAAAAAAGTATGTCTCACTTTGTTAATGTGCTGCTCAT  
 TGACCTGGAAAAATGAAAAAAATAAGCAAATGGTAAGACCCCTAAAAAAAAAAAAAA

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**FIGURE 392**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEWSREPYYARPEPELETFSPLPA  
GPGEWERRPQEPRPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHSVR  
VAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRRLNIQAGINENDFYDGAWCAGR  
DLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIFEGNS  
EKEIPVLNELPVPMVARYIRINPQSFDNGSICMRMEILGCPLPDPNYYHRRNEMTTDDLD  
FKHHNYKEMRQLMKVNEMCPNITRIYNIGKSHQGLKLYAVEISDHGEHEVGEPEFHYIAGA  
HGNEVLGRELLLVQFVCQEYLARNARIVHLVEETRIHVLPSSLNPDGYEKAYEGGSELGGWS  
LGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFSENATVAAETRAVIW  
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAGSYASTHRLMTDARR  
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENN  
ESLIVFMEQVHRGIKGLVRDSHGKGIPNAIIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKA  
EGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVS LPARRLKLRGRKRRQG

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**FIGURE 393**

GTCCCCACATCCGTCAACTGGTCAGGTCCCTCTTAGACCAGCTTGTCCATCATTTGCTGAAGTGGACCAAC  
 TAGTTCCCCAGTAGGGGTCTCCCTGGCAATTCTTGATCGGCCTTGGACATCTCAGATCGCTTCCAATGAAGA  
 TGGCCTGCCCTGGGGCTCTGGCTTGTCTCATATACTCATCTAAGTATGGACAAGGGTGTGCCGCCAGCTCTGGGG  
 AAGGAGCACGGGGCTGATCAAGGCATCCAGGAAACACTGGGACTCTGTCCAGCCTTGAAAGAACACTAGTGGTT  
 TCTGAATCTAGCCCCTTGGCGTAAGCAGTATGCAACTCTGCAACTCTGCTGGGCTTTGGGCCAGGTGG  
 CTACTTATTCTTTAGGGGATTGTCAAGGGTGCAGGACTCTCACGGTAAAGTACAGGCTTGGGCTTTGGGCCAGGTGG  
 ATCTGGTACAGTGTGGAGCTGGGAAAGCTGCTCCAGGAACGGCCGGAGGGAGGGCAGGCTGGGGCCCGCTT  
 CCAGGTGTTGCAGCTGCCCTCAGCGCTCCCCATTAGGTGGACTCTGAGGAAGGGTGTGAGCAGGCCACAGGCAGGC  
 GCTGGATCGAGAGCAGCTGTGCCAGTGGGATCCCTGCCCTGGTTCTGATGTGCTTGGCCACAGGGGATT  
 GGCTCTGATCATGGAGATCCAAGTGTGGACATCAATGACCACAGCCACGGTCTTGGACTCCAATGACAATAG  
 GCTGGAAATCTGTGAGAGCGCTCTGCCAACCCGGATCCCCCTGGACAGAGCTTGTGACCCAGACACAGGCC  
 TAACACCCCTGCACACCTACACTCTGTCTCCAGTGTGAGGACTTTGCTTGGATGTCAATTGTGGGCCCTGATGAGAC  
 CAAACATGCAGAACTCATAGTGTGAGGAGCTGGGAGGGAAATCATTCAATTGTGGATCTGGTGTAACTGC  
 CTATGACAATGGGAAACCCCCCAAGTCAGGTACAGCTTGTCAAGGCAACGCTTGGACTCCAATGACAATAG  
 CCCTGCTTGTGAGAGTTCAGTGGACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAGT  
 GACCGCCACAGACCTGACCAAGGCCAAATGGGAGGTGGAGTTCTCTCATGAGCACATGCCCTCAGAGGT  
 GCTGGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTATTCTGCTGACCTCTAGACTATGAAAAGACCC  
 TGCTTACAGGGTGGATGTTCAGGCAAGGACTGGTCCAATCTATCCCAGCCATTGCAAAGTTCTCATCAA  
 GTTCTGGATGTCAATGACAACATCCAAAGCATCCACGTACATGGGCTTCCAGGCATCACTGGTGTCAAAGC  
 TCTTCCCAGGACAGTATTGTCTTGTCAATGGAGGTGACTTGGATTTCAGGACACAATGGTTGGTCCACTG  
 CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAGAAACTATGCAACACATACATGGTGTCAAACATGC  
 CAACACTGGACAGAGAGCAGTGGCCAAATATACCCCTACTGTGTTAGGCAAGACAGGACTCCAGGCCATTATC  
 AGCCAAGAAACAGCTCAGCATTCAAGTCAAGTACAGTACATCAACGACAATGCAACCTGTGTTGAGAAAAGCAGGTATGA  
 AGTCTCCACGGGAAACAACTACCCCTCTTCACCTATTACCATCAAGGCTCATGATGCAAGACTTGGCATT  
 TAATGGGAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTACTATTGACTCAACACAGGAGA  
 GGTCACTGCTCAGAGGTCACTGAACATGAAGAGATGGCCGGCTTGAGTTCCAGGTGATCGCAGAGGACAGCGG  
 GCAACCCATGCTTGCATCCAGTGTCTCTGGTGGCTCAGGCTCTGGATGCCAATGATAATGCCAGAGGTGGT  
 CCAGCCTGTGTCAGCGATGGAAAGCCAGCCTCTCGTGTGTTGAGTGCCTCACAGCTCCAGGCCATT  
 CATCGAGACTCCCAATGGCTTGGGCCAGGGCACTGACACACCTCCACGGCCACTCACAGCTCCAGGCCATT  
 CCTTTGACAACCATGTGGCAAGAGATGCAACTCGGGGAAATGGAGAGGCCCTCTACAGCATCCGCAATGG  
 AAATGAAGCCCACCTCTCATCTCAACCCCTACACGGGGCAGCTGTGTCATGTCACCAATGCCAGCAGCCT  
 CATTGGGAGTGGAGCTGGAGATAGTAGAGGAGCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT  
 GAGGGTCACTGTCACCATGTGGACACCTGAGGGACTCAGCCGCAAGCTGGGCTTGAGCATGTCGAT  
 GCTGACGGTGTCTGCCCTGACTGTGGCATCTCCGGTTGATCTGCTTGTGTCATGTCATCTGCCG  
 GACAGAAAAGAAGGACAACAGGGCTACACTGTGGGGAGGCCAGTCCACAGCCAGCAGGCCAAGAGGCC  
 CCAGAAACACATTCAAGAGGAGCAGCATCCACCTCTGGCTGTGTCAGGGTCAAGGAGCTTGTGAAGT  
 CGGGCAGTCCCACAAAGATGTGGACAAGGAGGGCATGATGGAAGCAGGCTGGGACCCCTGCTGAGGCCCCCTT  
 CCACCTCACCCGACCCGTACAGGAGCGTGTGAAATCAAGGCAACCCAGGGAGCACCCGGAGAGGCCAGAGGT  
 GCTGCAACACCGTCAACCTCTTCAACCATCCCAGGAGGAAATGCTCCCGGGAGAACCTGAACCTTCC  
 CGAGCCCCAGGCCACAGGCCACGCTTCCAGGCCTGTAAGGTTGCAAGGAGCAGGCCACAGGGAGGCTGGC  
 TTGGAGACAGGGCAGTGGAGAAGGCCACAGAGGGCACCCAGGAGGCTCTGCAACCCCTGAGACGGCAGCGACATCT  
 CAATGGCAACAGTGTCCCCTGAGAAAAGAATCAGGGCCCTGAGATCTCTGGGAGCTGGCTGGCTGTGTC  
 TGCTTCCGGAGCGGGACCCCGTGGAGGAGCTACTGTGAGTCTCTCTCTGTCAGCAAATCTCCAGCTGCT  
 GTCTTGTGTCATCAGGGCAATTCTCAGGCCAAACCAACCCAGGAGGAAATAAGTACTTGGCCAAGGCCAGGAG  
 CAGCAGGAGTGAATCCAGACACAGATGGCCAAGTGTCAAGGGCTGGGCCAGACAGGCCAGAACAGGAGGA  
 AGGGCCTTGGATCTGTGAGAGGACCTCTGTGAGAAGCAACTGCTAGAAGAAGAGCTGTCAGTCTGCTGGACCC  
 CAGCACAGGCTGGCCCTGGACCGCTGAGGCCCTGACCCGGCTGGATGGCGAGACTCTTTGCCCTCAC  
 CACCAACTACCGTGACAATGTGATCTCCCGGATGCTGCAAGCCACGGAGGAGGCCAGGACCTTCCAGACGTTGG  
 CAAGGCAGGGCACAGGCCAGGAGCTGAGGCCACAGGCCAGGAGCTGGGCCAGACAGGCCAGAACAGGAGGA  
 GCTGGAGATGCTGTGAAACAGCGCTCCAGCATGCCGTGGAGGCCCTGGAGGGCTGCGCCGGCTCTGGT  
 CTGGGGAGGACCCCTGAGTTAGACTTGGCCACCATGCAAGGCTCAGGCCATGAAAGTGAAGGGACCCAGGTGG  
 AAAGACGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGCAGCAGGAGCTGGTGAAGGGACCCAGGTGG  
 CTGGATCCAAGAACCAAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTCTAAATCTGTAACTCACTAGCTAG  
 CGGCGGCCCTGAGAACTTTAGGGTCACTGATGCTACCCCCACAGAGGAGGCAAGAGGCCAGGACTAACAGCTGAC  
 TGACCAAAGCAGCCCTGTAAAGCAGCTGTGAGTCTTGTGAGGAGCAGGGACGGTTGTGGCTGAGATAAGTGT  
 TCCTGGCAAACATATGTGGAGCACAAAGGGTCACTGCTCTGGCAGAACAGATGCCACGGAGTATCACAGGAGG  
 AAAGGGTGGCCTTCTGGGTAGCAGGAGTCAGGGGGCTGTACCCCTGGGGGTGCCAGGAATGCTCTGACCTAT  
 CAATAAAGGAAAAGCAGTAAAAAAAAAAAAAA

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**FIGURE 394**

MMQLLQLLLGLPGGGYLFLGDCQEVTTLTVKYQVSEEVPSGTIVGKLSQELGREERRQAG  
AAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVLTGDLALIHVEIQVL  
DINDHQPRFPKGEOQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIGPD  
ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESSLALE  
IQEDAAPGTLLIKLTATDPDQGPNGEVEFFSKHMPPEVLDTSIDAKTGQVILRRPLDYEKN  
PAYEVVDVQARDILGPNPPIAHCKVLIKVLVDVNDNIPSIVHTWASQPSLVSEALPKDSFIALVMA  
DDLDSGHNGLVCWLSQELGHFRKLRTNGNTYMLLTNATLDREQWPKYTLTLLAQDQGLQPLS  
AKKQLSIQISIDINDNAPFEKSRYEVSTRENNLPSLHLITIKAHADLGINGKVSYRIQDSPV  
AHLVAIDSNTGEVTAQRSINYEEMAGFEFQVIAEDSGQPMЛАSSSVWVSLLDANDNAPEVVQ  
PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTTIVARDADSGA  
NGEPLYSIRNGNEAHLFILNPTHGQLFVNVTNASSLIGSEWELEIVVEDQGSPLQTRALLRV  
MFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGI FGLLALFMSICRTEKKDNRAYNCREAE  
STYRQQPKRPQKHIQKADIHLVPVLRQAGEPCEVGQSHKDVDKEAMMEAGWDPCQLQAPFH  
PTLYRTLNRNQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
EPEPQPATGQPRSRLKVASPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKV  
SPEKESGPRQILRSVRLSVAFAE  
RNPVEELTVDSPPVQQISQLSLLHQGOFQPKPNHRGNKYLAKPGGSRSA  
IPDGDGPSARAGG  
QTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRD  
NVISPDAAAATEEPRTFQTFGKAEAPELSPGTTRLASTFVSEMSSLLEM  
LEQRSSMPVEAASE  
ALRRLSVCGRTLSLDLATSAASGMKVQGDPGGKTGTEGKSRGSSSSRCL

**Important features:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 395**

CCCAGGCTCTAGTGCAGGAGGAAGGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG  
CTCCAGAACATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCTCCTCCACTGGGTCCGAATC  
AGTAGGTGACCCGCCCTGGATTCTGGAGACCTCACCATGGACGCCCGACCTCGTGCG  
GCCAAGACGTGGATGTTCTGCTCTGCTGGGGGAGCCTGGGAGGACACTCCAGGGCACAG  
GAGGACAAGGTGCTGGGGGTCAATGAGTGCAACCCCATTGCAGCCTGGCAGGCGGCCTTG  
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTGTAGGTGGCAACTGGGTCTTACAGCT  
GCCCACTGTAAAAAACGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAATAAGAT  
GGCCCAGAGCAAGAAATACCTGTGGTTCACTGCAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT  
GTGGAGGACCACAACCATGATCTGATGCTTCAACTGCAGTCCATCCCTGGTCC  
AAAGTGAAGCCCATTGCAGCCTGGCAGATCATTGCACCCAGCCTGGCAGAAGTGCACCGTCTCA  
GGCTGGGCACTGTCAACCAGTCCCCGAGAGAATTTCCTGACACTCTCAACTGTGCAGAAGTA  
AAAATTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC  
TGTGCAGGCAGCAAAGGGCTGACACGTGCCAGGGCGATTCTGGAGGGCCCTGGTGT  
GATGGTGCACTCCAGGGCATCACATCCTGGGCTCAGACCCCTGTGGAGGTCCGACAAACCT  
GGCGTCTATAACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC  
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCTGGTTTC

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**FIGURE 396**

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQWPWQAALFQGQQLLCGGVLV  
GGNWVLTAAHCKKPKYTVRLGDHSLQNKGDPQEIPVVQSIPHPCYNSSDVEDHNHDLMQL  
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYP  
GQITDGMVCAGSSKGADTCQGDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDWI  
KKIIGSKG

**Important Features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

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**FIGURE 397**

GGCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGATCCAGAGCCATGTCGGACCTGCTAC  
TACTGGGCCTGATTGGGGCCTGACTCTTACTGCTGCTGACGCTGCTGGCCTTGCCGGGT  
ACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGTCACCCCCCATCCGAACGTCACTG  
TGGCCTACAAGTCCACATGGGCCTATGGTGAGACTGGCGGCTTTCACTGAGAGCTGCA  
GCATCTCTCCAAGCTCCGCTCCATCGCTGTACTATGACAACCCCCACATGGTGCCCCCTG  
ATAAGTGCCGATGTGCCGTGGCAGCACCTGAGTGAAGGTGAGGAATGCCCTCCCTGAGC  
TCATCGACCTCTACCAGAAATTGGCTCAAGGTGTTCTCCTCCGGCACCCAGCCATGTGG  
TGACAGCCACCTCCCCTACACCACATTCTGTCCATCTGGCTGGCTACCCGCCGTGTCATC  
CTGCCCTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATCCTCGGCTGGAGATCTACC  
AGGAAGACCAAGATCCATTCTAGTGCCCACGGCACGGCAGGGAGACTTCTATGTGCCGTGAGA  
TGAAGGAGACAGAGTGGAAATGGCGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA  
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCCCTGGCAGCCGG  
AGACTTCAGCTGCCACACTGTCACCTGGGCGAGCAGCCGTGGCTGGATGACGGTGACACCC  
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGCTCCCTTTGAGGAGCTGGACTTGG  
AGGGCGAGGGGCCCTAGGGGAGTCACGGCTGGACCCCTGGGACTGAGCCCTGGGACTACCA  
AGTGGCTCTGGAGGCCACTGCCCTGAGAAGGGCAAGGAGTAACCCATGCCCTGCACCCCTCC  
TGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCTCCAGCCCTTTCCCT  
TCCTCTGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTGCTCCAGGCCTTTGCTAAG  
CCTTCTCCTCACTGCCCTTAGGCTCCAGGGCAGAGGAGCCAGGGACTATTTCTGCACCA  
GCCCCAGGGCTGCCGCCCTGTTGTCTTTTCAGACTCACAGTGGAGCTCCAGGACC  
CAGAATAAAGCCAATGATTACTGTTCACCTGGAAAAAAAAAAAAAAA

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**FIGURE 398**

MSDLLLGLIGGLTLLLLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGRL  
FTESCSISPRLRSIAVYYDNPHMVPDKRCAVGSILSEGEESPSPLEIDLYQKFGFKVFSFP  
APSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPALARQGD  
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDLSSVSLEVSPGSRETSAAATLSPGASSRGW  
DDGDTRSEHSYSESAGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEKGKE

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**FIGURE 399**

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCCGGGC  
TCCGTGCCGCCAAGTTTCATTTCACCTCTGCCTCCAGTCCCCCAGCCCCCTGGCCGAG  
AGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTGTTTTAAA  
TCTGTTCTTGGAGGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCTGCTCTGTT  
TGGAGCCTCTGCTATTGCTTGCTGCAGGGAGCCCCGTACCTTTGGTCCAGAGGGACGGCTG  
GAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGGTTAAC  
CTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCACAGCCAGCCC  
TTAGAAGACTGCAGTTCAACATGACAGCTAAAACCTTTCATCATTACGGATGGACGATG  
AGCGGTATTTGAAAACGGCTGCACAAACTCGTGTCAAGCCCTGCACACAAGAGAGAAAGAC  
GCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTACACGGATGCGGTCAAT  
ATAACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGGAGAAGGACGAT  
TTTCCTCTCGGAATGTCCACTTGATCGCTACAGCCTCGAGCGCACGTGGCCGGGTATGCA  
GGCAACTCGTGAAAGGAACGGTGGCGAATCACAGGTTGGATCCTGCCGGGCCATGTT  
GAAGGGGCCACATCCACAAGAGGCTCTCCGGACGATGCAGATTGTGGATGTCCTCCAC  
ACCTACACGCCTCCTCGGTTGAGCATTGGTATTCAAGATGCCTGTGGGCCACATTGACATC  
TACCCCAATGGGGTGACTTCCAGCCAGGCTGGAACGATGCTGGACTCAACGATGTCTGGATCAATTGCA  
TATGGAACAATCACAGAGGTGGTAAATGTGAGCATGAGCGAGCCGTCCACCTTTGTTGAC  
TCTCTGGTGAATCAGGACAAGCCGAGTTTGCTTCCAGTGCAGTCACTCCAATCGCTTCAAA  
AAGGGGATCTGTCAGCTGCCAAGAACCGTTGTAATAGCATTGGCTACAATGCCAAGAAA  
ATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAACCCGGGCAGGCATGCCTTCAGAGGT  
AACCTCAGTCCCTGGAGTGTCCCTTGAGGAAGGCCCTTAATACCTCTTAAATACCATGCT  
GCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCACAATCAAATCGTTGCAA  
ATCAGATTACACTGTGCATGCCTAGGAAAGGAATTTACAAAATAACAGTGTGGACCCC  
TAATAAA

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**FIGURE 400**

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFLRTSKDPEHEG  
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWLPL  
AHQLYTDAVNNTRVVGHSIARMLDWLQEKKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI  
TGGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIPNGGDFQPGC  
GLNDVLGSIAYGTTIEVVKCEHERAVHLFVDSLNVQDKPSFAFQCTDSNRFKKGICLSCRKNR  
CNSIGYNAAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:****Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

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**FIGURE 401**

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTGCAGAACTTCTACTTGCCTG  
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCCTCAGCTCCTCTGATGGGACCTCCTGT  
CAGTTCCCAGACAGTCCTGGCCAGCTGGATGCAGTGCCTGGTCTTCCCAGGCCAAGTGGCTC  
AACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCCTGGTACC  
AGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC  
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCTGTGTC  
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCCGGATTACTACTGCTCTGTTGGCTACGGCT  
TTAGTCCCTAGGGTGGGTGTGAGATGGGTGCCTCCCCCTGCCTCCCATTCTGCCCTGA  
CCTTGGGTCCCTTTAAACTTCTCTGAGCCTGCTCCCCCTGTAAAATGGGTTAATAATA  
TTCAACATGTCAACAAAC

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**FIGURE 402**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS  
APRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPQPEDDADYYCSVGYGFSP

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**FIGURE 403**

CGCGCCGGGCCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG  
GCAGAGCAGGGCTGCATTCAGCAGGAGCTGCGAGCACAGTGCAGCTGGCTCACAAAGAATGCTCAAGGTGTCAGC  
CGTACTGTGTGTGAGCCGCTTGGTGCAGTCAGTCTCTCGCAGCTGCCGCCGGTGGCTGCAGCGGGGG  
GCGGTCGGACGGCGTAATTTCTGGATGATAAACAAATGGCTACCACAATCTCTCAGTATGACAAGGAAGTCGG  
ACAGTGGAAACAAATTCCGAGACGAAGTAGAGGGATGATTATTCGCACCTGGAGTCCAGGAAAACCCCTCGATCA  
GGCTTAGATCCAGCTAAGGATCCATGCTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTGCTCAAGATT  
TCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG  
GAGGGTCCCATAATTATCCACCTGCAAGCAGTGCCTAGGTCTATCCAGCCCTGTTGTGGTCAGATGGTCA  
TACCTACTCTTCAGTGCAAACAGAAATATCAGGCATGTGCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG  
ACATTGCCATGTCCTCAGATAAGCCCACCAAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT  
CAGGGAAAGTGGCAAACAGATTGCGGACTGGTCAAGGCCCTCATGAAAGTGGAAAGTCAAAACAAGAACAAA  
AACATTGCTGAGGCCTGAGAGAACAGATTGCAAGGACTCAGTGCAGGACTCACTGGCTGGAT  
GTTAACAGACTTGATAACAAACTATGACCTGCTATTGGACCAAGTCAGAGCTCAGAACGATTACCTGATAAGAA  
TGAACAGTGTACCAAGGCATTCTCAATTCTGTGACACATAACAGGACAGTTAATATCTAATAATGAGTGGTG  
CTACTGCTTCCAGAGACAGCAAGACCCACCTGCCAGACTGAGCTCAGCAATATTCAAGCGGCAAGGGTAAA  
GAAGCTCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTIACTACAAGCCAACACAATGTCATGGCAGTGT  
TGGACAGTGTGGTGTGACAGATATGAAATGAAGTGCATGGGATCCAGAATAATGGTGTGAGATTGTGC  
TATAGATTTGAGATCTCGGAGATTTGCTAGTGGCATTTCATGAATGGACTGATGATGAGGGATGATGAAGA  
CGATATTATGAATGATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGATGATGATGATGGTGGTGTGATGA  
CCATGATGTATACTTGATTGATGACAGTTGAAATCAATAAAATTCTACATTCTAATATTACAAAAATGATAG  
CCTATTAAAAATTATCTTCTTCCCAATAACAAATGATTCTAAACCTCACATATATTGTATAATTATTGAA  
AAATTGCAGCTAAAGTTATAGAACATTATGTTAAATAAGAATCATTGCTTGAGTTTATATTCTTACACA  
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAGTTGAAGTGCCTACTATAATAAATTTCAGGAGA  
ACAAACTTGTAAATCTCCATAAGCAAATGACAGCTAGTGCCTGGGATCGTACATGTTAATTGGTAAAGAT  
AATTCTAAGTGAATTAAATAAAATTGTTAATGACCTGGTCTTAAGGATTAGGAAAATATGCATGCT  
TTAATTGCATTCCAAAGTAGCATCTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA  
AAAAAAAAAAAAAA

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**FIGURE 404**

MLKVS A V L C V C A A W C S Q S L A A A A V A A G G R S D G G N F L D D K Q W L T T I S Q Y D K E V G Q W N K F R D  
E V E D D Y F R T W S P G K P F D Q A L D P A K D P C L K M K C S R H K V C I A Q D S Q T A V C I S H R R L T H R M K E A G V  
D H R Q W R G P I L S T C K Q C P V V Y P S P V C G S D G H T Y S F Q C K L E Y Q A C V L G K Q I S V K C E G H C P C P S D K  
P T S T S R N V K R A C S D L E F R E V A N R L R D W F K A L H E S G S Q N K K T K T L L R P E R S R F D T S I L P I C K D S  
L G W M F N R L D T N Y D L L L D Q S E L R S I Y I L D K N E Q C T K A F F N S C D T Y K D S L I S N N E W C Y C F Q R Q Q D P  
P C Q T E L S N I Q K R Q G V K K L L G Q Y I P L C D E D G Y Y K P T Q C H G S V G Q C W C V D R Y G N E V M G S R I N G V A  
D C A I D F E I S G D F A S G D F H E W T D D E D D E D D I M N D E D E I E D D D E D E G D D D G G D D H D V Y I

**Important features:****Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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**FIGURE 405**

GGAAGGGGAGGGAGCAGGCCACACAGGCACAGGCCGTGAGGGACCTGCCAGACCTGGAGGGCTCGCTCTGTCA  
 CACAGGCTGGAGTGCAGTGGTGTGATCTTGCTCATCGTAACCTCACCTCCGGGTTCAAGTGATTCTCATGCC  
 TCAGCCTCCCAGTAGCTGGGATTACAGGTGGTGAACCTCCAAGAGTGACTCCGTCGGAGGAAATGACTCCCCAG  
 TCGCTGCTGCAGACGACACTGTTCTCTGTGAGTCTGCTCTCTGGTCAAGGTGCCACGGCAGGGGCCACAGG  
 GAAGACTTCTGCTCTGCAGCCAGCGAACAGACACAGGAGCAGCCTCACTACAAACCCACACCAGACCTG  
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTCTGGCAGGCCACCCCTGCTTCCCGA  
 TCCCTCCCTGACCCCCAGGGGCCCTTACCACTCTGCCTACTGGAAAGCAGACATGCTGGAGATTACATCTCTC  
 TATGGCAAGCGTGAACCTCTGCTGAGTGACAAAAGCCTCTAGCCTCTGTGCTTCCAGCACCCAGGAGGAGCCTG  
 GCTCAGGGCCCCCGCTGTTAGGCACCTCTGTCACCTCTGGTGGAGCCCTCAGAACATCAGCTGCCAGTGCC  
 GCCAGCTTCACTTCTCCACAGTCTCCACAGGCCGTCAACAATGCCCGTGGACATGTGCGAGCTC  
 AAAAGGAGACCTCCAGCTGCTCAGGCCAGTCTGAGCAGCATCCCCAGAAGGCCCTCAAGGAGGCCCTGGCTGCC  
 GCCAGCAGCAGTTCAGAGCCTGGAGCTGAAGACTGACCTCTGTGAGATTATGGGGACATGGTGTCTTCAG  
 GAGGACCGGATCAACGCCACGGTGTGAGCCTCAGGCCACAGCCGGCTCAGGACCTGCACATCCACTCCGG  
 CAGGAGGAGGAGCAGAGCAGATCATGGAGTACTCGGTGCTGCTGCCGAACACTTCCAGAGGAGCAGAACGG  
 CGGAGCGGGGAGGCTGAGAAGAGACTCCTCTGGTGGACTTCAGCAGCCAAGGCCCTGTTCCAGGACAAGAATTCC  
 AGCCAAGTCTCTGGTGAGAAGCTTGGGATTGTGTTACAGAACACCAAAGTAGGCCAACCTCACGGAGGCC  
 GTGCTCACTTCCACCCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTTCTGGGTTAAGACCCACA  
 TTGAGCAGCCCCGGGATTGGAGCAGTGTGGTGTGAGGACCGTCAAGGAGAGAAACCCAAACATCCTGCTTCTGC  
 AACCACTTGAACCTACTTGCAGTGTGATGGTCTCTCCGGTGGAGGGACGCCGTGACAAGCAACTACCTGAGC  
 CTCCCTCTCCTACCTGGCTGTGCTCTGCCCTGGCCTGCTGTACCCATTGCCCTACCTCTGCTCCAGG  
 GTGCCCTGCGCTGCAAGGAGAACCTCGGGACTACACCATCAAGGTGACATGAACCTGCTGCTGGCGCTCTC  
 CTGCTGACACGAGCTCTGTCAGCGAGCCGGTGGCCTGACAGGCTGAGGCTGGCTGCCAGGCCAGTGC  
 ATCTTCTGCACTTCTCCCTGTCACCTGCCCTTCTGGATGGCCTCGAGGGTACAACCTCACCGACTCGT  
 GTGGAGGCTTTGGACCTATGTCCTGGTACCTACTCAAGCTGAGGCCATGGCTGGGCTTCCAGG  
 CTGGTGACGCTGGCCCTGGGGATGTGGACAATATGGGACCATCTTGGCTGTGCACTAGGACTCCAGAG  
 GCCGTCATCTACCTCTCATGTCGGTGGATCCGGGACTCCCTGGTCAGCTACATCCAACCTGGCCTTTCAGC  
 CTGGTGGTTCTGTTCAACATGGCATGCTAGGCCACCATGGTGGTGCAGATCCTGGCTGCCCTGGGCTTGA  
 AAGTGGTCACATGTGCTGACACTGCTGGGCCAGGCTGGTCTGAGGAGGAGGGCCCTTGGCTGGGCTTGA  
 TTTGCTCTGGCACCTCCAGCTGTCCTCTACCTTTGAGCATCATCACCTCTTCAAGGCTTCCATC  
 TTCATCTGGTACTGGTCCATGCGGCTGCAAGGCCGGGGTGGCCCTCCCTCTGAAGAGCAACTCAGACAGGCC  
 AGGCTCCCCTCAGCTCGGGCAGCACCTCGTCCAGCGCATCTAGGCCCTCCAGGCCACCTGCC  
 CAGAGATGGGCCCTCGCAGCACACTGCTGTGGGGGGAGGCCAGGCCAGGCCAGTGCAGGCCAGACT  
 TTGGAAAGCCCAACGACCATGGAGAGATGGGGCTTGGCATGGTGGACGGACTCCGGCTGGCTTTGAATTG  
 GCCTGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCCATGCTGCCCTAGGTACTG  
 TCCCCACATCTGTCACCCAGCTGGAGGCCCTGGCTCTCTTACAACCCCTGGGCCAGGCCCTCATTGCTGG  
 GGCCAGGCCCTGGATCTGGAGGGTCTGGCACATCTTAACTCTGCCCCCTGGCTGGAGAACAAATGTGGCT  
 GTTGCTCTGCTCTCGTGGTACCCCTGAGGGACTCTGCATCCTCTGTCTATTAACTCAGGTGGCACCCAGG  
 CGAATGGGCCAGGGCAGACCTCAGGGCAGAGGCCCTGGGGAGGGCCCTTGGCAGGAGCACAGCAGC  
 AGCTCGCCACTCTCTGAGGCCAGGCCCTCCCTCAGCCCCCAGTCTCCCTCATCTCCCTGGGTT  
 TCCCTCTCTCCAGGCCCTTGTCTCTTACAGCTGGGGTCCCGATTCCAATGCTGTTTTGGG  
 GTGGTTCCAGGAGCTGCTGGTGTGTAATGTTGCTACTGCAACAGGCCCTGGCTGCC  
 GGCTCGGTACCGATGCGTGGCTGGCTGGTGTGTAATGTTGCTACTGCAACAGGCCCTGGCTGCC  
 CTCACCCCTGACCAAGCACAGGCCCTCAGGGGCCCTCAGCTCTCTGAAAGGCCCTGGCAAGAAC  
 CCATGCCAGTCCCGTCTGGTTCCATCCACACTCCAAGGACTGAGACTGACCTCTCTGGTGAACACTGG  
 GAGCCTGACACTCTCTTAAGAGGTTCTCCAAAGCCCCAAATAGCTCAGGCCCTGGCCGCC  
 TAATTCTGTCACAAACACACACGGTAGATGCTGGCTGTTGAGGTGGTAGGGACACAGATGACCGACTG  
 GTCACTCTCTCTGCCAACATTCACTGCTGGTAGGTGAGGCGTGCAGTGAAGCAAGAAC  
 CCCCTGGAGCTACAGGCCCTGGCTGGAGACTTCCGAGGAGTCAGCGTTCAATCTGACCTTG  
 GGGAGCCATCTCTGCTGGGAATCTGGAGAGACTTCCGAGGAGTCAGCGTTCAATCTGACCTTG  
 GGGAGGATGTTCTTTACGTACCAATTCTTTGTTGATATTAAAAAGAAGTACATGTT  
 ATTGGAAACTGTAGAAGAGAATCAAGAAGAAAATAAAAATCAGCTGTTGAA  
 TCTGCTAGCAAAAAAAAAAAAAAA

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**FIGURE 406**

MTPQSLLQTTLFLLSLLFLVQGAHGRGHREDFRFCRSQRNQTHRSSLHYKPTPDLRISIENSEE  
ALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGRDFLLSDKASSLLCFQHQE  
ESLAQGPPLLATSVTSWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDQLLSQF  
LKHPQKASRRPSAAPASQQLQSLESKLTsvrfmgdmvsfeedrinatvwklqptaglqdlhih  
SRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAERKRLLVDFSSQALFQDKNSSQVLGEKVLGI  
VVQNTKVALTEPVVLTFQHQLQPKNVTLQCVFWVEDPTLSSPGHWSAGCETVRRETQTSCF  
CNHLTYFAVLMSSVEVDAVHKHYLSLLSYVGCVVSALACLVTIAAYLCSRVPPLCRRKPRDY  
TIKVHMNLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLEGYNLYRLV  
VEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS  
LVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVGLPWALIFFSF  
ASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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**FIGURE 407**

TTGTGACTAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGTGGCAGGAG  
CCGCAGAGCCAGAGCAGACAGCCGAGAACAGGTGGACAGTGTGAAAGAACCAAGTGGTCTCGC  
TCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA  
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGACTCCAGGGTGCACTCAAGCCC  
TGTTCCTCTCCTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCACTCCAAAGCTC  
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAACGCCAGGAGCAGGGC  
TCTCAGAAGGCAGGTGGTGCCTCAGCTGGGATCATGTGTTGCCCTGGTCTGTCTGCTCAGCTG  
CCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAAC TGCCAGAGTGCCTACATGA  
CTTCGGGCTGGACGGATACCGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTCA  
AAGCGGTTCAACGCAGCTGCTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT  
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCCAACGTCCCCAACGTGTGCCGGAT  
GTACTGCTCAGATTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC  
CCAAGAGCCTCAGGGTCTGGTTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT  
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGAA  
ATGTGGTTGGTCTGACCTAGGTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG  
TGAAA

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**FIGURE 408**

MLLALVCLLSCLLPSSREAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAALDY  
EADGSTNNGIFQINSRRWCNSLTPNVPNVCRMYSIDLNPNLKDTVICAMKITQEPQGLGYWE  
AWRHHCQGKDLTEWVDGCDF

**Important features:****Signal peptide:**

amino acids 1-18

**N-myristylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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**FIGURE 409**

CAGACTCCAGATTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCCGGAGACAAACAGTACCTGACGC  
CTCTTCAGCCCCGGATCGCCCCAGCAGGGATGGCAGAAGATCTGGCTGCCCTCCCGTCTCCCTCTGGCC  
GCTCTGCCCTCGGTGCTGCTGGCTGGGGCGCCGGCTTCACACCTTCCCTCGATAGCGACTCACCTTACCCCT  
CCCGCCGGCCAGAAGGAGTGCTCTACCAAGCCCAGGCCCTGAAGGCCCTCGTGGAGATCGACTACCAAGTTA  
GATGGAGCAGGATTAGATATTGATTTCATCTGCTCTCCAGAAGGCAAAACCTAGTTTGAAACAAAAGAAAA  
TCAGATGGAGTTCAACTGTAGAGACTGAAGTTGGTATTACATGTTCTGCTTGAACAATACATTGACCCATT  
TCTGAGAAGGGATTTCTTGAAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAGAACAGATTGGAAG  
AAATATATTACTGGCACAGATATTGGATATGAAACTGGAGACATCTGGAAATCCATCAACAGCATCAAGTCC  
AGACTAAGCAAAAGGGCACATACAAATTCTGCTTAGAGCATTGAAAGCTGTGATCGAAACATACAAGAAAAGC  
AACTTGATAGAGTCATTTCTGGTCTATGGTAAATTAGTGTAGCTGGTGGTGTAGCCATTCAAGTTAT  
ATGCTGAAGAGTCTGGTGAAGATAAGAGGAAAGTAGAAACTTAAACTCCAAACTAGAGTACGTAAACATTGAAA  
AATGAGGCATAAAAATGCAATAAAACTGTTACAGTCAGGAACTTAAACTGGTCTCTCCAAAATTTTGGATATA  
AAAGTAGGAAACAGGTATAATTAAATGTGAAAATTAAAGTCTTCACTTCTGTGCAAGTAATCTGCTGATCCAG  
TTGACTTAAGTGTAAACAGGAATATTGCGAGAATAGTTAACTGAATGAAGCCATATAAACTGCAAT  
TTTCTAACTTTGAAAATTGCAAATGCTTAGGTGATTTAAATAATGAGTATTGGCCTAATTGCAACACC  
AGTCTGTTTAAACAGGTTCTATTACCCAGAACTTTTGTAAATGGCAGTTACAATTAAACTGTGGAAGTT  
TCAGTTTAAAGTTAAATCACCTGAGATTACCTAAATGATGGATTGAAATAATCTTAGACTACAAAGCCAA  
CTTTCTCTATTACATATGCACTCTCTTAAATGTAATAAGTAAATAGTTGAAATACAATTAGGTTTTG  
AGATTTTATAACCAAATACATTTCAGTGTACATATTAGCAGAAAGCATTAGCTTGTACTTGTACTTGTACATT  
CCAAAAGCTGACATTTCAGATTCTAAAACACAAAGTTACACTTAAATAGGACATGTTCTCTTTG  
AAATGAGAATATAGTTAAAGCTCTCCCATAGGGACACATTCTCTAAACCTTAACTAAAGTGTAGGA  
TTTAAATTAATGTGAGGTAAGTTATTAAATAGTATCTGTCAAGTAATATGTCAACAGTTAA  
TAATCATGTTATGTTAAATTAAACATGATTGCTGACTTGATAATTCAATTACAGCAGTTGAAGGAAATA  
TTGCTAAATGATCTGGCCTACATATAAAATCTCTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
AGAATTAGAAAACCTAACTGAGAAACCTAACTCCTAAATAAAATCCTAACTTAAGTAACTATAAAATATCTAGA  
ATCTGACTGGCTCATCATGACATCCTACTCTAAACATAAACTCAAGGAGATGATTAATTCCAGTTAGCTGGAAG  
AAACTTGGCTGTAGGTTTATTTCTACAGAAATTCTGGTTGAATTATTTGTAAGCAGGTACATT  
AAATGTAAGCCCTACTGTAAGTTAGCACTGGGTGACATATTAAATAACACTTTAT  
TAAATGCCCTCTGAAACACTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCAAAGTTAAA  
CACCTAAATGTAACCCATATACAAACAAAGTTCTGCCATCTAGCTTGTAAAGTCTATGGGGCTCTAC  
TCAAGTACTAGTAATTAACTTCATCATGAACTGAACTATAATTAAAGTTGCCCATTAAACGTTGTTAT  
GACTACATTGTGAGTTAGAAACAAACTTAAATTGGGTATGAAACCCCTCAACAGGTTAGTAATGCTGGAATT  
CTTGATGAGCAATAATGATAACCAAGAGAGTGATTCAATTACACTCATAGTAGTAAAGAGGATACATT  
TCTTAGGCCCTGGAGAACAGCAGTTAGATTCCCTACTGGCAAGGTTTAAAGGTTAAATGCCGTAT  
ATGATCAATTACCTTAATTGCCAAGAAAATGCTTCAGGTGCTAGGGTATCTCTGCAACACTTGAGAACAA  
AGGTCAATAAGATCTTGCTATGAAATACCCCTCCCTTGCCTGTTAAATTGCAATGAGAACAAATTACA  
GTACCATTAACATAAAAGCAGGTACAGATATAAAACTACTGCATCTTCTATAAAACTGTGATTAAGAATTCTA  
CCTCTCTGTATGGCTGTTACTGACTCTGACTCTTACCTAAACATGAAATTGTTACATAATCTCT  
ACATGATGATTGATTTGCCCCACTGATCTAAACCTATGATTCACTTAAGTCTTACCATATAAAAGATAATTGCTT  
TATTGAAAAAGATTAGGAATAACTAGGACAATTATTTATAGACAAAGTAAAGACAGATAATTAAAGAGG  
CATAACCAAAAAGCAAACCTGTAACACAGAGTAAAGTAAAGACAGATAATTAAAGG  
CATATGCTTTTTAATTCACTATTCACTTCTAAATTAAAGTTGCTAAATTGAGTAAGCTGTTTACT  
AACAGCTCATTGCTTTCAATATACAAATTAAAGTAAACTACATATTAAACTAAGGCCAACCGATTT  
CATAAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCAGAGTTGCTCTGATATGCAATTGGATGATTAAT  
GTTATGCTGTTCTCATGTGAATGTCAGAACATGGAGGGTGTGTAATTGTTATGTAATTAAATCCTTCTTA  
CACATAATGGTCTTAAATTGACAAAAAGTGGCAACTTACAATTGATGTCTCCTCAAATGAAGATTCTTAT  
GTGAAATTAAAGACATTGATTCCGATGTAAGGATTTCATCTGAAGTACAATAATGCAACATCAGTGTG  
CTCAAACTGCTTATACATTAAACAGCCATCTTAAATAAGCAACGTATTGAGTACTGATATGATATAATA  
AAATTATCAAAGGAAA

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**FIGURE 410**

MGDKIWLFPVLLAALPPVLLPGAAAGFTPSLSDFTFTLPAGQKECFYQPMPPLKASLEIEYQ  
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCFDNTFSTISEKVIFFELIL  
DNMGEQAQEQQEDWKYITGTDILDMLKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE  
SNFDRVNFWSMVNLVVVVSAIQVYMLKSLFEDKRKSRT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 411**

CCCAAGCTGAGGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTTCCCAGGGGACCGCATTCCAGAGTC  
GTACTCTGTGAAGCACCCACATCTACCTCTGCCACGTCCCCACGGGCTGGGGGAAAGATGGTGGGGACCAA  
GCCTGGGTCTCTTCTGGTCTGGGAAGAGAACCCCCACGATCTTGCAACATCTGTGTTGGGAGACAGACGATGCTCACCCAGTCAGTA  
AGAAGAGTCCAGCTGGGAAGAGAACCCCCACGATCTTGCAACATCTGTGTTGGGAGACAGACGATGCTCACCCAGTCAGTA  
TGGACACATGGTCAACATCGACTACCCAGCGGGAGGGCAGACTATGAGCGCTGGTGGACGCCATTCTGGCTTCTAC  
TATGGGGACGGCTGTAGTGGCCGCTCCCCCTGCGGCTAGAGGCTCGGACCCTGACTGGACACCTGCGGGCAGCACT  
GGCAGGTGGCTCATGGTAGTCCCCCTGCGGCTAGGGGTTCTGGTGCCTCAACAGGGAGCAGCGGCCCTGGCAGAGA  
TCTAATTACACCGTACGCTTCTGCCACAGGATCCTCGCAGGGAGACACAGAGCGCATCTGGAGGCCATTGG  
TCTCCCTGGAGCAAGTGCTCAGCTGCGCTGTGTCAGACTGGGGTCCAGACTCGCAGACAGCATTGGTCTTGG  
ATGGTGTGCTGTGAGGGCAGGGAGGGTCAAGCTGATGGGAGGGACTGTACAGCTGTGACCTG  
ACCTGCCCAATGGGCCAGGTGAATGCTGACTGTGATGCCCTGATGTGCCAGGACTCTATGCTTATGGGCTGTC  
TCCCTTCCGGAGGTGCCCCAGCTCAGGGGCTGCTATCTACCTCTGACCAAGACGCCAGGCTGTCAGGCCAG  
ACAGACAGTGTGGGAGATTCGAATCTCTGGCTTGTGCTGTGATGGCAGAAAGCATTCTGAAGATCAAAGGTC  
AAAGTTGGCCCCCATTTGTAACATGCCCCAGACTAGGCTGAAGGCAGGCCATTCAAGGCAGAGTGGTGG  
GCAGAGACTCATACTGGTGAACCTGGAGACACAAAGCAGGGAGAGCTGGCAGAGTGGTGG  
AAGGCCACAGGGAGGCCAGGGCAGACAAGTATTTTGATCATATAATGACACATTGCTGGATCTTCTTCTAC  
AAGCATGAGAGCAACGCTGGTCTGGGAAACTGCAAGCAGCACCAGCTGGGGAGTACTCTTGG  
GATGCTGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGCTACAGCATCTGATGAGACTCTTGCAGCTG  
CCTGAGAGCTATCTTATCCGCTGCCCCATGATTGCTTCAAGATGCCACCAACTCTTCTACTATGACGGTGG  
CGCTGCCCTGTTAAGACTTGTGAGGGCAGCAGGATAATGGGATCAGGTGCGCTGATGCTGTGAGAACTGCTGT  
GGCATCTCAAGACAGGAGAAGGGAGATCAGCTGGAGCTGGCTACAGGCTACCCACCAAGGTGCCAGAGGTC  
AGCTGCCAGGGTGTACGGAAACTCGGAGCATCGTGGGGGCTGTCAGTGTGCTGACAATGGGAGGCCATTG  
CGCTTGGCCATGTGTCATGGGAAACAGCGGTGTAAGCATGACTGGCTACAAGGGCACTTCCCTCCATGTC  
CCCCAGGACACTGAGGGCTGGTGTCTCACATTGTGAGCAGGCTGCAAGAGTTGTCACACCAACCAAAAGTCTA  
CTTTCAACAAGAAGGGAGTGGCTGTTCCATGAAATCAAGATGCTTCTGCGGAAAGAGGCCATTCTTGGAA  
GCCATGGAGGACCAACATCATCCCCCTGGGGAGGTGTTGCTGAAGACCCATGGCTGAACGGAGATTCCATCC  
AGGAGTTTCTACAGGCCAGAATGGGAGGCCATAGGAAAGTGAAGGCCAGTGTGACCTTCTGGATCCCCGG  
AATATTTCCACAGCCACAGCTGCCAGACTGACCTGATCTGAGGAGACACTTCTGGGCTTCTGGATCCCCGG  
ACGTATGCGATGTTCTCTGTGGACTTCAGAGATGAGGTCACTCAGAGCACTTAATGCTGCCAAAGTGAAGGT  
CACCTGTACTGCGACCCAGGTCAAGATGCGAGACACATCTCCAGTGGAAACTCTGCTCACTCA  
GGGCTGGGGAGGGAGGAAGGTGATTCTCAAAATTGAAAATCAAGGGAGGAACAAAAGAGACAGAACCTTCTG  
GTGGGCAACCTGGAGATTCTGTGAGAGGGCTTTAACCTGGATGTTCTGAAAGCAGGGCTGTTGTTAAG  
GTGAGGGCTTACGGAGTGGAGGAGTTCTGGCTAGTGTGAGCAGATCCAGGGGGTGTGATCTCCGTGATTAACTG  
GAGCTAGAACTGGCTTCTGTCACACCTTGGGCTCTGGGGCTTGTGACAGTGTCACTACAGGCCAAAGGG  
GCCCTGTGCTGCCCTCTGTGATGAGCTGCCCTGATGCCCTACTCTGCTTGTGCTTGTGCAAGGCTGGCTGG  
GAGGAACAGCAAGCAGGGACTCTTCTGGCTTGTGAGGACTCTGGGCTGATGGCAACATGGCGATGGAAATT  
AAGCTCAACTACCGTGGCAGGCCAGTGGGAGATCTGGGACTCTGGGCTGATGGCAACATGGGGGCACTCATGGGG  
CCAAGGCCAACTCAGCTGAGGAGACCAATGGGCCCCATCTATGCTTCTGGAGAACCTTCCGGGATGTGAAGAGGCA  
CCACCAAGTGCAGGCCACTTCCGGTCTTACAGATTGAGGGGGATCGATATGACTACAACACAGTCCCCCTCAAC  
GAAGATGACCTATGAGCTGGACTGAAGACTATCTGGGACTCTGGGACTCTGGGCTGATGGCAACATGGCT  
ATCAAGGTGAAGATTGTGGGCCCCACTGGAAAGTGAATGTGCGATGCCCAACATGGGGGCACTCATGGGG  
GTGGGGAGCTGTGATGAAATGGAGATGTGAGGAGCACTCGGGACAGGGACGCCAGGCTTGTGAGGT  
CTGGAGTTCAAGTGCAGTGGGACTCTATGCTGAGGACCTGGGACGCCAGGCTTGTGAGGT  
GGCAGCTGGCTGCCAGGCCAGTGTGAGACCCCATGCTGATGAGTACTCTGGTCAACACTTGCAGTCAC  
AACAGACACCAAGTGTGAGTACACCATGTCGGCACCTTGGGCCACTGGGCCACAACATGTCAGTCA  
GACCAAGGCCCTCGCAGGGAGAGATCGCGCTCGGCCGTGTTTGATGGCACATCGATGGCTCTCCAGA  
ATCATGAAGACCAATGTGGGAGTGGCTTCTCTTCAACTCTGTGAGAGGGCAAGTGGGCCAGAGTGCCTTC  
CAGTACCTCCAAAGCACCCTGGCCAGCTGGCTGAGGAGCACTGGTCAAGGAAGAGTGGCTCTGGAGGGAG  
CAGCGAGGAGGCCAGGGGGTGGCCAGCGCCAGGGTGGAGTGGTGGCTCTGGAGATTCTAGGTTGCTCAACAG  
CCCCCTGTACACTAATGGTTTGTGACTTCCACCTTCTGCCCCATGGCTTGTGAAATTGCTGTTCTCTG  
TGCAACAAACTGTCACTGGTAAATTAAAGCATTCTGCTTCTGTGAAATTGCTGTTGTTCTCTG  
CTTAACTTGTCCCCATGCTACTGATTGGCACGGGCCCCACAAATGGCACAATAAGGCCCCCTTGTGAAACTGTT  
TTAAATGAAACACAAAGAAATTGGGCCACTGGTAAACTCTGCACTGTCAGCTTCACTGTA  
GCAAAATATGCTTCTCTTCTGGCTTGTGCAACAGGACATAGGCAAGCCCTGGTCAAGATGGCT  
ATAACCAATATAAGCATATTCTGGCTTGTGCAACAGGACATAGGCAAGCCCTGGTCAAGATGGCT  
AAATGAGTGGTGAAGATAAAAGAATAAAACACAAACTTACTTACTTGTGAAATGTA  
AATTTGGAAATTCTACTGGCACATTCAAGTTAGGACTTAAATAGGGTGTGATCATAGTGGCT  
AAAGAACATCTCTGGTATCCACATTACACCGAGGGTGTCAACTGTGATTTGTGACCTTCC  
TGTGCTAGAACCCAGTGTAGGCCAGGGCAGATGTCAATAATGCACTCTGTGTTTGGAAAAAA

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**FIGURE 412**

MVGTKAWVFSFLVLETSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNID  
YPGGKGDYERLDAIRFYGYDRVCARPLRLEARTTDWTPAGSTGQVVHGSREGFWCLNREQRP  
GQNCSNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS  
EEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAWSLPGGAPASGAAIYLLTTPKL  
LTQTDSDGRFRIPGLCPDGKSILKITVKVFAPIVLTMPKTSLSKAATIKAEFVRAETPYVMNP  
ETKARRAGQSVLCCCATGKPRPDKYFWYHNDLDPNSLYKHESKLVLRLQQHQAGEYFCKA  
QSDAGAVKSVAQLIVTASDETPCNPVPESYLIRLPHDCFQNATNSFYYDVGRCPVKTCAQQ  
DNGIRCRDAVQNCCGISKEEREIQCSCGYTLPTKVAKECSCQRCTETRSIVGRVSAADNGEP  
MRFGHVYMGNSRVSMTGYKGTFTLHPQDTERLVLTFVDRQLKFVNNTKVLPFNKKGSASFHE  
IKMLRRKEPITLEAMETNIIPLGEGVVEDPMAELEIPSRSFYRQNGEPYIGKVKA  
SFTVKLWSLN PDTGLWEEE GDFKFENQRRNKREDRTFLVGNL  
EIRERRLFNLDVPE SRRCFVKV  
RAYRSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFD  
SVITGPNGACVPAFCDDQSPDA  
YSAYVLA SLAGEELQAVESSPKFN  
PNAIGVPQPYLNKL  
NYRRTDHEDPRVKKTA  
FQISMAKPR  
PNSAEESNGPIYAFENLRACEEAPP  
SAAHFRFYQIEGDRYDYNT  
VPFNEDDPM  
SWTEDYLA  
WW  
PKPM  
EFRACYIKV  
KIVGPLEVNVR  
SRNMGGTH  
RRRTVGKLY  
GIRDVR  
STRDRD  
QPNV  
AACLE  
F  
KCSGMLYDQDRV  
DRTL  
VKVI  
PQGS  
CRR  
RAS  
VN  
P  
N  
M  
L  
H  
EY  
LV  
NL  
PL  
AV  
NN  
DT  
SE  
Y  
T  
ML  
A  
PL  
D  
PL  
G  
HNYGIY  
TV  
TD  
QDP  
RTAKE  
IAL  
GRC  
FDGT  
SDG  
SSR  
IMK  
S  
NV  
G  
VAL  
T  
FNC  
VER  
Q  
V  
GR  
Q  
SAF  
Q  
Y  
L  
Q  
STPAQ  
SPAAG  
TV  
Q  
GR  
V  
P  
S  
RR  
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R  
A  
S  
RGG  
Q  
RG  
VV  
A  
SL  
RF  
P  
R  
V  
A  
QQ  
PL  
IN

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**FIGURE 413**

GCCACGTTGTCTTCTTCACCACCAACCCAGGAGCTCAGAGATCTAAGCTGCTTCCATC  
TTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGATGGGCCGCTCTTGCCCTTCTC  
ATCCTAAATCCCCCTCTCAGCTGATCAACCCGGGAGTACTCAGTGTCCCTAGACTCCGTT  
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG  
AAGCTCTCGTGTGCTAGTGTAAAAGCCAAGGCAGACCGTCCTGCCCTGCTGGATGGCT  
GTCACTGGCTGTGTTGGCTATGGCTGTGGATGTTAGCTGGAAACCACCTGC  
CACTGCCAGTGCAGTGTGGACTGGACCACTGCCGCTGCCACCTGACCTGACAGGGA  
GGAGGCTGAGAACTCAGTTTGACCATGACAGTAATGAAACCAGGGTCCAACCAAGAAAT  
CTAACTCAAACGTCCCACCCATTGTTCCATTGCTGATTCTGGGTAAATAAGACAAACTTT  
GTACCTCAAAAAAAAAAAAAAA

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**FIGURE 414**

MGPSCLLILIPLLQLINPGSTQCSLDVMDKKIKDVLSLEYSPSPISKLSCASVKS  
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

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**FIGURE 415**

CAGAAGAGGGGGCTAGCTAGCTGTCTGCGGACCAGGGAGACCCCCCGGCCCGGTGTG  
AGGC GG C CT ACAGGGCCGGGTGGCTGGCGAGCCGACGCCGGCGGAGGAGGCTGTGAGGA  
GTGTGGAACAGGACCCGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTGCC  
TGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGACAGAGATTCTATAAGATCTTGGGG  
TGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAAACTAGCCTGCAGCTTC  
ATCCC G ACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGTGCTGCTT  
ATGAGGTTCTGTCAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAAGGATTAA  
AAGATGGTCATCAGAGCTCCATGGAGACATTTTACACTTCTTGGGGATTTGGTTCA  
TGTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG  
ATCTAGAAGTCACTTGGAAGAAGTATATGCAGGAAATTGTGGAAGTAGTTAGAAACAAAC  
CTGTGGCAAGGCAGGCTCCTGGCAAACCGGAAGTGCACCGAATTGTCGGCAAGAGATGCCGACCC  
AGCTGGGCCCTGGCGCTTCAAATGACCCAGGAGGTGGCTGCGACGAATGCCCTAATGTCA  
AACTAGTGAATGAAGAACGAAACGCTGGAAGTAGAAATAGAGCCTGGGTGAGAGACGGCATGG  
AGTACCCCTTATTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGGAGATTACGGTTCC  
GAATCAAAGTTGTCAGCACCCAAATATTGAAAGGAGAGGAGATGATTGTACACAAATGTGA  
CAATCTCATTAGTTGAGTCAGTGGCTTGGGATGGGAGGAGATGATTGTACACAAATGTGA  
AGGTACATATTCGGGATAAGATCACCAAGGGCTTTGATAATCAGTGGGATGGTACACAAATGTGA  
GGCTCCCCAACTTGACAACAACAATATCAAGGGCTTTGATAATCAGTGGGATGGTACACAAATGTGA  
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT  
CAGTGCAGAAGGTATACAATGGACTGCAAGGGATTGAAGGTGAATAAAATTGGACTTTGTTT  
AAAATAAGTGAATAAGCGATATTATCTGCAAGGTTTTGTGTGTTTTGTTTA  
TTTCAATATGCAAGTTAGGCTTAATTTTTATCTAATGATCATGAAATGAATAAGAGG  
GCTTAAGAATTGTCATTGCAAGGGCTTGAGTTCAAGAATTAAAGCTGCAAGAGG  
TCCCTTGGGATTTAATGTCTGGTGCCTGAGTTCAAGAATTAAAGCTGCAAGAGG  
ACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGAGGTGTTAGCAATTCAATTCAAATG  
CCAAGTGGAGAAGTCTGTTAAATACATTGTTGTTATTGTTA

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**FIGURE 416**

MAPQNLSTFCLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYE  
VLSDSEKRKQYDTYGEEGLKDGHQSSHGDIFSHFFGDFGMFGGTPRQQDRNIPRGSDIIVDLEVTLEEVYAGNF  
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVVCDCECPNVKLVNEERTLEVEIEPGVRDGMEYPFI  
GEGEPEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFMEDITHLDGHKVHISRDKITRPGAKLW  
KKGEGLPNFDNNNIKGSLIITFDVDFPKEQILTEEARREGIKQLLKQGSVQKVYNGLQGY

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

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**FIGURE 417**

CGGCGGCGCTGCGGGCGCGAGGTGAGGGCGCGAGGTGAGGGCGCGAGGTCCCAGCAGGA  
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAAGAGAGGCCGGAGAGGGCCAGCCGCCGGCAG  
**GATGACCAAGGCCGGCTGTTCCGGCTGTGGCTGGTCTGGGTGGTGTTCATGATCCTGCT**  
GATCATCGTGTACTGGACAGCGCAGGCCGCCACTTCTACTTGCACACGTCTCTCTAG  
GCCGCACACGGGCCGCCGTGCCACGCCGGACAGGGACAGGGAGCTCACGGCGA  
CTCCGATGTCGACGAGTTCTGGACAAGTTCTCAGTGCTGGCGTAAGCAGAGCGACCTTCC  
CAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA  
CTGGTCCCCGCGCGACGCCCGCGCAGCCCAGACCAGGGCCGGCAGCAGGGAGCGAGGAG  
CGTGCTGCGGGCTTCTGCGCCAACCTCCAGCCTGGCTTCCCCACCAAGGAGCGCGATTGCA  
CGACATCCCCAACCTCGGAGCTGAGCCACCTGATCGTGGACGACCGGACGGGCATCTACTG  
CTACGTGCCAACGGTGGCCTGCAACCAACTGGAAGCGCGTATGATCGTGTGAGCGGAAGCCT  
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCGCGAGCACGTGACAACGC  
CAGCGCGACCTGACCTTACAACAAGTTCTGGCGCCGCTACGGGAAGCTCTCCGCCACCTCAT  
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTCGTGCACGACCCCTCGTGCCTGAT  
CTCCGCCCTCCGCAAGTTGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTGCCGTGCC  
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCGCCCTGGCGCGAGGCCTCCGCGC  
TGGCCTCAAGGTGCTTCCGCAACTTCATCCAGTACCTGCTGGACCCGACACGGAGAAGCT  
GGCGCCCTTCAACGAGCACTGGCGCAGGTGTACCGCCTCTGCCACCGTGCCAGATCGACTA  
CGACTTCGTGGGAAGCTGGAGACTCTGGACGAGGACGCCCGCAGCTGCTGCAGCTACTCCA  
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGAACAGGACGCCAGCAGCTGGAGGA  
GGACTGGTTGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCTGTATAAAACTCTACGAGGCCGA  
CTTTGTTCTCTCGGCTACCCCAAGCCGAAACCTCCTCCGAGAC**TGA**AAGCTTGCCTG  
CTTTTCTCGCGTGCCTGGAACCTGACGCACGCCACTCCAGTTTTATGACCTACGATT  
TGCAATCTGGCTTCTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT  
TTTAAGATTAATATATTCAAGGTATTAATACGA

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**FIGURE 418**

MTKARLFRLWLVLSVFMILLIIVYWDSAGAAHFYLHTFSRPTHGPPPLPTPGPDRDRELTAD  
SDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAERRS  
VLRGFCANSSLAFPTKERAFFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGL  
LHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPFVRLI  
SAFRSKFELENEEFYRKFAVPMRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDPHTEKL  
APFNEHWQRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRTASSWEE  
DWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

**Important features:****Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

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**FIGURE 419**

GGCACGAGGCTGAACCCAGCCGGCTCATCTCAGCTCTGGTTCTAAGTCCATGTGCCAAAG  
GCTGCCAGGAAGGAGACGCCCTCCTGAGTCCTGGATCTTCTTCCTCTGGAAATCTTGACT  
GTGGGTAGTTATTCTGAATAAGAGCGTCCACGCATTGGACCTCGCGGACTGCTGA  
AGTCTCAGTCCGTGCCACCTGGCTTCTGCTACGTCTTATTGCCCTCAGGGCTAACATCA  
ACACCATTCACTCTCCTCTGGCCATTAAACAAGCAGCTTCCGGAAGATCA  
ACTGCAGACTGCTCTATTGCATCTCAAGCCAGCTGGTATGCTGCTGGAGTGGTGGTCGGCA  
CGGAATGCACCCTTCACGGACCCGCGCGCTACCTCAAGTATGGAAAGGAAAATGCCATCG  
TGGTTCTCAACCACAAGTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGAACGCTTG  
GGCTGTTAGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCTATGTCCAATTATCGGCT  
GGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGAGCAGGATCGCAAGACGG  
TTGCCACCAGTTGCAGCACCTCCGGACTACCCCGAGAAGTATTTTCTGATTCACTGTG  
AGGGCACACGGTTCACGGAGAAGAACATGAGATCAGCATGCAGGTGGCCCGGGCAAGGGG  
TGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGCTCGCCATCACCGTGAGGAGCT  
TGAGAAATGTAGTTCAGCTGTATATGACTGTACACTCAATTCAAGAAATAATGAAAATCCAA  
CACTGCTGGAGTCCTAACGAAAGAAATACCATGCAGATTGTATGTTAGGAGGATCCCAC  
TGGAAAGACATCCCTGAAGACGATGACCGAGTGCTCGGCTGGCTGCACAAGCTTACCAAGGAGA  
AGGATGCCCTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGAGACGCCATGGTGGCC  
CCCGGGGCCCTGGACCCCTCGTAAGTGGCTGTTGGCCTCGCTGGTGTCTACCCCTTCT  
TCCAGTCCCTGGTCAGCATGATCAGGAGCGGTCTCCCTGACGCTGCCAGCTTCATCCCG  
TCTTCTTGTGGCCTCCGTGGAGTTCGATGGATGATTGGTGTGACGGAAATTGACAAGGGCT  
CTGCCTACGGCAACTCTGACAGCAAGCAGAAACTGAATGACTTGACTCAGGGAGGTGTCACCAT  
CCGAAGGAAACCTGGGAACTGGTGGCCTCGCATATCCTCCTTAGTGGACACGGTGACAA  
AGGCTGGGTGAGCCCTGCTGGCACGGCGGAAGTCACGACCTCTCCAGCCAGGGAGTCTGGT  
CTCAAGGCCGGATGGGAGGAAGATGTTGTAATCTTTTCCCCATGTGCTTAGTGGC  
TTTGGTTTCTTTGTGCGAGTGTGTGAGAATGGCTGTGTGGTGAAGTGTGAACCTTGTTC  
TGTGATCATAGAAAGGGTATTTAGGCTGCAGGGAGGGCAGGGCTGGGACCGAAGGGGACA  
AGTTCCCCTTCATCCTTGGTGCTGAGTTCTGTAACCCCTGGTGCAGAGATAAGTGA  
AAAGTCTTGTAGGTGAGATGACTAAATTATGCCTCCAAGAAAAAAATTAAAGTGTCTTCT  
GGGTCAAAAAAAAAAA

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**FIGURE 420**

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWINKQLFRKINCRLSYCISSQLVM  
LLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGGSKVLAKKEL  
AYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHEISM  
QVARAKGLPRLKHLLPRTKGFAITVRSLRNVSAYDCTLNFRNNENPTLLGVNLNGKKYHAD  
LYVRRIPLEDIPEDDDECASAWLHKLYQEKDAFQEYYRTGFPETPMVPPRRPWTLVNWLFWA  
SLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDSKQKLND

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**FIGURE 421**

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGCGGACGCGTGGCTGGGTGCCTGCATC  
GCCATGGACACCACCAGGTACAGCAAGTGGGGCGCAGCTCCGAGGAGGTCCCCGGAGGGCCC  
TGGGGACGCTGGGTGACTGGAGCAGGAGACCCCTTTCTTGGCCCTGGCTGTCCTGGTCACC  
ACAGTCCTTGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGCG  
CTGCTTGACGCCACGACCTGCTGAGGACAAACGCCCTGAAGCAGACGGCGCGCTGGGTGCC  
CTGAAGGAGGAGGTCGGAGACTGCCACAGCTGCTGCTGGGACGCAGGCGCAGCTGCAGACC  
ACGCGCGCGAGCTTGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCTGCAGGAA  
CTGCGTGAGCGCGTGACCCAGGGCTGGCTGAAGCCGGCAGGGCCGTGAGGACGTCCGACT  
GAGCTGTTCCGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCGTGCCACG  
TCGTGGCTGTCCTCGAGGGCTCTGCTACTTTCTGTGCCAAAGACGACGTGGCGCG  
GCGCAGGATCACTGCGCAGATGCCAGCGCACCTGGTGATCGTTGGGGCCTGGATGAGCAG  
GGCTTCCACTCGAACACCGCGTGGCGTGGTTACTGGCTGGCCCTGAGGGCTGTGCCAT  
CTGGGCAAGGTCAGGGTCTACCGAGTGGGTGGACGGAGTCTCTCAGCTTCAGCCACTGGAAC  
CAGGGAGAGCCAAATGACGCTTGGGGCGCGAGAACTGTGTCATGATGCTGCACACGGGCTG  
TGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAGAAAAGGCACAACG  
TGAACCCGCCAGTGCCCTGGAGCCGCCATTGCAAGCATGTCGTATCCTGGGGCTGCTCA  
CCTCCCTGGCTCTGGAGCTGATTGCCAAAGAGTTTTCTTCCTCATCCACCGCTGCTGAG  
TCTCAGAAACACTGGCCAAACATAGCCCTGTCAGCCAGTGCCTGGCTCTGGACCTCCA  
TGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAACCTCCACTAGCTCCAAATCC  
CTGCTCTGCGTCCCCGTGATATGCCCTCACTTCTCCCTAACCAAGGTTAGGTGACTGAGG  
ACTGGAGCTGTTGGTTCTCGCATTTCACCAAAGCTGGAGCTGTTTGAGCCTGAGG  
AAGCATCAATAAATATTGAGAAATGAAAAAA

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**FIGURE 422**

MDTTRYSKWGGSEEVPGGPWGRVHWSSRRPLFLALAVLVTTLWAVILSILLSKASTERAAL  
LDGHDLRLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALREL  
RERVTQGLAEAGRGRREDVRTELFRALEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTWAAA  
QDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFSHWNQ  
GEPNDAWGRENCVMMHLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:****Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

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**FIGURE 423**

CGGCCGCCAGGCGTAGGCAGGGTGGCCCTTGCCTCCCCTCCTGAAAAACCCGGCGGGC  
GAGCGAGGCTGCGGGCGCCGCTGCCCTCCCCACACTCCCCGCCAGAACGCGCTCGCTCGGC  
GCCCAACATGGCGGGTGGCGCTGCCGCCGAGCTAACGGCGCTCGCCGCCCTGGATCGC  
GGCTGTGGCGCGACGGCAGGCCAGGAGGGCAGCTGCCGCCAGCACAGCCGGTCCA  
GCCCATGACCGCCTCCAACGGACGCTGGTGATGGAGGGCAGTGAAATTTCACGC  
CCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAAGAATGGGAGGCTTTGAAAGAATGGTGA  
AATACTTCAGATCAGTGTGGGAAGGGTAGATGTCATTCAAAGAACCAGGTTGAGTGGCCGCTT  
CTTGTCAACCACCTCTCCAGCATTTTATGCAAAGGATGGGATATTCCGCCGTATCGTGG  
CCCAGGAATCTCGAAGACCTGCAGAAATTATCTTAGAGAAGAAATGGCAATCAGTCGAGCC  
TCTGACTGGCTGGAAATCCCCAGCTCTCAACGATGTCGGAATGGCTGGCTTTTAGCAT  
CTCTGCCAAGATATGGCATCTTCACAACATTTCACAGTGACTCTTGGAAATTCTGCTTGGT  
TTCTTATGTGTTTCTGTCATAGCCACCTGGTTTTGGCTTTATGGGCTGGTCTGGT  
GGTAATATCAGAATGTTCTATGTGCCACTTCCAAGGCATTATCTGAGCGTTCTGAGCAGAA  
TCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGAGGATGCGGAGGAGGAGGAGGAAAGATGA  
TTCAAATGAAGAAGAAAACAAAGACAGCCTTGAGATGATGAAGAAAGAGAAAGATCTGG  
CGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTGCTGGTGGATGAGGA  
GAGAAGTGGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTGACCCGGGAGGAAGTGA  
GCCTGAGGAGGCTGAAGAAGGCATCTGAGCAACCCTGCCAGCTGACACAGAGGTGGTGA  
AGACTCCTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGACTGTAGATTAAATGATGCGT  
TTCAAGAATACACACAAAACAATATGTCAGCTCCCTTGGCCTGCAGTTGTACCAAATC  
CTTAATTTCCTGAATGAGCAAGCTCTCTAAAGATGCTCTAGTCATTGGTCTCATG  
GCAGTAAGCCTCATGTATACTAAGGAGAGTCTCAGGTGTGACAATCAGGATATAGAAAAAC  
AAACGTAGTGTGGGATCTGTTGGAGACTGGGATGGGACAAGTTCATTTACTTAGGGTCA  
GAGAGTCTGACCCAGAGGAGGCCATTCCAGTCTAATCAGCACCTCCAGAGACAAGGCTGC  
AGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTGGCTCTGAGCATCCCCAAAGTGTAAACGT  
AGAAGCCTGCACTCTTCTGTAAAGTATTATTTGTCAAATGAGGAAACATCAG  
GCACCCACAGTGCATGAAAATCTTCACAGCTAGAAATTGAAAGGGCTTGGGTATAGAGAGC  
AGCTCAGAAGTCATCCCAGCCCTCTGAATCTCTGTCTATGTTTATTCTTACCTTAATT  
TTTCCAGCATTCCACCATGGCATTAGGCTCTCCACACTCTTCACTATTATCTGGTCA  
GAGGACTCCAATAACAGCCAGGTTACATGAACTGTGTTGTCATTCTGACCTAAGGGTTT  
AGATAATCAGTAACCATAACCCCTGAAGCTGTGACTGCCAACATCTCAAATGAAATGTTGT  
GCCATCAGAGACTCAAAAGAAGTAAGGATTTACAAGACAGATTAAGGAAATTGTTTGT  
CCAAAATATAGTTGTTGATTTTTTAAGTTCTAAGCAATTTCAAGCCAGAAG  
TCCTCTAAAGTCTGCCAGTACAAGGTAGTCTGTGAAGAAAAGTTGAATACTGTTTGT  
ATCTCAAGGGTCCCTGGCTTGAACTACTTTAATAACTAAAAACACTCTGATT  
TCCTTCAGTGTGCTTTGGTGAAGAATTATGAACTCCAGTACCTGAAAGTGAAGAGATT  
TGATTTGTTCCATCTCTGTAATCTTCAAAGAATTATCTTGAAATCTCAACT  
CAATCTACTGTAAGTACCCAGGGAGGCTAATTCTT

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**FIGURE 424**

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMGEWMLKFYAPW  
CPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPLSGRFFVTTLPAFFHAKDGIFRRYRGPG  
IFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAWCSY  
VFFVIATLVFGLFMGLVLVVISECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEKDDSN  
EEENKDSLVDDEEEKEDEAEEEEEDNLAAGVDEERSEANDQGPPGEDGVTRREEVEPE  
EAEEGISEQPCPADTEVVVEDSLRQRKSQHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins. (homologous region to disulfide isomerase)**

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

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**FIGURE 425**

GAGGAACCTACCGTACCGCCGCGCTGGTAGTCGCCGTGTGGCTGCACCTCACCAATCCGTGCGCCGCG  
 CTGGGCCGTCGGAGAGTCGCTGCTCTCCTGCACGCCGCTGGCTGCCAGGCGGGTCCGCCGCCA  
 GGGTTGAGGATGGGGAGTAGCTACAGGAAGCAGCACCAGGGATGCCAAGGTATTTTGTTGGAATGAAAAGGA  
 AGTATTAGAAATGAGCTGAAGACCATTACAGATAATTTTGGGAGAGATTTGTGATGTTGATTCAACCT  
 TGAAGTAATGTAGACAGAAGTCTCAAATTGATATTACATCAACTGGAACCCAGCAGTGAATCTTAATGTTCAC  
 TTAAATCAGAACTTGATAAGAAAGAGAATGGAGCTGGTAAATAAGATGACTATATCAGAGACTTGAAGAAG  
 GATCATTCTGTGTTCTGATAGTGTATGGCATTAGGGCACAGATCAGGATTTACAGTTACTGG  
 AGTGTCCAAAAGTCAAGCAGTAGAGAAATAAGACAAGCTTCAGAAATTGGCATTGAAAGTACATCTGATAA  
 AAACCCGAAATAACCCAAATGCACATGGCATTAAAAAAATAAGAGCATATGAAGTACTCAAAGATGAAGA  
 TCTACGGAAAAAGTATGACAAATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
 CTATTATCGTTATGATTGGTATTATGATGATGATCCTGAAATCAACATTGAAAGAAGAGAATTGATGC  
 TGCTGTTAATTCTGGAGAACTGTGGTTGTAATTTACTCCCCAGGCTTCAACTGCCATGATTTAGCTCC  
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTTACTCGAATTGGAGCTTAAGTGTGATGATAAAT  
 GCTTGGCGAATGAAAGGAGTCACAGCTATCCCAGTCTTCATTTCCGGCTGGAATGGGCCCAGTGAATA  
 TCATGGAGACAGATAAGGAGACTTGTAGTGTAGTTGAGCTTGCAGCATGTTAGAAGTACAGTGACAGAACTTG  
 GACAGGAAATTGGTCAACTCCATACAAACTGCTTTGCTGCTGTATTGGCTGGCTGATCAGTTTGTTCAAA  
 AGGAGGAGATTGTTGACTTCACAGACAGCTCAGGCTAGTGCATGTTCTCAACTCATTGGATGCTAA  
 AGAAATATATTGGAAGTAATACATAATCTTCAGATTTGAAACTACTTCGGAAACACACTAGAGGATCGTT  
 GGCTCATCATCGTGGCTGTTATTTTCATTTGGAAAAAAATGAAATTCAGATCTGAGCTGAAAAACT  
 AAAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTGACTGTTCTGACCAGACATCTGAGTAA  
 TCTGTATGTTTCAGCGTCTAGCAGTATTTAAAGGACAAGGAAACAAAGAATGAAATTCATCATGGAAA  
 GAAGATTCTATGATATACTTCCTTGGCAAAGAAAGTGTGAATTCTCATGTTACACGCTGGACCTCAAA  
 TTTCTGCCAATGACAAAGAACATGGCTGTTGATTCTTGGCCACCAGTGTGAGCTTACT  
 ACCAGAGTTACGAAGGACATCAATTCTTATGGTCGCTTAAGTTGGTACACTAGATTGATCAGTTCATGA  
 GGGACTCTGTAACATGTATAACATTCAAGCTTACAGCTTACAAACAGTGGTATTCAACAGTCCAACATTCTGAGTA  
 TGAAGGACATCACTCTGCTGAACAAATCTGGAGTTCATAGAGGATCTTGAATCTCAGTGGTCTCCCTTAC  
 ACCCACCCACCTCAACGAACATGTTACACAAAGAAACACAACGAAGTCTGGATGGTGTATTCTCCGTG  
 GTGTCATCTTGGCAAGTCTTAATGCCAGAATGGAAAAGATGGCCGGACATTAACAGTGTGATCAACGTGG  
 CAGTATAGATTGCCAACAGTATCATTCTTTGTGCCAGGAAACGTTCAAAGATAACCTGAGATAAGATT  
 TCCCCCAAAATCAAAAGCTTACAGTACAGTTACAATGGTGAATAGGGATGTTATTCCCTGAGAAT  
 CTGGGGCTAGGATTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTCAGTGAAGAAGTCTACAAGG  
 GAAAATCATGGGTGATTGATTCTATGCTCTTGGTGGACCTTGCAGGAAATTGCTCCAGAATTGAGCT  
 CTTGGCTAGGATGATAAAGGAAAGTGAAGCTGGAAAAGTAGACTCTCAGGCTTATGCTCAGACATGCCAGAA  
 AGCTGGGATCAGGCTATCCAACGTGTTAAGTTTATTCAGAAAGGACAAGGAAATTTCAGAAGAGACA  
 GATAAAATACCAAGAGATGCAAAGAACATCGTCGCTTAATAACTGAAAATGGAAACTCTCCGAAATCAAGGCAA  
 GAGGAATAAGGATGAACTTTGATAATGTTGAAGATGAAGAAAAGTTAAAAGAAATTCTGACAGATGACATCAG  
 AAGACACCTATTAGAATGTTACATTATGATGGGAATGAATGAACATTCTTAGACTTGCAAGTTGACTGCCA  
 GAATTATCTACAGCACTGGTAAAGAAGGCTGCAAACATTGTAAGGGCGTTATAAATATT  
 GACTTTGCCAGGCTATAATATGGTACACATGAGAACAGAATAGAGTCATCATGTTATTCTGTTATTGCT  
 TTTAACACCTTAAAAAATATTAAAACGATTCTAGCTCAGGCCATACAAAGTAGGCTGGATTCTAGTCCATG  
 GACCATAGATTGCTGCCCCCTCGACGGACTTATAATGTTCAGGTGGCTGGTGAACATGAGTCTGCTGCT  
 ATCTACATAATGTCTAAGTTGATAAAAGTCCACTTCCCTCACGTTTTGGCTGACCTGAAAAGAGGTAAC  
 TAGTTTGGTCACTTGTCTCTAAAGTCTGTTAGTTGCTGATCATCCAGGAAACCTGAGGGAAAAAATTA  
 GATGTTGACAGTAAACAAACCCGTTATGCTGTTAGTTGAGGAGATTCTCATTGTTCTTCCCTCTCA  
 AAGGGTGAAGAAAATGCTTTAATTTCACAGCCGAGAAACAGTGCAGCAGTATGTCACACAGTAAGTACAC  
 AAATTGAGAACAGTAAGTCACAAATTCTGTTAGTTGCTGATCATCCAGGAAACCTGAGGGAAAAAATTA  
 TAGCAATTAACTGGGCAATTGAGTATCTAAATATGTTATCAAGTATTAGAGTTCTATATTAAAGATATA  
 TGTGTTCATGTTCTGAAATTGCTTCTAGAAATTCTCCACTGATAGTTGATTTTGAGGCATCTAATAT  
 TTACATATTGCTCTGAACTTGTGTTGACCTGTTATCCTTATTACATTGGGTTTTCTTCTCATAGTTG  
 TTTTCACTCCCTGTCAGTCTATTATTACAAATAGGAAAATTACTTACAGGTTGTTACTGTAGCTTAT  
 AATGATACTGTAGTTATTCCAGTTACTAGTTACTGTCAGGGCTGCCCTTCTAGATAAAATATTGACATAATA  
 ACTGAAGTATTAAAGAAAATCAAGTATATAAACTAGGAAAGGATCTCTAGTTCTGTTAGTTAATCAGAGTGT  
 ACAGAATGGTAAAAAATTCTAAAGAATCAGTAACTGTTAGTTAGTTAATCAGAGTGTACAGAATGGTAAAAAATT  
 CCAATCAGTCAAAAGAGGTCATGAATTAAAGGCTTGCACATTTCAAAAA

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**FIGURE 426**

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKLHPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGIYDDDEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTRDFAKEVDGLLRIGAVNCDDRMLCRMKGVNNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNSIQTAFAAGIGWLITFCSKGGDC LTSQTRLRLSGMLFLNSDAKEIYLEVIHNLPDFELLSANTLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLKNDHIQVGRFDCCSAPDICSNLVVFQPSLAVFKGQGTKEYEIHHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFAPWCPCRALLPELRRASNLLYQQLKF GTLDCTVHEGLCNMYNIQAYPTTVFNQSNIHEYEGHHSAEQILEFIEDLMNPSVSVSLTPPTTFNELVTQRKHNEWMVDFYSPWCHPCQVLMPEWKRMA RTLTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPKSNKAYQYHSYNGWNRDAYSRLI WGLGFLPVSTDLTPQTFS EKV LQGKNHWVIDFYAPWCGPCQNFAPEFELLARMIKGKV KAGKVDCQAYA QTCQKAGIRAYPTVKFYFYERAKRN FQEEQINTRDAKAIAALISEKLETLRNQGKR NKDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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**FIGURE 427**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGACCCCTGACTCTGCAGCGAACCGGCA  
CGGTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCACTTCTCTTCTCCCTCTGA  
GTCCTCTGAGATGATGGCTCTGGGCCAGCGGGAGCTACCCGGGTCTTGTGCGATGGTAG  
CGGCAGCTCTGGCGGCCACCCCTGCTGGGAGTGAGGCCACCTGAACCTGGTCTCAATT  
CCAACGCTATCAAGAACCTGCCCCACCGCTGGCGCTGCGGGCACCCAGGCTCTGAG  
TCAGCGCCGCAGGGAACTCTGTACCCGGGGATAAGTACCAAGACCATTGACAACCTACC  
AGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGTCCCACCC  
GCGGAGGGGACCGCAGGCGTCAAATCTGCTGCCCTGCAGGAAGGCCGAAACGCTGCATGC  
GTCACGCTATGTGCTGCCCGGGAAATTACTGCAAAAATGGAATATGTGTCTTGTGATCAA  
ATCATTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTGGTAATGATCATAGCACCT  
TGGATGGTATTCCAGAAGAACCAACCTTGTCTTCAAAATGTATCACACCAAAGGACAAGAAG  
GTTCTGTTGTCTCCGGTCATCAGACTGTGCCCTCAGGATTGTGTTGCTAGACACTTCTGGT  
CCAAGATCTGTAACCTGCTCTGAAAGAAGGTCAAGTGTGACCAAGCATAGGAGAAAGGCT  
CTCATGGACTAGAAATATTCCAGCGTTACTGTGGAGAAGGTCTGTCTGCCGGATACAGA  
AAGATCACCACATCAAGCCAGTAATTCTCTAGGCTCACACTGTCAGAGACACTAAACAGCT  
ATCCAATGCAGTGAACCTCTTATATAATAGATGCTATGAAAACCTTTATGACCTTCATC  
AACTCAATCTAAGGATATAAGTTCTGTGGTTCAAGTTAACGATCCAATAACACCTTCCA  
AAACCTGGAGTGTAAAGAGCTTGTCTTATGGAACCTCCCTGTGATTGAGTAAATTACT  
GTATTGTAATTCTCAGTGTGGCACTTACCTGAAATGCAATGAAACTTTAATTATTTCT  
AAAGGTGCTGCACTGCCTATTTCTTGTATGAAATTGGTACACATTGATTGTTAT  
CTTGACTGACAAATATTCTATATTGAAACTGAAGTAAATCATTCAAGCTTATAGTTCTAAAAG  
CATAACCTTACCCATTAAATTCTAGAGTCTAGAACGCAAGGATCTTGGAAATGACAAAT  
GATAGGTACCTAAATGTAACATGAAAATACTAGCTTATTTCTGAAATGTAATCTTAAATG  
CTTAAATTATATTCCCTTAGGCTGTGATAGTTTGAAATAAAATTAAACATTAAAAAA  
AAAAAA

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**FIGURE 428**

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSAA  
PGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRKRCMRHAM  
CCPGNYCKNGICVSSDQNHFREGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEGSVC  
LRSSDCASGLCCARHFWSKICKPVLKEGQVCTKRRKGSHGLEIFQRCYCCEGLSCRIQKDHH  
QASNSSRLHTCQRH

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

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**FIGURE 429**

GAGAGGGACGAGGTGCCGCTGCCCTGGAGAACCTCCCGCTGCCGTGGCTCCGGAGCCCAGCCC  
TTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCAGCGCCTGTCACGGACCC  
CAGCGTTACCATGCATCCTGCCGTCTCCTATCCTAACCGACCTCAGATGCTCCCTCTGCT  
CCTGGTAACTGGGTTTTACTCCTGTAACAACAGAAATAACAAGTCTTGCTACAGAGAAATAT  
AGATGAAATTAAACAATGCTGATGTTGCTTAGTAAATTTATGCTGACTGGTGTGCTT  
CACTCAGATGTTGCATCCAATTTGAGGAAGCTCCGATGTCATTAAGGAAGAATTCCAAA  
TGAAAATCAAGTAGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATA  
CAGGATAAGCAAATACCCAACCCCTCAAATTGTTGTAATGGGATGATGATGAAGAGAGAATA  
CAGGGGTCA CGCATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAGTGACCCAT  
TCAAGAAATTGGGACTTAGCAGAAATCACCCTTGATCGCAGCAAAGAAATATCATTGG  
ATATTTGAGCAAAGGACTCGGACAACATAGAGTTTGAAACGAGTAGCGAATATTTGCA  
TGATGACTGTGCCTTCTTCATGGGATGTTCAAAACCGGAAAGATATAGTGGCGA  
CAACATAATCTACAAACCACCAAGGGCATTCTGCTCCGGATATGGTGTACTTGGGAGCTATGAC  
AAATTTGATGTGACTTACAATTGGATTCAAGATAATGTGTTCTCTTGCCGAGAAATAAC  
ATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTCTCATACTTTCACATGAA  
AGAAGATAACAGAAAGTTAGAAATATTCCAGAACATGAAGTAGCTCGGAATTAAAGTAAAAA  
AGGTACAATAAACTTTTACATGCCGATTGTGACAAATTAGACATCCTCTGCAACATACA  
GAAAACCTCCAGCAGATTGCTCTGTAATCGTATTGACAGCTTAGGCATATGTATGTGTTGG  
AGACTTCAAAGATGTATTAATTCCCTGGAAAACCTCAAGCAATTGTATTGACTTACATTCTGG  
AAAACCTGCACAGAGAAATTCCATCATGGACCTGACCCAACTGATAACAGCCCCAGGAGAGCAAGC  
CCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTCCAGAAACTAGCACCCAGTGAATATAG  
GTATACTCTATTGAGGGATCGAGATGAGCTTTAAAACTTGAAAACAGTTGTAAGCCTTTC  
AACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTATATTTCATATTCTATGTGTAT  
TTTATTTGAATAAACAGAAAGAAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAA

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**FIGURE 430**

MHPAVFLSLPDLCRCSLLLLTVWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRCFSQM  
LHPIFEEASDVIKEEFPNENQVVFARVDCDQHSIAQRYRISKYPTLKLFRNGMMMKREYRGQ  
RSVKALADYIRQQKSDPIQEIRDIAETTLDRSKRNIIGYFEQKDSNDNYRVFERVANILHDDC  
AFLSAFGDVSKPERYSGDNIIFYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREITFEN  
GEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLHIQKTP  
ADCPVIAIDSFRHMYVFGDFKDVLIPGKLQFVFDLHSGKLHREFHHGPDPDTAPGEQAQDV  
ASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:****Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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**FIGURE 431**

GAGCAGGACGGAGCC**ATGG**ACCCCCGCCAGGAAGCAGGTGCCAGGCCATGATCTGGACTGCA  
GGCTGGCTGCTGCTGCTGCTGCTCGCGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCGTG  
CAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGCGTG  
GACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGCAGTG  
CGGGGTTGCGGTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTCACGGGTTCTG  
GCGTTCATCCAGCTGCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTAACCTCACCTCG  
CGGGCGCTCGACCCGGCAGGTAATGAGAGTGCAATACCCGCCAACGGCGTGGAGTGCTACAGC  
TGTGTGGGCCTGAGCCGGGAGGCCTGCCAGGGTACATGCCGCCGGTCGTGAGCTGCTACAAC  
GCCAGCGATCATGTCTACAAGGGCTGCTTGACGGCAACGTCACCTGACGGCAGCTAATGTG  
ACTGTGTCCCTGCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGATGGAGTAACA  
GGCCCAGGGTTCACGCTCAGTGGCTCTGTTGCCAGGGTCCCGCTGTAACTCTGACCTCCGC  
AACAAAGACCTACTTCTCCCCTCGAATCCCACCCCTGTCCGGCTGCCCTCCAGAGCCCACG  
ACTGTGGCCTCAACCACATCTGTCACCACATTCTACCTCGCCCCAGTGAGACCCACATCCACC  
ACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAGAACACAGGAGCCTCC  
CGGGATGAGGAGGCCAGGTTGACTGGAGGCGCCGCTGCCACCAGGACCGCAGCAATTCAAGGG  
CAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAAGGCTGTGGCTCCACAGCT  
GGATTGGCAGCCCTCTGTTGCCGTGGCTGCTGGTGTCTACTG**TGA**GCTTCTCCACCTGGA  
AATTCCCTCTCACCTACTTCTCTGCCCTGGTACCCCTCTCATCACCTCCTGTTCCA  
CCACTGGACTGGCTGCCAGCCCCCTGTTTCAACATTCCCAGTATCCCCAGCTTCTGC  
TGCCTGGTTGGCTTTGGAAATAAAATACCGTTGATATATTCTGCCAGGGTGTCTA  
GCTTTTGAGGACAGCTCCTGTATCCTCTCATCCTGTCCTCCGCTGTCCCTTGTGATG  
TTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGAAGGTGAGAGAGAGGATGCTAAGCTCC  
TACTCACTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGGGTGGGACAATGGCTCCCC  
ACTCTAACGACTGCCCTCCCTACTCCCCCATCTTGGGAATCGGTTCCCCATATGTCTCC  
TTACTAGACTGTGAGCTCCTCGAGGGGGGCCGGTACCCAATTGCCCTATAGTGAGTCGTA

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**FIGURE 432**

MDPARKAGAQAMIWTAGWLLLLLRLGGAQALECYSCVQKADDGSPNKMKTVCAPGVDVCTE  
AVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRALDP  
AGNESAYPPNGVECYSCVGLSREACQGTSPPVSCYNASDHVYKGCFDGNVTLTAANVTVSLP  
VRGCVQDEFCTRDRGVTGPGFTLSGCCQGSRCNSDLRNKYFSPRIPLVRLPPPPEPTTVAST  
TSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGVEHEASRDEEPRLTGGAAGHQDRNSNSQYPAK  
GGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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**FIGURE 433**

CGGGACTCGGCGGGCCTCCTGGGAGTCTCGGAGGGACCGGCTGTGCAGACGCCATGGAGTT  
GGTGCCTGGTCTTCCTCTGCAGCCTGCTGGCCCCATGGCCTGCCAGTGCAGCTGAAAAGGA  
GAAGGAAATGGACCCTTTCATTATGATTACCAAGACCCCTGAGGATTGGGGACTGGTGTGCG  
TGTGGCCTCTCTCGGTTGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTTCAA  
TCAGAACGCCCCGGGCCCCCAGGAGATGAGGAAGCCCAGGTGGAGAACCTCATCACGCCAATGC  
AACAGAGCCCCAGAACGAGAGAACTGAAGTCAGCCATCAGGTGGAAGCCTCTGGAACCTGAG  
GCGGCTGCTTGAACCTTGGATGCAAATGTCGATGCTTAAAAAACCGGCCACTTCAGCAACA  
GCCCTTCCCCAGGAGAACGCAAGAACCTGTGTGCCCCCACCCTATCCCCTTAACACCAATT  
CCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCCCTGCCAACCTC  
CCGTGATGTGTGTGTGTGTGTGACTGTGTGTTGCTAACTGTGGTCTTGTGG  
CTACTTGTGGATGGTATTGTGTTGTTAGTGAACGTGGACTCGCTTCCCAGGCAGGG  
GCTGAGCCACATGGCATCTGCTCCTCCCTGCCCGTGGCCCTCCATCACCTCTGCTCCTA  
GGAGGCTGCTTGTGCCCCGAGACCAGCCCCCTCCCTGATTAGGGATGCGTAGGGTAAGAGC  
ACGGGCAGTGGTCTTCAGTCGTCTGGGACCTGGGAAGGTTGCAGCACTTGTCACTATTCT  
TCATGGACTCCTTCACTCCTTAACAAAAACCTTGCTCCTTATCCCACCTGATCCCAGTCT  
GAAGGTCTCTAGCAACTGGAGATAAAAGCAAGGAGCTGGTGAGCCCAGCGTTGACGTCAAG  
CAGGCTATGCCCTCCGTGGTTAATTCTCCAGGGCTCCACGAGGAGTCCCCATCTGCC  
CCGCCCTTCACAGAGGCCGGGATTCCAGGCCAGGGCTCTACTCTGCCCTGGGAAT  
GTGTCCCTGCATATCTCTCAGCAATAACTCCATGGCTCTGGGACCCCTACCCCTCCAACC  
TTCCCTGCTCTGAGACTCAATCTACAGCCCAGCTCATCCAGATGCAGACTACAGTCCCTGC  
AATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCCGTTGGGCCAGCACACCGGGA  
TGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTGCCTACGTCCCTAGATGGCAGCAGAG  
GCAACTCCGCATCCTTGCTCTGCCTGCGTGGTCAGAGCGGTGAGCGAGGTGGTTGGAG  
ACTCAGCAGGCTCCGTGCAGCCCTGGAACAGTGAAGGTTGAAGGTCAAAACGAGAGTGGG  
AACTCAACCCAGATCCC GCCCTCCTGCTCTGTGTTCCCGCGAAACCAACCAACCGTGC  
GCTGTGACCCATTGCTGTTCTGTATCGTATCCTCAACAAACAACAGAAAAAGGAAT  
AAAATATCCTTGTTCCT

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**FIGURE 434**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHODYQTLRIGGLVFAVVLFSVGILLILSRRCKC  
SFNQKPRAPGDEEAQVENLITANATEPQKQRTEVQPSGGSLWNLRRLLEPLDANVDA

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**FIGURE 435**

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTCTGTGCCTCCGCTTGTCTCCTGC  
TGTCCGGCTGGTCCCAGGGCTGGCGAGCCGACCCCTCACTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTAGCAGACCTGGACCACGGTGGTGTGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTGCCCTGGGGAGAAACTAA  
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTAGCTGGAGAATTACACACCCAGGAACCCCTCACCTGCAGGCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCACTTCGATG  
GGCAGATCTCCTCCTCTTGACTCAGAGAAGAGAATGTGGACAACGGTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCATGTCCTCCATTACTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCACCGCCATGTCCTCAGGCACAACCCACTCAGGCCACAGCCACCC  
TCATCCTTGCTGCCTCCTCATCATCCTCCCTGCTCATCCTCCCTGGCATCTGAGGAGAGT  
CCTTAGAGTGACAGGTTAAAGCTGATACAAAAGGCTCCTGTGAGCACGGCTTGATCAAAC  
TCGCCCTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGTGGCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTGATTCCCTTGCAACAATTAA  
CCAGCAGTTACACATATTATGCAATTTCCTTGTGCTACCTGATGGAATTCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTCCTTCTCTTTGGAAAAA  
TCAAGTACTTCTTGATGATCTTCTTGAAATGATATTGTCAGTAAATAATCACG  
TTAGACTTCAGACCTCTGGGATTCTTCCGTGCTGAAAGAGAATTAAATTATTAAT  
AAGAAAAAATTATTAATGATTGTTCTTAGTAATTATTGTTCTGTACTGATATTAA  
ATAAAAGAGTTCTATTCCCCAAAAAAAAAAAAAA

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**FIGURE 436**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF LH  
YDCGNKTVTVPSPGLGKKLNVT TAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
CEQKAEGHSSGSWQFSFDQI FLLFDSEKRMWTTVHPGARKMKEKWENDKV VAMSFH YFSMGD  
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGT TQLRATATT LILCCLLII LPCFILPGI

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**FIGURE 437**

GTTCTCCTTCCGAGCCAAAATCCCAGGCATGGTGAATTATGAACGTGCCACACCATGAAGCTTGTGGCAGG  
TAACTGTGCACCACACACCTGGAATGCCATCCTGCTCCGTTCTACCTCACGGCGCAAGTGTGGATTCTGT  
GTGCAGGCCATCGCTGCTGCCGCTCAGCCGGGCCAGAACTGCCCTCCGTTGCTCGCAGTAACCAGTTCA  
GCAAGGTGGTGTGCACGCCGGGCCCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACC  
TCATGGAGAACACATCCAGATGATCCAGGGCGACACCTCCGCCACCTCCACCGAGGTCTGCAGTTGG  
GCAGGAACACTCCATCCGGCAGATTGAGGTGGGGCCTTCACAGGCCCTGCCAGCCTAACACCCGGTGGAGCTGTTCG  
ACAACAGCTGACAGTCATCCCTAGCGGGGCCCTTGAAATACCTGTCCAAGCTGGGGAGCTCTGGCTTCGAACA  
ACCCCCATCGAAAGCATCCCTCTTACGCCCTCAACCGGGTGCCTCCCTCATGCCCTGGACTTGGGGAGCTCA  
AGAAGCTGGAGTATATCTGAGGGAGCTTTGAGGGCTGTTCAACCTCAAGTATCTGAACCTGGGAGCTGCA  
ACATTAAGACATGCCAATCTACCCCCCTGGTGGGGCTGGAGGGAGCTGGAGATGTCAGGGAACCACTCCCTG  
AGATCAGGCCTGGCTCCCTCCATGCCCTGAGCTCCCTCAAGAAGCTGGGTCTGAACAGTCACAGGTGAGCTGA  
TTGAGCGGAATGCTTGTGGCTGGCTTCACTTGTGGAACCTAACCTGGCCACAATAACCTCTTCTTGC  
CCCATGACCTCTTACCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCTGGAACCTGTGATTGTG  
ACATTCTGTGGCTAGCCTGGCTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCTG  
CCATGCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAAGGCCCTCCAGTGCCTGTGCCCCCTTCATCATGG  
ACGCACCTCGAGACCTCAACATTCTGAGGGCTGGATGGCAGAACTTAAGTGTGGACTCCCCCTATGTCTCCG  
TGAAGTGGTTGCTGCCAATGGACAGTGCTCAGCCACCCCTCCGCCACCCAAAGGATCTCTGTCTCAACGACG  
GCACCTTGAACCTTCCCACGTGCTGCTTCAAGACACTGGGGTGTACACATGCATGGTACCAATGTCAGGCA  
ACTCCAACGCCCTGGCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCAACTACAGCTCTCACCAACAG  
TAACAGTGGAGACCACGGAGATCTGCCCTGAGGACACAACGCAGAAAGTACAAGCCTGTTCTACCACGTCCACTG  
GTTACCAAGCCGGCATATACCACCTCTACCACGGTGCTCATTCAAGACTACCCGTGTGCCAACGAGGTGGCAGTAC  
CCGGCAGACACCACTGACAAGATGCAGACAGCAGCTGGATGAAGTCATGAAGACCAACGATCATATTGGCT  
GCTTGTCAGTGCAGTCTGCTAGCTGCCGCATGTTGATTGTTCTATAAAACTCTGAAGGGCACAGCAGCAG  
GGAGTACAGTCACAGCCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGAG  
CAGCAACAGCAGCTCCGTCGGTGTACAGGTGAGGGGGCAGTAGTGTGCTGCCACATTGACCATATTAAC  
ACAACACCTACAAACCAACGACATGGGCCACTGGACAGAAAACAGCCTGGGAACCTCTGCACCCACAGTCA  
CCACTATCTGAAACCTTATATAATTCAAGACCCATACCAAGGACAAGGTACAGGAAACTCAAATTGACTCCCT  
CCCCAAAAAAACTTATAAAATGCAATAGAATGCACACAAAGACAGCAACTTTGTACAGAGTGGGAGAGACTT  
TTCTGTATATGCTTATATATTAAGTCTATGGGCTGGTAAAAAAACAGATTATATTAAAATTAAAGACAAAA  
AGTCAAAACA

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**FIGURE 438**

MKLLWQVTVHHHTWNAILPFVYLTAQWILCAAIAAAASAGPQNCPSCSNCFSKVVC  
RGLSEVPQGIPSNTTRYLNLMENNIQMIQADTFRHLHHLEVQLGRNSIRQIEVGAFNGLASLN  
TLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEYISE  
GAFEGLFNLKYLNLCMCNIKDMPNLTPLVGLEELEMMSGNHFPEIRPGSFHGLSSLKKLWVMNS  
QVSLIERNADFGLASLVELNLAHNNLSSLPHDLFPLRYLVELHLHHNPWNCDCDILWLAWWL  
REYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAELKCRTPP  
MSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFHVLLSDTGVTMCVTNVAGNSNASAYLNV  
STAELNTSNYSFFTTVTVETTEISPEDTRKYKPVPTTSTGYQPAYTTSTTVLIQTRVPKQV  
AVPATDTTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAMLIVFYKLRKRHQQRSTVTAARTVE  
IIQVDEDIPAATSAATAAPSGVSGEAVVLPITHDHINYNTYKPAHGAHWTENS LGNSLHPT  
VTTISEPYIIQTHTKDKVQETQI

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**FIGURE 439**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCTG  
TCAGTGTGTCTCCTGATGGTCTCGCTGCCCTTGCTGCTACCAGGCCATGCTCTGCTGC  
CCAGCTGTTGCTTCTGAGATCACAGTCTTATTCTTAAGTGACGCTGCCGTAAACCTCCAA  
GTTGCCAAACTTAATCCACCTCCAGAAGCTCTGCAGCCAAGTTGGAAGTGAAGCACTGCACC  
GATCAGATATCTTTAAGAACGACTCTCATTGAAAAAGTCCTGGTGGAATAGTGAAAAAAT  
GTGGTGTGTGACATGTAAAAATGCTAACCTGGTTCCAAAGTCTTCAACGACACCCCTGATC  
TTCACTAAAATTGTAAAGGTTCAACACGTTGCTTTAATAAATCACTGCCCTGC

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**FIGURE 440**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAALKLEVK  
HCTDQISFKKRLSLKKSWWK

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**FIGURE 441**

GAACATTTAGTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGATG  
GGGTTGCTGGTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCACC  
ACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCCAGG  
GACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCATGGCAGGCTCCAG  
CTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCAAGAAGCCACCAGCAA  
GCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCGGAAAGATGGAGGTCAAGCAGAAGGGC  
AGAGGATGAACTGGAAGTCCGGTTAACGCCCTTGATGTTGGAATCAAGCTGTCAGGGT  
TCAGTACCAAGCAGCACAGCCAGGCCCTGGGAAGTTCTCAGGACATCCTCTGGGAAGAGGC  
CAAAGAGGCCAGCCGACAAGTGATCGCCCACAAGCCTACTCACCTCTCTAAGTTAGA  
AGCGCTCATCTGGCTTTCGCTTGCTGCAGCAACTCCCACGACTGTTGTACAAGCTCAGG  
AGGCGAATAAATGTTCAAAGTGA

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**FIGURE 442**

MPSPGTVC~~S~~LLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDGG  
QAEGAED~~E~~LEVRFNAPFDVG~~I~~KLSGVQYQQHSQALGKF~~L~~QDILWEEAKEAPADKO

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**FIGURE 443**

CGGCCACAGCTGGCATGCTCTGCCTGATGCCATCCTGCTGTATGCCTCGTCCAGTACCTCG  
TGAACCCCAGGGTGCCTCCGACGGACCCCAGATGTCAAGAATTGAACACGTGGCTGCTGTT  
CTCCCCCTGTTCCCGGTGCAGGTGCAGACCCCTGATAGTCGTGATCATCGGGATGCTCGTGC  
CTGCTGGACTTCTTGGCTTGGTGACCTGGGCCAGCTGCTCATCTTCCACATCTACCTGAGT  
ATGTCCCCCACCTAACGCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATCTTACA  
CCTCTACTTGAGTATGCTCTAACCTGAGCCCCCACGCCCTGGGCCAGAGTCTTGTCCCC  
CGTGTGCGATGTGTTCAAGGGTCAGGCTCTCCAGAAGTGAGATCATGGACAAAAAGGGAAA  
TCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAACTCACGCCG  
AGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTAAAATGTTAGAGACAATGGA  
ATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTTCCAAAACAC  
AAAGTAGAAATTCTAACATGAAATATATTACAGGCAGGTACCCACTAACCAAACAATGAAG  
CGAGAGCTGTGGTCTTGCTCACAGTGGGCACAGCGTAGGGCGTCAGTCATGTTGCT  
GAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAAGTAACAACAACCTCC  
CTGCTCTGGCACCCAGCGTTGGTCTAGGTGGCCAGCTGCAAAGCGTCTTCATTCTG  
GGCAGTGGTGGCCCCGAGGCTGTGGCTCTCAGGGGTTCTGTGGACACGGCAGCAGAGTG  
TGTCCAGGCCAGCCCCAAGAATGCCCTGCTCTGACAGCTGGCAACCCCTGGTCAGGGCA  
GAGGGAGTTGGTGGTCAGGCTCTGGCTCACCTCCATCTCCAGAGCATCCCCCTGCCTGCAG  
TTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGAGCCTCTGTTCAAAACC  
ACAGGTTACCCCTACAAACCACTGTCCCCACACAACCTGGGATGTTTAAAACACACACCTC  
TAACGCATATCTTACAGTCAGTCACTGTTGCTTGCTGAGGGTTGAATTTTTTAATGAAAGTGC  
AATGAAAATCACTGGATTAAATCCTACGGACACAGAGCTGAAAAAAAAAAAAAAAAAAAA  
AAAAAAA

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**FIGURE 444**

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLLDFLGLVHLGQLLIFHIYLSMSPTLSPRSPQGWV  
VRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQAQ  
QEAELETPRPAGVVPGA

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**FIGURE 445**

AGGCAGGGCAGCAGCTGCAGGCTGACCTGCAGCTGGCGGAATGGACTGGCCTCACAAACCTGC  
TGTTTCTTCTTACCATTTCCATCTTCCTGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGA  
GGAAGGGGCAAGGGCGGCCTGGGCCCTGGCCCTGGCCCTACCAGGTGCCACTGGACCTGG  
TGTCACGGATGAAACCGTATGCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGG  
CCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTGCAGCTGTGGA  
TGTCCAACAAGAGGAGCCTGTCTCCCTGGGCTACAGCATCAACCACGACCCCAGCCGTATCC  
CCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGAACCCCTTACCATGCAGG  
AGGACCGCAGCATGGTGAGCGTGCCGTGTTCAGCCAGGTTCCGTGCGCCGCCCTTGCC  
CGCCACCGCCCCGCACAGGGCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCT  
GCACCTGCATTTCTTGAATCACCTGGCCAGAACGCCAGGCCAGCAGCCGAGACCATCCTCCT  
TGCACCTTGTCAGAACAGGCTATGAAAAGTAAACACTGACTTTGAAAGCAAG

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**FIGURE 446**

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRGPLAPGPHQVPLDLVSRMKPYARMEYE  
RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVVDLPEARCLCLGC  
VNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

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**FIGURE 447**

GGAGTGCAGATGGCATCCTCGGTTCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAGA  
TGGAGCTCTCGAAGGCCTCTCTGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCTAT  
CACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTGTGGGCACACAGAAAGGTGC  
CCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTGACATGCCAGTGTCCCTGGATG  
GAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGAGACTGGGGATGACCGGT  
TCTCCTTCCGGAGCTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAGAACCGAG  
GGGAGAGGTGCCGAAGTTCAATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAAGGACTAC  
TGGAAATTGCCACGTTGCAAGGCCATGTCACCCCACCTCTCGATTGGAGGGAAAGCGGTTGA  
TGGAGAAGGCTCCCTCCCCCTCCCTGGGGCTTGTGGCAAAAATCCTATGGTTATCC  
CTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTCCTCCTGCTACTAACAGAC  
TTGCTACTCACTGGAACCCCTGCCTGTGGCTCAAACGTGAGCGCCTTGCTGCTGTTCCCT  
GTCCTGTCAGGTCTCCTGGGATGGTGGCCCACATGATGTATTCAAACTGCTTCCAAAGCGACT  
GTCAACTGGGTCCAGAAGACTGGAGACCACATGTTGAAATTATGGCTGGCCTTCTACATG  
GCCTGGCTCTCCTCACCTGCTGCATGGCGTGGCTGTCAACCACCTCAACACGTACACCAAGG  
ATGGTGCAGGAGTTCAAGTGAAGCAAGTAAGAGCTCAAGGAAACCGAACTGCCTACCA  
CATCACCATCAGTGTTCCTCGCGGCTGTCAAGTGCAGCCCCACCGTGGGTCTTGACC  
AGCTACCACCAAGTATCATAATCAGCCCATCCACTCTGTCTTGAGGGAGTCGACTTCTACTCC  
GAGCTGCGGAACAAGGGATTCAAAGAGGGCCAGCCAGGAGCTGAAAGAAGCAGTTAGGTCA  
TCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTGGGGAGTAGGCTTGAGCCCTACCT  
TACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCGTCTTGAGCATGGTTTTA  
GAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTAAGTCCTAAGGGATTCCCTGGGTGCCA  
CTGCTCTCTTCTACAGCTCCATCTGTTCACCCACCCACATCTCACACATCCAGAA  
TTCCCTCTTACTGATAGTTCTGTGCCAGGTTCTGGGCTAAACCATGGAGATAAAAGAAG  
AGTAAAATACACTCCCCGACCTAAGGATCTGAAA

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**FIGURE 448**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNWFVGTQKVPKPLCEKGLAAKCFDMPV  
SLDGDTNTSTQEVVQYNWETGDDRFSFRSFRSGMWLSCEETVEEPGERCRSIELTPPAKRGE  
KGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQQLPPA  
TNRLATHWEPCILWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCLEWLG  
LLHGLALLHLLHGVGCHHIQHVHQDGAGVQVQA

## FIGURE 449

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**FIGURE 450**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPHN  
LSGLLGLSLRYNSLSELРАGQFTGLMQLTWLYLDHНHICSVQGDAFQKLRRVKELTЛSSNQIT  
QLPNTTFRPMNPRLSVDLSYNKLQALAPDLFHGLRKLTTLHMРANAIQFVPVRIFQDCRSLKF  
LDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIVSSL  
DWVWNLEKMDLSGNEIEYMEPHVFETVPHLQLDSNRLTYIEPRILNSWKSLTSITLAGNL  
WDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDavyAFHLCEDGAEPSTGHLLSAV  
TNRSDLGPPASSATTLADGGEQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMALIFSLI  
VVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNHIEGALVII  
NEYGSCTCHQQPARECEV

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FIGURE 451

TTGAGCGCAGGTGAGCTCTGCGCGTCCGGGGCGTTCCAGTCACCCTCCGCCGTTAC  
CCGCAGCGCGCCCGAGGGAGTCTCCTCCAGACCCCTCCCGTTGCTCCAACATAACGGA  
CTGAACGGATCGCTGCGAGGGTGGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACT  
ACCATCCATAGCCAGATAGATTATCTTACACTGAACGTGATCAAGTACTTTGAAAATGACTTCG  
AAATTATCTGGTGTCTCATACTTGCTGCACTGAGTCTTCACCACCTTCTCTCCAA  
CTAGACCAGCAAAGGTTCTACTAGTTCTTGATGGATTCCGTTGGGATTACTTATATAAA  
GTTCCAACGCCCATTTCTTATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAAT  
GTTTTATTACAAAAACCTACCCCTAACATTATACTTTGTTAACTGGCCTCTTGAGAGAAT  
CATGGGATTGTTGCAAATGATATGTTGATCCTATTCGGAACAAATCTTCTCCTGGATCAC  
ATGAATATTTATGATTCCAAGTTGGGAAGAAGCAGACACCAATATGGATCACAAACCAGAGG  
GCAGGACATACTAGTGGTGCAGCCATGTGGCCCGAACAGATGTAaaaATACATAAGCGCTT  
CCTACTCATTACATGCCTTACAATGAGTCAGTTCATTTGAAGATAAGTTGCCAAAATTGTT  
GAATGGTTACGTCAAAGAGCCCATAATCTGGTCTCTATTGGGAAGACCCCTGATGAC  
ATGGGCCACCATTGGGACCTGACAGTCCGCTATGGGGCCTGTCATTCAGATATTGACAAG  
AAGTTAGGATATCTCATACAAATGCTGAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATC  
ATCACAAGTGATCATGGAATGACCGAGTCTGAGGAAGGTTAATAGAACATTGACCAAGTAC  
CTGGATAAAGACCACTATACCCCTGATTGATCAATCTCCAGTAGCAGCCATCTGCCAAAAGAA  
GGTAAATTGATGAAGTCTATGAAGCAACTAACGCAGCTCATCCTAATCTTACTGTTACAAA  
AAAGAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTCAACCAATCATAGCA  
GTGGCTGATGAAGGGTGGCACATTACAGAATAAGTCAGATGACTTCTGTTAGGCAACCAC  
GGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTAGCCCATGGCCTGCCTTCAGA  
AAGAATTCTCAAAGAACGCATGAACCTCCACAGATTGACCCACTATGCCACCTCCTC  
AATATCACTGCCATGCCACACAATGGATCATTCTGAATGTCAGGATCTGCTCAATTCA  
ATGCCAAGGGTGGCCCTTATACACAGACTATCTCCCTGGTAGTGTAAACCAGCA  
GAATATGACCAAGAGGGGTATACCCCTATTCTAGGGGTCTCTTGGCAGCATTATAGT  
ATTGTATTTTGTAATTTCATTAAGCATTAACTCACAGTCAAATACCTGCTTACAAGAT  
ATGCATGCTGAAATAGCTCAACCATTATTACAAGCT**TAATGTTACTTGAAGTGGATTG**CAT  
ATTGAAGTGGAGATTCCATAATTATGTCAGTGTAAAGGTTCAAATTCTGGAAACAGTT  
CCAAACATCTGCAGAACCATTAAGCAGTTACATATTAGGTATACACACACACACACA  
CACATACACACACGGACAAAATACTACACCTGCAAGGAATAAGATGTGAGAGTATGT  
CTCCATTGTTACTGTAGCATAGGGATAGATAAGATCCTGCTTATTGGACTGGCAGAT  
AATGTATATATTAGCAACTTGCACATATGTAAGTACCTTATATATTGCACTTAAATTCT  
CTCCTGATGGGTACTTTAATTGAAATGCACTTATGGACAGTTATGTCTTATAACTTGATTG  
AAAATGACAACCTTTGCACCCATGTCACAGAATACTTGTACGCATTGTCAAACTGAAGGA  
AATTCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAAATTGAGAGAAGAAGAA  
GGTGATAAGTGTGAAAATTAAATGTGATAACCTTGAACCTTGAATTGGAGATGTATTCC  
CAACAGCAGAATGCAACTGTGGCATTCTGTCTTATTCTTCCAGAGAACGTGGTTTCA  
TTTATTCTCCTCAAAAGAGAGTCAAATACTGACAGATTGTTCTAAATATATTGTTCTGT  
CATAAAATTATTGTGATTCTGTGAGTCATATTACTGTGATTTCATAATAATGAAGACAC  
CATGAATATACTTTCTTCTATAGTCAGCAATGGCCTGAATAGAAGCAACCAGGCACCAT  
CTCAGCAATGTTCTTGTGTTGAATTATTGCTCCTTGAAAATTAAACTATTAAATT  
ACATTAATAATCAAATTGGATAAAAAAAAAAAAAAA

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**FIGURE 452**

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSDGFRWDYLYKVPTPHFHYIMKYGVHVQ  
VTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMMNIYDSKEWEEATPIWIT  
NQRAGHTSGAAMWPGBTDKIHKRFPTHMPYNESVSFEDRVAKIVEWFTSKEPINLGLLYWED  
PDDMGHHHLGPDSPLMGPVISIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEERLIEL  
DQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKNSRIQP  
IIAVADEGWHLQNKSDDFLLGNHGYDNALADMPIFLAHGPAFRKNFSKEAMNSTDLYPLLC  
HLLNITAMPNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYFIGVSLGS  
IIVIVFFVIFIKHLIHSQIPALQDMHAETIAQPLLQA

**Important features:****Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372,  
382-385, 389-392**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

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**FIGURE 453**

GGCCGCCTGGAATTGTGGAGTTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGAC  
**TATGGCTCCCCAGAGCCTGCCTCATCTAGGATGGCTCTGGCATGCTGCTTGGCTGCT**  
GATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTGCCCTGACCAA  
CCCAGAGAAGAGCAGCACAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGCTGGA  
TGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTCAGCCAGGGCAGGC  
TGTCCCTGCAGGATCCCACGTACGGCTGAATCTCAGACTGGGAAAGAGAGGCAAAACTCCA  
ATATGAGGACAAGTTCCGAAATAATTGAAAGCAGGCTGGATATCAACACCAACACCTA  
CACATCTCAGGATCTCAAGAGTCAGTGCAGTGGCAAAATTCAAGGAGGGGGCAGAGATGGAGAGTTC  
AAAGGAAGACAAGGCAGGCTGAGGTAAAGCGGCTTCCGCCATTGAGGAAGTGAA  
GAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGGTACGGCTGAT  
CAACAAGTTCAATAGTCCAGCTCCAGTTGGAAGAGAAGATTGCTGCGCTTTGATCTTGA  
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTCCCTTGGTGGTCTTCAAGTGGT  
GATCAATGGCTAACAGCACAGAGGCCCTCGTAAGGAGTATGCTGCGTTGTGCTGGCGC  
TGCCTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGAGGCCCTGCAGAAGCT  
GCTGGTCATCCTGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGTCTGTTGCACTGTG  
CTCCCTGCTGCCACTTCCCTATGCCAGCGGAGTTCTGAAGCTCGGGGCTGCAGGT  
CCTGAGGACCTGGTCACGGAGAAGATGTTGCCAGGAGGAGGCTGAGCTGACCCAGGAGATGTC  
CTACGACCTGGTCACGGAGAAGATGTTGCCAGGAGGAGGCTGAGCTGACCCAGGAGATGTC  
CCCAGAGAAGCTGCAGCAGTATGCCAGGTACACCTCCTGCCAGGCCCTGTTGGAACAGGGCTG  
GTGCGAGATCACGGCCACCTCCTGGCGCTGCCAGCATGATGCCGTGAGAAGGTGCTGCA  
GACACTGGCGTCCCTGACCACCTGCCGGACCGCTACCGTCAGGACCCCCAGCTGGCAG  
GACACTGGCCAGCCTGCAGGCTGAGTACCAAGGTGCTGGCCAGCCTGGAGCTGCAGGATGGTGA  
GGACGAGGGCTACTTCCAGGAGCTGCTGGCTCTGTCACAGCTTGCTGAAGGAGCTGAGA**TG**  
**A**GGCCCCACACCAGGACTGGACTGGGATGCCGTAGTGAGGCTGAGGGGTGCCAGCGTGGGTG  
GGCTTCTCAGGCAGGAGGACATCTGGCAGTGCTGGCTTGGCATTAAATGGAAACCTGAAGG  
CCAAAAAAA  
AAAAAAAA  
AAAAAAAA  
AAAAAAAA  
AAAAA

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**FIGURE 454**

MAPQLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPDKSSTKETERKETKAEEELD  
AEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGRKDINTNTY  
TSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMVRLI  
NKFNSSSSSLEEKIAALFDLEYVHQMDNAQDLLSFGGLQVINGLNSTEPLVKEYAAFVLGA  
AFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKVLFALCSLLRHFPYAQRQFLKGGLQV  
LRTLQEKGTTEVLAVRVVTLLYDLVTEKMFAEEEAEALTQEMSPEKLQQYRQVHLLPGLWEQGW  
CEITAHLALPEHDAREKVLQTLGVLLTCRDYRQDPQLGRTLASLQAELYQVLASLELDGE  
DEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

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**FIGURE 455**

GCCCCAGGGAGCAGTGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAGT  
GGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACCCCTA  
CCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGGCAGGGAAAGGAGAGGTGT  
CTGTGCGTCCTGCACCCACATCTTCTCTGTCCCCTCCTGCCCTGCTGGAGGCTGCTAGAC  
TCCTATCTTCTGAATTCTATAGTGCCTGGTCTCAGCGCAGTGCCATGGTGGCCGTCCTTG  
TGGTTCTCTTACCTGGGAAATAAGGTGCAGCGGCCTGGCTACAGCAAGACCCCCCTGGA  
TGTGGGTGCTCTGTGCTCTGATCACAGCCTGCTCTGGGGTACAGAGCATGTTCTGCCA  
ACAATGATGTTTCTGTGACCACCCCTAACACCGTGCCCTCTGGGAGCAACCAGGACCTGG  
GAGCTGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGATCATCAATGGATCCG  
ACTGCGATATGCACACCCAGCCGTGGCAGGCCGCTGTTGCTAAGGCCAACAGCTACT  
GCGGGGCGGTGTTGGTCATCCACAGTGGCTGCTCACGGCCGCCCAGTCAGGAAGAAAGTT  
TCAGAGTCCGTCTGGCCACTACTCCCTGTCACCAGTTATGAATCTGGCAGCAGATGTTCC  
AGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCTAACGACCTCATGC  
TCATCAAACGTAAACAGAAGAATTGCTCCACTAAAGATGTCAGACCCATCAACGTCTCCTCTC  
ATTGTCCTCTGCTGGACAAAGTCTGGTGTCTGGCTGGGGACAACCAAGAGCCCCAAG  
TGCACCTCCCTAACGTCTCCAGTGCTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGG  
ATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACT  
CCTGCCAGGGTGATTCTGGGGGCCTGTTGCAATGGCTCCCTGCAGGGACTCGTGTCC  
GGGGAGATTACCTTGTGCCCGGCCAACAGACGGGTGTCTACACGAACCTCTGCAAGTTCA  
CCAAGTGGATCCAGGAAACCATCCAGGCCACTCCTGAGTCATCCAGGACTCAGCACACCG  
CATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTCAGACCCCTCATTCCTCCAGAGA  
TGTTGAGAATGTTCATCTCTCCAGCCCTGACCCCATGTCCTGGACTCAGGGCTGCTTCC  
CCCACATTGGCTGACCGTGTCTCTAGTTGAACCTGGAAACAATTCCAAAATGTCCAG  
GGCGGGGGTTGCGTCTCAATCTCCCTGGGCACCTTCATCCTCAAGCTCAGGGCCATCCCT  
CTCTGCAGCTCTGACCCAAATTAGTCCCAGAAATAACTGAGAAGTGGAAAAAA

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**FIGURE 456**

MATARPPWMWVLICALITALLGVTEHVLANNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDDS  
SSRIIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLTAHCRKKVFRVRLGHYSLSPV  
YESGQQMFQGVKSIPHGYSHPGHSNDLMLIKLNRRIRPTKDVRPINSSHCPAGTKCLVSG  
WGTTKSPQVHFPKVLQCLNISVLSQRCEDAYPRQIDDTMFCAGDKAGRDSQGDGGPVVCN  
GSLQGLVSWGDPCARPNRPGVYTNLCKFTKWIQETIQANS

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**FIGURE 457**

GCAGTCAGAGACTTCCCTGCCCTCGTGGAAAGAACATTAGGAATGCCCTTAGTGCCCTGCTCCTGAAC  
AGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTCACTCTCACCGCTGTAGGAATCCAGATGCAGG  
CCAAGTACAGCAGCACGAGGGACATGCTGGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTG  
CCACAACCTGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTCAACGTGGCACCAGTGGCCCTGA  
CCCTGCTGACTTTGTGCTGGTGTGATAGGGCTGGCAGCCCTGGGGCTTTGTTTCAGTACTACCAGC  
TCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCCAAGAGTTGCAATCTC  
TTCAACTCCAGAATATAAGCTTGCAGGAAGTCTGCAGCAGTGGCTGAAAAACTCTGTCGTGAGCTGTATAACA  
AAGCTGGAGCACACAGGTGCAGCCCTGTACAGAACATGGAATGGCATGGAGACAATTGCTACCAGTTCTATA  
AAGACACGAAAAGTGGGAGGACTGTAATATTCTGCCTTAGTGAAACTCTACCATGCTGAAGATAAACAAAC  
AAGAAGACCTGGAATTGCCCGTCTCAGAGCTACTCTGAGTTTCTACTCTTATTGGACAGGGCTTTGCGCC  
CTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTCACCTCTGAACGTGTTCCATATTATAATAGATG  
TCACCAGCCAAGAACAGCAGAGACTGTGTGGCCATCCTCAATGGATGATCTCTCAAAGGACTGCAAAGAATTGA  
AGCGTTGTCTGTGAGAGAACGGCAGGAATGGTGAAGCCAGAGAGGCTCCATGTCCTTCTGAAACATTAGGCG  
AAGGTGACTTGATTGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCAAAGCAAGGGCTAGTTGAG  
ACATTGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGTTCTCGTGTTCCTGTT  
CAGGATCACCAGCATTCTGAGCTTGGTTTATGCACGTATTAACAGTCACAAGAAGTCTTACATGCCAC  
CAACCAACCTCAGAAACCCATAATGTCATGCTTCTGGCTTAGAGATAACTTTAGCTCTCTTCTCAA  
TGTCTAATATCACCTCCCTTTCTGACAGTCAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTAC  
CAGCAAATACACAAGGAATTCTTTGTTCTGAGTCATACTAGCCCTCCCAATCCATCAGTAAAGACCC  
CATCTGCCTTGTCCATGCCGTTCCAAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
GCATTCCTTCTGTGCCATTAAAGACTCTGATAATTGTCTCCCTCCATAGGAATTCTCCAGGAAAGAAATAT  
ATCCCCATCTCCGTTCATATCAGAAACTACCGTCCCCGATATTCCCTCAGAGAGATTAAGACCAAGAAAAAGT  
GAGCCTCTCATCTGCACCTGTAATAGTTCTGAGTCATACTGACCCATATTACCTTCAAGGT  
ACTGAAGATTAATAATAATGTAATAGTAAACTGTGAAAAA

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**FIGURE 458**

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLTLCLVLLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCREL  
KRCVCERRAGMVKPESLHVPPETLGEGL

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**FIGURE 459**

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGCAGGAGCAGCTGGCCAC  
TGGCGGCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCTGT  
GAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAACGCTGGCCAGGGTGGTGGT  
CAGCTGGTCAGGGACCTACGGCACCTGCTGGACCACCTGCCTCTCCATCGAAGCAGGGAA  
GTGGGAGCCTCGAGCCCTCGGGTGBAAGCTGACCCAAAGCCACCCCTCACCTGGACAGGA**ATGA**  
GAGTGTCAAGGTGTGCTTCGCCTCCTGGCCCATCTTGCCATAGTCACGACATGGATGTTA  
TTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCAGCCTCGC  
CCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCAGCCA  
ACTTTGCCTTAAATCTGCAGTGGGCCAACGTCGTGGCCCTACTATGTGCTTGAAAG  
ACCGCATGATCATGAGTCTGTGAAAAACAATGTGGCAGAGGCCTAAACATGCCCTGGTGA  
ATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGGAGATGTTATGC  
ACCTAGTGAATTCCCTTAAAGAAATTCCGGGGGTGCACTGGTGTGGCTGCCCTACGACG  
ATCCAGGGACAAATGAACGATGAAAGCAGGAAACTCTCTGACTTGGGAGTTCTACG  
CAAACAAACTGGCTCCGGACAGCTGGTCTCATAGGAGCAAAGACCTCAGGGTAAAA  
GCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATCGAGGGATGCCAGAGC  
TGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATT**TAGGTGGCTGTGGCTTCCCTCAG**  
CCAGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCAGGGCTGAGGAGGA  
GGAGCAGGGGGTGTGCTGGAGGTGCTGCAGGTCTGCACGCTGTGTCGCCCTCCCTC  
CTCGGAAACAGAACCCCTCCACAGCACATCCTACCCGAAGACCAGCCTCAGAGGGTCTTCT  
GGAACCAAGCTGTGTGGAGAGAATGGGGTGTTCGTCAGGGACTGCTGACGGCTGGTCTG  
AGGAAGGACAAACTGCCAGACTTGAGCCAAATTAAATTATTTGCTGGTTTGAAAAAA  
AAAAAAAAAAAAAA

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**FIGURE 460**

MRVSGVLRLLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCPA  
NYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNNGTTGAVLGQKAFCDMYSGDV  
MHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWFIGAKDLRG  
KSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

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**FIGURE 461**

AAACTCAGCACTGCCGGAGTGGCTATTGTTAAGACAAAGGGTGTGCACTTCCTGCCAGGA  
AACCTGAGCGGTGAGACTCCCAGCTGCCATCACAGGCCAGGACATGCAGAACCTCC  
TAGAACCGACCCACCACCATGAGGTCTGCCGTGGAGATGCAGGCACCTGAGCCAAGGC  
CCAGTGGTCTTCTGGCTGTCTTCTCTTCTTCGCCCTGCCCTTTATTAA  
GGAGCCTCAAACAAAGCCTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCTCTACA  
GTCCCTGGCAAAGCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTATGCAGA  
GCCAGGCCAGAGAACAACTGCCCTCAACACACAACAAAGGCCAGGCCACACCCACGGAGA  
CAGAGGAAAGGAGGCCAACCGAGCAGGCCGGAGGAGCAGGACAAGGTGCCACACAGACA  
GAGGGCAGCATGGAAGAGGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTCACCCAGGAG  
GCAAGATGCAGGGATGCCCTGGCAGGACAGAGGCACAATCATGGAAGAGCCAGGACACAAA  
GACGCCAACGAAATGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACGGTGTAGAGAA  
GCACCAAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCAAAAGTCAGCACAGAATGCT  
GGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCACAGCAGTCATCCC  
ACCTAAGGAGAAGAACCTCAGGCCACCCACCCCTGCCCTTCCAGAGGCCACGACGCA  
GAGAAACCAAAGACTGAAGGCCAACCTCAAATCTGAGCCTCGGTGGGATTGAGGAAAA  
ATACAGCTTCGAAATAGGAGCCTCAGACGACTGCCCTGACTCTGTGAAGATCAAAGCTC  
CAAGTCGCTGTGGCTCCAGAAACTCTTCTGCCAACCTCACTCTTCTGGACTCCAGACA  
CTTCAACCAAGAGTGGACGGCCCTGGAACACTTTGACCCACCCCTGGCTCATGGAGCT  
CAACTACTCCTGGTGCAGAAGGTCGTGACACGCTTCCCTCAGTGCCCAAGCAGCAGTC  
CCTGGCCAGCCTCCCCGCTGGAGCCTCCGGTGCATCACCTGTGCCGTGGCAACGGGG  
CATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCACGACTACGTGTTCCGATTGAG  
CGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGACTCGGACATCCTCTACGGCTTAC  
CGCCTCTCCCTGACCCAGTCACTCCTATATTGGCAATCGGGTTCAAGAACGTGCCTCT  
TGGGAAGGACGTCCGCTACTGCACTCCTGGAAGGCACCCGGACTATGAGTGGCTGGAAGC  
ACTGCTTATGAATCAGACGGTGATGTCAAAAACCTTCTGGTTCAAGGACAGACCCAGGA  
AGCTTTGGAAAGCCCTGCACATGGACAGGTACCTGTTGTCGACCCAGACTTCTCCGATA  
CATGAAGAACAGGTTCTGAGGTCTAAGACCCGGATGGTGCCTGGCAACGGGCTACAGATGA  
ACCCACTGGGCCCTCTGCTGCTCACTGCCCTCAGCTGTGACCGAGGTGAGTGCTTATGG  
CTTCATCACTGAGGGCCATGAGCGCTTCTGATCACTACTATGATACATGGAAGCGGCT  
GATCTTACATAAACCATGACTTCAAGCTGGAGAGAGAAGTCTGGAAGCGGCTACAGATGA  
AGGGATAATCGGCTGTACCGCTCTGGTCCCGGAACTGCCAAAGCCAAGAAC**TGA**CCGG  
GCCAGGGCTGCCATGGCTCCTGCCGTCCAAGGCACAGGATACAGTGGGAATCTTGAGAC  
TCTTGGCCATTCCCATGGCTCAGACTAAGCTCCAAGCCCTCAGGAGTTCCAAGGGAACAC  
TTGAACCATGGACAAGACTCTCTCAAGATGGCAAATGGCTAATTGAGGTTCTGAAGTTCTCA  
GTACATTGCTGTAGGTCTGAGGCCAGGGATTAAATTAAATGGGGTGTGGGTGGCCAATA  
CCACAATTCTGCTGAAAAACACTCTCCAGTCCAAGCTCTTGATACAGAAAAAGAGCC  
TGGATTACAGAACATATAGATCTGGTTGAATTCCAGATCGAGTTACAGTTGTGAAATCT  
TGAAGGTATTACTTAACTCACTACAGATTGTCTAGAAGACCTTCTAGGAGTTATCTGATT  
TAGAAGGGTCTATACTTGTCCCTGTCTTAAGCTATTGACAACACTACGTGTTGAGAAC  
TGATAATAATACAAATGATTGTTGTCCATGGAAAGGCAAATAAATTCTACAGTGA  
AAAAAAA

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**FIGURE 462**

MRSCLWRCRHLSQGVQWSLLLAVLVEFLFALPSFIKEPQTQPKSRHQRTENIKERSLQLAKPK  
SQAPTRARRTTIYAEPAPENNALTQTPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAWKS  
PEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNGGQTRKLTAASRTVSEKHQGKAA  
TTAKTLIPKSQHRLMLAPTGAVSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPTTQRNQRLK  
AANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHFNQSEW  
DRLEHFAPPFGFMELNYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGGILNNSH  
MGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLLILGNRGFKNVPLGKDVRY  
LHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFREALHMDRYLLLHPDFLRYMKNRFL  
RSKTL'DGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYYDTSWKRLIFYINH  
DFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

**Important features:****Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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**FIGURE 463**

GGGGGAGCTAGGCCGGCGCAGTGGTGGCGGCGCAAGGGTGAGGGCGGCCAAC  
 CCCAGGTAGGTAGAGCAAGAAGATGGTGTTCCTGCCCCCTAAATGGTCCCTGCAACCATGTC  
 ATTTCTACTTTCCCTCACTGTTGGCTCTCTTAACGTGTCCACTCCTCATGGTGTCAAGAC  
 TGAAGCATCTCCAAAACGTAGTAGTGTGGACACCATTCCCTGGAATAAAATACGACTTCTGA  
 GTACGTATCCCAGTTATGATCTGTGATCCATGCAAACCTTACACGCTGACCTCTG  
 GGGAAACACGAAAGTAGAAATCACAGCCAGTCAGGCCACCCAGCACCATCCTGCATAGTCA  
 CCACCTGCAGATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGGAAGAAC  
 CCTGCAGGTCCCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAGCCCCCT  
 TGCGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTCGGAGACTTCCACGG  
 ATTTCACAAAAGCACCTACAGAACCCAAGGAAGGGAACTGAGGATACTAGCATCAACACAATT  
 TGAACCCACTGCAGCTAGAATGGCCTTCCCTGCTTGTGATGAACTGCCTCAAAGCAAGTTT  
 CTCAATCAAATAGAAGAGAGCCAAAGGCACCTAGCCATCTCAATATGCCATTGGTGAATC  
 TGTGACTGTTGCTGAAGGACTCATAGAACCAATTGATGTCAGTGTGAAGATGAGCACCTA  
 TCTGGTGGCCTTCATCATTCAGATTGAGTGTGTCAGCAAGATAACCAAGAGTGGAGTCAA  
 GGTTCTGTTATGCTGTGCCAGACAAGATAATCAAGCAGATTATGCACTGGATGCTGGGT  
 GACTCTCTAGAATTTATGAGGATTATTCAAGCATAACCGTATCCCTACCCAAACAAGATCT  
 TGCTGCTATTCCGACTTCACTGCTGGCTATGGAAAACCTGGGACTGACAACATATAAGAGA  
 ATCTGCTCTGTTGTTGATGCAAGAAAAGTCTTCAGTCAGTAAGCTGGCATCACAGTGAC  
 TGTGGCCATGAACTGGCCACCACTGGTTGGAACCTGGTCACTATGGAATGGTGGAAATGA  
 TCTTGGCTAAATGAAGGATTGCAAATTATGGAGTTGTGTCAGTGTGACCCATCC  
 TGAACCTGAAAGTTGGAGATTATTCTTGGCAAATGTTTGACGCAATGGAGGTAGATGCTT  
 AAATCCCTCACACCCCTGTCTCACACTGTTGAAAATCTGCTCAGATCCGGGAGATGTTGA  
 TGATGTTCTTATGATAAGGGAGCTGTATTCTGAATATGCTAAGGGAGATCTTAGCGCTGA  
 CGCATTAAAAGTGGTATTGTCAGTATCTCCAGAACAGTAGCTATAAAAATACAAAAAACGA  
 GGACCTGTGGATAGTATGCAAGTATTGCCCACAGATGGTGTAAAAGGGATGGATGGCTT  
 TTGCTCTAGAAGTCACATCATCTTCATCCTCACATTGGCATCAGGAAGGGGTGGATGTGAA  
 AACCATGATGAACACTGGACACTGCAGAGGGTTTCCCTAATAACCATCACAGTGAGGGG  
 GAGGAATGTACACATGAAGAACAGACTACATGAAGGGCTCTGACGGCGCCCGACACTGG  
 GTACCTGTGGCATTTCCATTGACATTCACCCAGAACATGGTCCATCGATT  
 GCTAAAAACAAAACAGATGTGTCATCCTCCCCAGAAGAGGTGGATGGATCAAATTAAATGT  
 GGGCATGAATGGTATTACATTGTGCATTACGAGGATGATGGATGGACTCTTGACTGGCCT  
 TTAAAAGGAACACACACAGCAGTCAGCAGTAATGATCAGGCAAGTCTCATTAAACATGCA  
 TCACTCGTCAGCATTGGAAAGCTGTCCTGAAAAGGCCCTGGATTATCCCTGACTTGAA  
 ACATGAAACTGAAATTATGCCGTGTTCAAGGTTGAATGAGCTGATTCTATGTATAAGTT  
 AATGGAGAAAAGAGATATGAATGAAGTGGAAACTCAATTCAAGGCCTCCCTCATCAGGCTGCT  
 AAGGGACCTATTGATAAGCAGACATGGACAGACGAGGGCTCAGTCAGAGCAAATGCTGCG  
 GAGTGAACTACTACTCCTCCCTGTGTGACAACATATCAGCCGTGCGTACAGAGGGCAGAAGG  
 CTATTTCAGAAAGTGGAAAGGAATCCAATGGAAACCTTGAGCCTGCGACGTGACCTGGC  
 AGTGGTGTGGGGGCCAGAGCACAGAACAGCTGGGATTCTTCTTATAGTAAATATCAGTT  
 TTCTTGTCCAGTACTGAGAAAAGCCTAAATTGAATTGCCCCCTGCAAGAACCCAAAATAAGGA  
 AAAGCTCAATGGCTACTAGATGAAAGCTTAAAGGGAGATAAAAATAAAAGCTCAGGAGTTCC  
 ACAAAATTCTTACACTCATTGGCAGGAACCCAGTAGGATACCCACTGCCCTGGCAATTCTGAG  
 GAAAAACTGGAACAAACTGTACAAAAGTTGAACCTGGCTCATCTCCATAGGCCACATGGT  
 AATGGGTACAACAAATCAATTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGGATTCTTCAG  
 CTCTTGGAAAGAAAATGGTCTCAGCTCCGTTGTGTCACAGACAATTGAAACCATTGAAGA  
 AAACATCGGTTGGATGGATAAGAATTGATAAAAATCAGAGTGTGGCTGCAAAGTGAAGAAGCT  
 TGAACGTATGTAAGGAAACTCTCCCTGCCCCGGTTCTGTTATCTCTAATCAGGAAACATTG  
 TGAGTGTATTTCAAACTAGAGATGGCTGTTGGCTCCACTGGAGATACTTTTCCCTTC  
 AACTCATTTTGACTATCCCTGTGAAAAGAATAGCTGTTAGTTTCTCATGAATGGCTTTT  
 CATGAATGGGCTATCGTACCATGTGTTTGTTCATCACAGGTGTGCCCTGCAACGTAAC  
 CAAGTGGTGGGTTCCCTGCCACAGAACATAAGTACCTTATTCTCTCAAAAAAAAAAAAA  
 AAAAAAAAAAAAAA

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**FIGURE 464**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVHY  
DLIHNLTTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLEHP  
PQEQLALLAPEPLLVLGPLYTVVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTAARM  
AFPCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVMSTYLVAIFIIS  
DFESVSKITKSGVKVSYYAVPDKINQADYALDAAVTLEFYEDYFSIPYPLPKQDLAAIPDFQ  
SGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELHQWFGNLVTMEWWNDLWLNEG  
AKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFDDVSYDKG  
ACILNMLREYLSADAFKGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDGFCRSQHS  
SSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPDTGYLWHVPL  
TFITSKSNMVHRFLKTQDVLLPEEVEWIKFNVGMNGYYIVHYEDDGWDSLTGLLKGHTA  
VSSNDRASLINNAFQLVSIKGKLSIEKALDLISLYLKHETEIMPVFQGLNELIPMYKLMERDMN  
EVETQFKAFIRLLRDLIDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCVQRAEGYFRKWKE  
SNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALCRTQNKEKLQWLLD  
ESFKGDKIQTQEFPQILTIGRNPVGYPLAWQFLRKWNWKLVQKFELGSSIAHMVMGTNQF  
STRTRLEEVKGFFSSLKENGSQLRCVQQTIETIEENIGWMDKNFDKIRVWLQSEKLERM

**Important features:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

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**FIGURE 465**

CAGCCACAGACGGGTCATGAGCGCGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCACT  
GCCAGGAGTGCAGGCGCTGCTCTGCCAGTTGGGACAGTCAGCATGTGTGGAAGGTGTCCGA  
CCTACCCC GGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGTGCCAGGACAC  
GTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTCTCTCCAAGGGCTGCACGGAGGC  
CAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATCTCCTA  
CACCTTCGTGTGCCGCCAGGAGACTCTGCAACAACCTCGTTAACCTCCCTCCGCTTGGC  
CCCACAGCCCCCAGCAGACCCAGGATCCTGAGGTGCCAGTCTGCTTGTCTATGGAAGGCTG  
TCTGGAGGGACAACAGAAAGAGATCTGCCCAAGGGGACCACACACTGTTATGATGGCCTCCT  
CAGGCTCAGGGAGGAGGCATCTCCAATCTGAGAGTCCAGGGATGCATGCCAGCCAGG  
TTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGTATGACTGAGAACTGCAATAG  
GAAAGATTTCTGACCTGTCATGGGGGACCACCATTATGACACACGGAAACTTGGCTCAAGA  
ACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGTGTCAAGGAGAC  
GCTGCTGCTCATAGATGTAGGACTCACATCAACCCCTGGTGGGACAAAAGGCTGCAGCACTGT  
TGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCTCCTGGGTGCTTGTGGCCTC  
CTATACCCACCTCTGCTCCTCGGACCTGTGCAATAGTGCAGCAGCAGCAGCGTTCTGCTGAA  
CTCCCTCCCTCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCTACCTGTGTGCAGCC  
CCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCAGGGCGCCACTCATTGTTA  
TGATGGGTACATTCTCATCTCAGGAGGTGGCTGTCCACCAAAATGAGCATTAGGGCTGCGT  
GGCCCAACCTCCAGCTTCTGTTGAACCACACCAGACAAATCGGGATCTTCTCTGCGCGTGA  
GAAGCGTGATGTGCAAGCCTCTGCCTCTCAGCATGAGGGAGGTGGGCTGAGGGCCTGGAGTC  
TCTCACTGGGGGGTGGGCTGGCAGTGGCCCCAGCGCTGTGGTGGGAGTGGTTGCCCTTC  
CTGCTTAACTCTATTACCCCCACGATTCTCACCGCTGCTGACCACCCACTCAACCTCCCTC  
TGACCTCATAACCTAATGGCTTGGACACCAGATTCTTCCATTCTGCTCATGAATCATCTT  
CCCCACACACAATCATTCTACTCACCTAACAGCAACACTGGGGAGAGCCTGGAGCAGCATC  
CGGACTTGCCTATGGGAGAGGGAGCCTGGAGGAGTGGCTGCATGTATCTGATAATACAGAC  
CCTGTCCTTCA

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**FIGURE 466**

MSAVILLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTCDSGLGCQDTLMLIE  
SGPVSLVLSKGCTEAKDQEPRVTEHRMGPGLSISYTFVCRQEDFCNNLVNSLPLWAPQPPA  
DPGSLRPCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRLGGGIFSNLRVQGCMPQPGCNLLN  
GTQEIGPGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETLLLID  
VGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSVLLNSLPPQ  
AAPVPGDRQCPTCVQPLGTCSSGSPPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGCVAQPSS  
FLLNHTRQIGIFSAEKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

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**FIGURE 467**

GAGGATTGCCACAGCAGCGGATAGAGCAGGAGAGCACCAACGGAGCCCTTGAGACATCCTG  
AGAAGAGCCACAGCATAAGAGACTGCCCTGTTGGTGTTCAGGATGATGGCCCTTCG  
AGGAGCTTCTGCATTGCTGGTCTGTTCTGCAGCTTCAGCCCCGCCAGTGTACCCA  
GGACCCAGCCATGGTGCATTACATCTACCAGCGTTCGAGTCTGGAGCAAGGGCTGGAAAA  
ATGTACCCAAGCAACGAGGGCATACTCAAGAATTCCAAGAGTTCTCAAAAATATATCTGT  
CATGCTGGGAAGATGTCAACACTACAAGTGAAGTACAAGAGTGCAGTGGTAACCTGGCACT  
GAGAGTTGAACGTGCCAACAGGGAGATTGACTACATAACACCTTCAGAGGGCTGACGAGTG  
CATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCAAGAAGCTGAAGAAGAGAAAAA  
GATCCGGACTCTGCTGAATGCAAGCTGTGACACATGCTGATGGCATAAAGTCTTGAAAAT  
AGTGAAGAAGATGATGGACACACATGGCTCTTGGTGAAGAGATGCTGTCTATAACTCTCCAAA  
GGTGTACTTATTAAATTGGATCCAGAAACAACACTGTTGGAAATTGCAAACATACGGGCATT  
CATGGAGGATAACACCAAGCCAGCTCCCAGCAAACTCTAACACTTCTGGCAGGGAAC  
AGGCCAAGTGAATCTACAAAGGTTTCTATTTTCTATAACCAAGCAACTCTAAATGAGATAAT  
CAAATATAACCTGCAGAAGAGGAAGTGTGGAAGATGCAATGCTGCTCCAGGAGGGTAGGCCG  
AGCATTGGTTTACCAAGCACTCCCCCTCAACTTACATTGACCTGGCTGTGGATGAGCATGGCT  
CTGGGCATCCACTCTGGGCAGGCACCCATAGCCATTGGTCTACAAAGATTGAGCCGG  
CACACTGGAGTGGAGCATCATGGGATACCCATGCAGAAGCCAGGATGCTGAAGCCTCATT  
CCTCTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGCCAGGGCCCTCATCGCATCAC  
CTGCATCTATGATCCACTGGGCACTATCAGTGAAGGAGACTGCCAACCTGTTCTCCCCAA  
GAGACCAAGAAGTCACTCCATGATCATTACAACCCCAGAGATAAGCAGCTATGCCCTGGAA  
TGAAGGAAACCAAGATCATTACAAACTCCAGACAAAGAGAAAGCTGCCCTGTAAGTAATGCAT  
TACAGCTGTGAGAAAAGAGCACTGTGGCTTGGCAGCTGTTCTACAGGACAGTGAGGCTATAGC  
CCCTCACAATATAGTATCCTCTAACTCACACACAGGAAGAGTGTAGAAGTGGAAATACGT  
ATGCCTCTTCCAAATGCACTGCCTTAGGTATCTTCAAAGAGCTTAGATGAGAGCATATC  
ATCAGGAAAGTTCAACAATGTCCATTACTCCCCAAACCTCCCTGGCTCTCAAGGATGACCAC  
ATTCTGATACAGCCTACTTCAGCCTTTGTTACTGCTCCCCAGCATTACTGTAACTCTG  
CCATCTCCCTCCCACAATTAGAGTTGATGCCAGCCCCCTAATATTACCAACTGGCTTTCTC  
TCCCCTGGCCTTGCTGAAGCTCTCCCTTTCAAAATGTTCTATTGATATTCTCCCATTT  
CACTGCCCAACTAAAATACTATTAAATATTCTTCTTTCTTTGAGACAAGGT  
CTCACTATGTGCCAGGCTGGCTCAAACCTCCAGAGCTCAAGAGATCCTCTGCCCTCAGCCT  
CCTAAGTACCTGGGATTACAGGCATGTGCCACCACACCTGGCTAAAATACTATTCTTATTG  
AGGTTAACCTCTATTCCCTAGCCCTGCTCCACTAAGCTGGTAGATGTAATAATAAA  
GTGAAAATTAACATTGAAATATGCCCTCCAGGTGTGGAGTGTGACATCATTGAATT  
TCGTTTCACCTTGAAACATGCACAAGTCTTACAGCTGTCAATTAGAGTTAGGTGAGT  
AACACAATTACAAGTGAAGAGATACAGCTAGAAAATACTACAAATCCCATAGTTTCCATTG  
CCCAAGGAAGCATCAAATACGTATGTTGTTCACCTACTCTTATAGTCATGCCTCATCGTT  
TCAGCCTAAAATTAATAGTCTGTCCTTCTAGCCAGTTTCTATGTCATGTCACAAGACCTTC  
AGGCCTTCAAATGATAATTCTCCAGAAAACCAAGCTCAAGGGTGAGGACCCCAACTCTAGCC  
TCCTCTGTCTGCTGCCTCTGTTCTCTTCTGCTTAAATTCAATAAAAGTGACACTG  
AGCAAAAAAAAAAAAAA

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**FIGURE 468**

MMVALRGASALLVLFLAAFLLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYIQEFQEF  
SKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRREIDYIQLREADECIVSEDKTLAEMLLQE  
AEEEKIRTLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTVWEF  
ANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVEDRMLL  
PGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDTPCRSQ  
DAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIHYNPRDK  
QLYAWNEGNQIIYKLQTKRKLPLK

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**FIGURE 469**

TGGCCTCCCCAGCTTGC CAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGGC  
AGT GTTTGCCTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCCTC  
CTAGTA ACT GTGTCTGACTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGTGGG  
GCAGGCACCTGCTGTGCCATCAGCCTGTGGCTCGAGGGCTGCGGATGTGCACCCGCTGGG  
CGGGAAAGGCAGGGAGTGCCACCCCGCAGCCACAAGGTCCCCTTCAGGAAACGCAAGCAC  
CACACCTGTCCTGCTTGCCAACCTGCTGTGCTCCAGGTTCCGGACGGCAGGTACCGCTGC  
TCCATGGACTTGAAGAACATCAATTTTTTAGGCGCTTGCTGGTCTCAGGATACCACCATCCT  
TTTCCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCATGACTCTCCAG  
TCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAGGCAGACATA  
CCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGGCTGTGGTGTG  
AAAGGTGCCAGCCTGGTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTAAATGGCAGAAA  
GGACATTCCCCCTCCCTCCCCAGGTGACCTGCTCTTCCCTGGGCCCTGCCCTCTCCCCA  
CATGTATCCCTCGGTCTGAATTAGACATTCTGGCACAGGCTCTGGGTGCATTGCTCAGAG  
TCCCAGGTCCCTGGCCTGACCTCAGGCCCTCACGTGAGGTCTGTGAGGACCAATTGTGGT  
AGTCATCTCCCTCGATTGGTTAACCTCTTAGTTTCAGACCACAGACTCAAGATTGGCTCTT  
CCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCAGGGAGGCCAATCAGCC  
CCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGACCTGTGACCTTCTGCCA  
GAATTGTATGCCCTGAGGCCCTTACACACTTACCAACTTAACCACACTGAAGCCCCA  
ATTCCCACAGCTTCCATTAAATGCAAATGGTGGTGGTCAATCTAATCTGATATTGACAT  
ATTAGAAGGCAATTAGGGTGTTCCTAAACAACCTCTTCCAAGGATCAGCCCTGAGGACAG  
GTTGGTGA CTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGTGGAGCAAGGGACAGGGAGC  
AGGGCAGGGCTGAAAGGGCACTGATTCA GACCAGGGAGGCAACTACACACCAACATGCTGG  
CTT TAGAATAAAAGCACCAACTGAAAAAA

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**FIGURE 470**

MRGATRVSIMLLLTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPG  
SHKVPFFRKHKHTCPCLPNLLCSRFPDGRYRCSDLKNINF

**Important features:**

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

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**FIGURE 471**

AGCGCCCCGGCGTCGGGCGGTAAAAGGCCGCAGAAGGGAGGCAC TGAGAAATGTCTTCC  
TCCAGGACCAAGTTCTCACCATGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGCTG  
CTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTCTGTCAGGCCAGAAAGCGGCC  
TGGAGTACCTGGAGGAATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTCAAAGCAA  
AGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGCCGTGCGGAGGCCAGGCTGTTCTCT  
GTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGCGTCCCC  
TCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTCCAGCCTATTTCAAAG  
GAGAAATCTCCTGGATGAAAAGAAAAAGTTCTATGGTCACAAAGGCCAGATGATGTTA  
TGGGATTTATCCGTCTGGGAGTGTGGTACAACCTCTCCGAGCCTGGAACGGAGGCTCTG  
GAAACCTGGAAGGAGAACGGCTTCATCCTGGGGAGTTTCGTGGTGGATCAGGAAAGCAGG  
GCATTCTCTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACTTCTGTT  
AAGCTGCTAAGATGATCAAACCACAGACTTGCCTCAGAGAAAAAATGATTGTGTGAAACTG  
CCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTCATGGATGTATTGTTCCACTCGT  
TCCCTAAGGAGTGGAGAACCCATTATACTCTACTCTCAGTATGGATTATTAATGTATTTAA  
TATTCTGTTAGGCCACTAAGGCAAAATAGCCCCAAACAAGACTGACAAAAATCTGAAAAA  
CTAATGAGGATTATTAAGCTAAAACCTGGAAATAGGAGGCTAAAATTGACTGCCAGGCTGG  
GTGCAGTGGCTCACACCTGTAATCCCAGCAGCTTGGGAGGCCAGGTGAGCAAGTCAC TGAG  
GTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCAGACCCGTCTCTACTAAAAATACAAAA  
ATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCGGAGGCTGAGGCAGGAGAA  
TCACCTGAACTGGAGGTGGAGGTTGCGGTGAGCTGAGATCACACCACTGTATTCCAGCCTG  
GGTACTGAGACTCTAACTAA

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**FIGURE 472**

MSFLQDPSFFTGMWSIGAGALGAAALLANTDVFLSKPQKAALEYLEDIDLKTLEKEPRT  
FKAHELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQP  
YFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEGFILGGVFVGS  
GKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 473**

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTATTCCAATAACACATTGGGTTT  
TGGGATTTAATTTCAAACACAGCAGAATGACATTTCCTGTCACTATTATTATTGTTGGT  
ATGTGAAGCTATTGGAGATCCAATTCAAGGAAGCAACACACATTGGAGAATGGCTACTTCATC  
AAGAAATAAAGAGAACCAAGTCACCCACACAATCATCTTAGAAGACAGTGTGACTCCTAC  
CAAAGCTGTCAAAACCACAGGCAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGAGGGTT  
AATTCTTGGTGCTGAAGCTGGGGCAGGGGTGTAAGAAAAACACTTAGATTCAATGATTGTA  
AATTAAAGGCAAATACACATATTAGTATTACCTAGTGTAAATGTATCCCTGTCATATATAACAA  
TAAGGTGAAATTATAAGTACCCCTATGCAGTTGGCTGGACAGTCTAAATTGGACTTTATTAAT  
TTTAAATCAGTAACTGATTATCAGTGGCTATGTGCTTAGATCTACAGGAGATCATATAAT  
TTGATACAAATAAAAGAAAAGTGTCTCTCCCTACAGAATTGACATTAAATGCGATACA  
GTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAAAGAAGGGAAAA  
TGTTGCCAAGGAAAAAAA

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**FIGURE 474**

MTFFLSLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGKG  
IVKGRNLDSRGLILGAEAWRGVKKNT

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**FIGURE 475**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGCCTGTCACCAAGAGCTGGAGACACCAT  
CTCCCACCGAGAGTCATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCCTC  
AGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTGAGAAATGCATG  
CAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGCTCAATCGGACCCCTGAAG  
CCCCAGAGGGTATTGTGGTGGCCTGGTGCCGGCTGGTGCCGCCAAGGTGCTCAGC  
GATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGCCATCTTCACC  
TACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAGCTCTCAC  
AGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTAACCTGACCAAGTTACCCAGTACGAC  
AAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAGAAGGTGCC  
GAGAAGCTGGGCTACGCCTGCGTCCCCAGGAAAAGGGCACTGCCGAAGACATCTACCAAG  
ATGGCTCTAACCAAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGGCATGAAGAAG  
TTTAAAGGCACACGCTCTTGAATATCTCTGGGGAGGGGAAACCTGAGCCGGCCGGCGTG  
CAGCTCTGGGAGACGTGATGTCCGAGGATGGCTTCTCTATCTCAGCTCGCCGAGGCCCTC  
CGGGCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGGTGGCTGGACCTG  
CTGCCGCGCGCTGCTGAGCTGCTGCCGGCTTGTGCTGTTAACGCGCCCGTGGTGGCG  
ATGACCCAGGGACCGCACGATGTGACGTGACATCGAGACCTCTCCCCGGCGCGGAATCTG  
AAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGGGGGTAAGCGCATCACC  
TTCTCGCCGCCGCTGCCCGCCACATGCAGGAGGCCTGCCGAGGCTGCACTACGTGCCGCC  
ACCAAGGTGTTCTAACGCTCCGAGGCCCTCTGGCGCGAGGAGCACATTGAAGGCCAC  
TCAAACACCGATGCCCGCGCATGATTTCTACCGCCGCCGCGAGGGCGCGCTGCTG  
CTGCCCTGTAACGTGGTGGACGACGTGGCGCATTGCACGGGCTGCGCCAGCTCTGGGAC  
GGCACCGCGCTCGTCAAGCGTTGGCGAGGACAGCACAGCCAGGGTGGCTTGTGGTACAG  
CCGCCGGCGCTGGCAAACCGAAAAGGATGACTGGACGGCCCTTATGCCGCATCTACTTT  
GCCGGCGAGCACACGCCCTACCGCACGGCTGGTGGAGACGGCGGTCAAGTCGGCGCTGCC  
GCCGCCATCAAGATCAACAGCCGAAGGGGCCTGCATCGGACACGCCAGCCCCGAGGGCAC  
GCATCTGACATGGAGGGCAGGGCATGTGCATGGGTGGCCAGCAGCCCTCGCATGACCTG  
GCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGGCCAGTTATCTCCAAAACACGACCCAC  
ACGAGGACCTCGCATTAAAGTATTTGGAAAAA  
AAAAAAAAAAAAAA

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**FIGURE 476**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRVI  
VVGAGVAGLVAAKVLSDAGHKVITLEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRLHK  
LCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMALNQ  
ALKDLKALGCRKAMKKFERHTLLEYLLGEGLSRPAVQLLGDMSEDGFYLSFAEALRAHSC  
LSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNLKVLKA  
DVVLLTASGPRAVKRITFSPPPLPRHMQEALRRLYVPATKVFLSFRRPFWREEHIEGGSNTDR  
PSRMIFYPPPREGALLLASYTWSAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDGTGVV  
KRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIFAGEHTAYPHGWVETAVKSALRAAIKI  
NSRKGPASDTASPEGHASDMEQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQNTTHRTSH

**Important features:**

**Signal peptide:**

amino acids 1-21

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**FIGURE 477**

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGTGGGACACTCTGGGCCGGCTTCTGCCTGCAT  
GGACGCTCTGAAGCCACCCCTGTCCTCTGGAGGAACCACGAGCAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA  
GAACTCAGAGCCGGAGGCCCAATTCACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGCTGAATTCT  
GCTGCTGTTCACAAAGATGCTTTTATCTTAACCTTTGTTTCCCACTTCCGACCCGGCGTTGATCTGCAT  
CCTGACATTGGAGCTGCCATCTCTGTGCTGATCACAGACCTAACCCGCTTACCTCTTGACCTGAA  
CAATCAGTCTGTGGAATTGAGGGAGGACCGGAAGGGGTTTCCCAGAAAGAACATGACCTAACAAAGTTGCTG  
CTTCTCAGATGCCAAGACTATGATGAGGTTTCCAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTTGGG  
ATATAGAAAACCAAAACCAGCCCTACAGATGCTATCTAACACAGGTTCTGATAGCAGAGTACCTGGGTT  
CTGTCTTGCATAAAGGTTATAAATCATCACCAGACCAAGTTGTCGGCATTTGCTCAGAAAGGCCAGACTG  
GATCATCTCGAATTGGCTTACACGTAACCTATGTAGCTGACACTCTGTATGACACCTTGGGACCAGAACG  
CATCGTACATATTGCAACAAGGCTGATATGCCATGGTGTGACACACCCAAAAGGCAATTGGTGTGAT  
AGGGAAATGTAGAGAAAGGCTTCACCCGGAGCTGAAGGCTGATCATCTTATGGACCCCTTGTGATGACCTGAA  
GCAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTACCTATGATGCTGAGAACACTAGGCAAAAGAGCACTCAG  
AAAACCTGTGCTCTAGCCAGAAGACCTGAGCGTACATGCTCAGGCTGACAGGTTGACCCCAAAGG  
AGCCATGATAACCCATCAAATATTGTTCAATGCTGCTCTTCTCAAATGTTGAGGCTGTTATGAGCC  
CACTCCTGATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA  
CAGCTGTGGAGCCAGAGTTGGATTCTTCAAGGGGATATTGGTTGCTGGCTGACGACATGAAGACTTGAAGCC  
CACATTGTTTCCCGGGTGCCTGACTCTAACAGGATCTACGATAAGGTACAAATGAGGCCAGACCC  
GAAGAAGTTCTGTGAAAGCTGGCTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
TTTCTGGACAAGCTCATTTGCAAGATCCAGGACAGCTGGGCGGAAGGGTTCTGTAATTGTCACTGGAGC  
TGCCCCATGTCCACTCAGTCATGACATTCTGGGGCAGCAATGGGATGTCAGGTGATGAAGCTTATGGTCA  
AACAGAAATGACAGGTGGCTGACATTACATTACCTGGGACTGGACATCAGGTCACGTTGGGGTGCCTGG  
TTGCAATTACGTGAAGCTGGAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
CAAGGGTACAAACGTGTCAGGATACCTGAAGGGACCTGAGAAGACACAGGAAGCCCTGGACAGTGTGCTG  
GCTTCACACAGGAGACATTGGTGGCTCCGAATGAAACTCTGAAGATCATGACCGTAAAAAGAACATT  
CAAGCTGGCCAAGGAGAACATATTGACACCAGAGAACAGGATAGAAAATATCTACAAACAGGAGTCACCAGTGTACA  
AATTGTTGACACGGGGAGAGCTACGGTCATCCTAGTAGGAGTGGGGTCTGACACAGGATGTACTTCC  
ATTGCAAGCTGGGGTGAAGGGGCTCTTGAGGAAGCTGCCCCAAAAGGAAAGGCAATT  
AGAAGACTTGCAGAAAATTGGGAAAGAAAAGTGGCTTAAACATTGAAACAGGTCAAAGCCATT  
AGAGCCATTTCATTGAAAATGGGCTTGTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTCAAATACTT  
TCGGACCCAAATTGACAGCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGGGGCCACTG  
TGCACCTGTTGTGAGAAAATGGATTAAAACATTCTACATTGTTGCTTCCCTATTTTTTAAC  
TGTAAACTCTAAAGGCATAGCTTTGTTTATATTGAGACATATAATGTAACACTAGTCCCAATAATCA  
ATCCTGCTTTCCCATCTCGATGTTGCTAAATTAAAGGCTCAGGGCTACTTTATCAACATGCCGTCTCAA  
GATCCCAGTTATGTCGCTCTCTCATGATTCCAAACCTTAATACTATTGAAACCAAAAGTCAAGGGT  
CAAAGGGACCCCTCTGTGGCTTCTTGTGTTGTGATAAAACATAACTTGCAACAGTCTATGCTTATTACA  
TCTTCTACTGTTCAAACAACTAAGAGATTAAAATTCTGAAAAGACTGCTTACAAATTGTTCTAGCCACTCCAC  
AAACCACTAAAATTAGTTAGCCTATCACTCATGTCATCATCTATGAGACAAATGTCGGATGCTCTT  
CTGCGTAAATTAAATTGTTGACTGAAGGGAAAGTTGATCATAACCAACATTCTCAAACCTCTAGTTAGATA  
TCTGACTTGGGAGTATTTAAATTGGGTCTATGACATACTGTCAGGAAATGCTGTTCTAAAGCATT  
CAGTAGGAACCTGGGAGTAAATGTTCCCTACAGTTGCTGAGCTGAGGCTGAGCTGTTGGGGAGGAGTTGACA  
GGTGGGCCAGTGAACCTTCCAGTAAATGAGGCAAGCAACTGAATAAAAACCTCTGAAACTGGGAACAAAGATCT  
ACAGGGCAAGCAAGATGCCACACAAACAGGCTTATTGTTGAGGAAACCAACTGATCTCCCCACCCCTGGATT  
AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTCTACTGTAAATGTAAGTCTTAAAATAAAC  
TATTACAGATAAAAAA

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**FIGURE 478**

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLFTKMLFIFNF  
LFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNSVGIEGGARKGVSQKNNDLTSCC  
FSDAKTMYEVFORGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQ  
FVGIFAQNRPWEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKALVLIG  
NVEKGFTPSSLVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPEDLSVIC  
FTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDVAISYPLAHMFERIVQAVVYSC  
GARVGFFQGDIRLLADDMKTLKPTLFPAPVRLLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFKE LQKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVM  
TFFRAAMGCQVYEAYGQTEC TGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTV  
NNEGEVCIKGTNVFKGYLKDP  
EKT QEA  
LDSDGWLHTGDIGRWPNGTLKIIDRKKNIFKLAQGEYIAPEK  
IENIYNRSQPVLQIFVH GESLRSSLVGVVVVPDTDV  
LPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKESGLKT  
FEQ VKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDS  
LYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

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FIGURE 479

GGAGGC GGAGGCC CGGGCAGCCGGCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGGC  
CCGGGGCCCCTAAGCCATT CCTGAAGTCATGGCTGGCCAGGACATTGGTGAACCGCCAATCC  
GGT**A**TGGACACTGGAAGCCCAGCCCCCTCATCAAGCCTTGGGGCTCGGAAGAACGGAGC  
TGGTACCTTACCTGGAAAGTATAAAACTGACAAACCAGCAGGGCCCTCGGGAGATCTGTCA  
GGGGCCGTGCTTTCTGCTGGTGA CTCATTGTCAATATCAAGTTGATCCTGGACACTCGG  
CGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCCCTAGGC  
CGCCTGGAGCCCCCACGGCGCAGAGGCAGTGGTCCCAGGGCTCTGGACGTAGAGGTGTAT  
TCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCA CGGTGCTGGAGGATGAGGCC  
GAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGCAGTGATGGCAAAA  
CGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCCCTAACATGGTA  
GCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTCCACCTCAAGGACACA  
GCCAAGGCTCTGCTGAGGAGCCTGGCAGCCAGGCTGGCCCTGGGCTGGAGGGACACA  
TGGGCCTCGTGGGACGAAAAGGAGGTCTGTCTCGGGGAGAAACATTCTAAGTCACCTGCC  
CTCTCTCCCTGGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGAGCTCAGCAGAACAG  
GCAGAGTGCCACTGGGAGACACAGAGCTGAACCGTGCAGCGCCGGCTCTGCAGCAAAGTT  
GAGGGCTATGGAAGTGTATGCAGCTGAAGGACCCACACCCATCGAGTCAGGCCCTGACCCA  
CTCCCAGACAACAAGGTCTCAATGTGCCCTGGCTGTCAATTGCAAGGGAACCGACCCAATTAC  
CTGTACAGGATGCTGCGCTCTGCTTCAGCCAGGGGTGTCTCTCAGATGATAACAGTT  
TTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGCACTGTTGGTCTGAGGGGCATC  
CAGCATACTCCCATCAGCATCAAGAAATGCCCGCTGTCTCAGCACTACAAGGCCAGCCTCACT  
GCCACTTCAACTGTTCCGGAGGCCAAGTTGCTGTGGTTCTGGAAAGAGGACCTGGACATT  
GCTGTGGATTTTCAGTTCTGAGCCAATCCATCCACCTACTGGAGGGAGGTGACAGCCTG  
TACTGCATCTCTGCTGGAAATGACCAGGGGTATGAACACACGGCTGAGGACCCAGCACTACTG  
TACCGTGTGGAGACCATGCCTGGCTGGCTGGTGCTCAGGAGGTCTTGTACAAGGAGGAG  
CTTGAGCCAAGTGGCCTACACCGGAAAAGCTCTGGATTGGACATGTGGATGCGGATGCC  
GAACAA CGCCGGGGCGAGAGTGACATCATCCCTGACGTTCCGATCCTACCACTTGGC  
CTCGGCCTCAACATGAATGGCTACTTCACGAGGCCTACTTCAAGAACGACAAGTTCAACACG  
GTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCTGAAGAAAGAAGCTTATGAAGTGGAA  
CACAGGCTGCTCAGTGAGGTGAGGTTCTGGACCACAGCAAGAACCTTGTGAAGACTCTTC  
CTGCCAGACACAGAGGGCCACACCTACGTGGCTTATTGCAATGGAGAAAGATGATGACTTC  
ACCACCTGGACCCAGCTGCAAGTGCTCCATATCTGGGACCTGGATGTGCGTGGCAACCAT  
CGGGGCTGTGGAGATTGTTGGAAGAACCACTTCTGGTGGTGGGGTCCGGCTTCC  
CCCTACTCAGTGAGAACGCCACCCCTCAGTCACCCCAATTTCCTGGAGGCCACCCCAAGGAG  
GAGGGAGCCCCAGGAGCCCCAGAACAGACAT**TGA**GACCTCCAGGACCCCTGCGGGCTGGT  
ACTGTGTACCCCCAGGCTGGCTAGCCCTTCCATCTGTAGGATTGTAGATGCTGGTA  
GGGGCTGGGCTACCTGTTAATCATGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCC  
CTGCTCCAACACCCCGTCTGAGTTAAAGTCTATTATTTACTCCTGTGGAGAACAGGGC  
AGGAGAGTACCTGGAATCATTACGATCCCTAGCAGCTCATCCTGCCCTTGAATACCCTCAC  
TTTCCAGGCCTGGCTCAGAACATCAACCTATTGACTGTCTGAGGGCCTTGAACAGGC  
CGAACCTGGAGGGCCTGGATTCTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTC  
TTACTCAGGAAACTGCTGTGCCCAACCCATGGACAGGCCAGCTGGGCCACATGCTGACAC  
AGACTCACTCAGAGACCCTAGACACTGGACAGGCCCTCTCAGCCTCTGTCCAGA  
TTTCAAAGCTGGATAAGTGGTCA TTGATTAAAAAGGAGAACCCCTCTGGAAAAAAA  
AAAAAAAAAAAAAAA

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**FIGURE 480**

MDDWKPSPLIKPGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTRR  
AISEANEDPEPEEQDYDEALGRLEPPRRRGSGPDRVLDVEVSSRSKVVAVDGTTLVLEDEARE  
QGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLKDTA  
KALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSSAEEA  
ECHWADTELNRRLRRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNVPAVIAGNRPNYL  
YRMLRSLLSAQGVSPQMITSVIFIDGYEEPMDVVALFGLRGIQHTPISIKNARVSQHYKASLTA  
TFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLY  
RVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVSRSYHFGIV  
GLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSKKEAYEVHRLNSEAEVLDHSKNPCEDSFL  
PDTEGHTYVAFIRMEKDDFTTWTQLAKCLHIWLDLVRGNHRLWRLFRKKNHFLVVGVPAASP  
YSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

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**FIGURE 481**

GAAAGA**ATGTTGTGGCTGCTTTTCTGGTACTGCCATT**CATGCTGAACCTGTCAACCA  
GGTGCAGAAAATGCTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT  
GCCTGGGATACCAATGAAGAATACCTCTCAAAGCGATGGTAGCTTCTCCATGAGAAAAGTT  
CCCAACAGAGAACGAAACAGAAATTCCCCTGTCCTACTTTGCAATGTAACCCAGAGGGTATCA  
TTCTGGTTGTGGTTACAGACCCTCAAAAAATCACACCCTCCTGCTGTTGAGGTGCAATCA  
GCCATAAGAATGAACAAGAACCGGATCAACAATGCCTCTTCTAAATGACCAAACCTGGAA  
TTTTAAAAATCCCTTCCACACTTGACCCACCATGGACCCATCTGTGCCATCTGGATTATT  
ATATTGGTGTGATATTTGCATCATCATAGTTGCAATTGCACTACTGATTTATCAGGGATC  
TGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAA  
AACATGATCACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGGGGCATATTA  
ATGATGCCTTC**TGACAGAGGATGAGAGGCTCACCCCTCTGAAGGGCTGTTGTTCTGCTTC**  
CTCAAGAAATTAAACATTGTTCTGTGTACTGCTGAGCATCCTGAAATACCAAGAGCAGAT  
CATATATTTGTTCAACCATTCTTCTTTGTAATAAATTGAAATGTGCTGAAAGTGAAAAG  
CAATCAATTATAACCCACCAACACCCTGAAATCATAAGCTATTGACGACTCAAAATATTCTAA  
AATATTTCTGACAGTATAGTGTATAATGTGGTATGTGGTATTGTTATTGATTAA  
GCATTTTAGAATAAGATCAGGCATATGTATATAATTTCACACTTCAAAGACCTAAGGAAAA  
ATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCATTGAAAATGGATCCTTT  
TGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAAGTAATTATTGTA  
AATGGATGGATAAAATGGAATTACTCATATAACAGGGTGGATTTCACACCA  
ACAGTTGATTATATATTTCTGAATATCAGCCCCCTAATAGGACAATTCTATTGTTGACCATT  
TCTACAATTGTAAGTCCAATCTGTGCTAACTTAATAAGTAATAATCATCTCTTTAAA  
AAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 482**

MLWLLFFLVTIAHAECLCQPGAEAFKVRSLIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPN  
REATEISHVLLCNVTQRVSFWFVVTDP SKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFL  
KIPSTLAPPMDPSVPIIIIFGVIFCIIIVAIALLILSGIWQRRRNKEPSEVDDAEDKCENM  
ITIENGIPSDPLDMKGIGLMMPS

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**FIGURE 483**

CGTCTCTGCGTTGCC **ATG** CGTCCGGGGGCCAGGGCACTCTGGCCTCTGCCCTGGGGGC  
CCTGGCTTGGGCCGTGGCTTCGTGAGCTCCATGGGCTGGGAACCCCGCGCCCGGTGGTGT  
TTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGTCCAGACTGATGTCAACCG  
GGCCGAGTGTGCTGCCCTCCGGCAACATTGACACCCTGGTCCAACCTCACCCACCCGGGAA  
CAAGATCAACCTCCTCGGTTCTTGGGCTTGCCACTGCCTCCCTGCAAAGATTGTGCGA  
CGGCGTGGAGTGCGGCCCCGGCAAGGCGTGCCTGCATGCTGGGGGCCCGCGCTGCGAGTG  
CGCGCCCAGCTGCTCGGGCTCCCGCGCGCTGCAGGCTGCCTGCAGACGGCGCCACCTA  
CCCGCAGCAGTGCAGCTGCGGCCGCGCTGCCCGGCCACCCGGACCTGAGCGTCATGTA  
CCGGGGCCGCTGCCGCAAGTCTGTGAGCACGTTGTGCCCCGCCACAGTCGTGCGTCGT  
GGACCAGACGGGCAGCGCCACTGCCTGGTGTGAGCGGCCCTGCCCTGTGCCCTCCAG  
CCCCGGCCAGGAGCTTGCCTGCGCAACAACACGTCACCTACATCTCCTCGTGCACATGCGCCA  
GGCCACCTGCTTCCGGGCCCTCATCGGCTGCCACGCCAGCTGCCAGGACCC  
TGAGGAGGCCAGGTGGTGTGAGTCAGAACAGAGGAAGAGAACCTCGTG**TGA**GCCTGAGGAC  
AGGCCTGGCCTGGTGCCTGGAGGGCCCCCATCATCCCTGTTATTATTGCCACAGCAGAGTC  
TAATTATATGCAACGGACACTCCTAGAGCCGGATTGGACCACTGGGGATCCAGAAC  
TCCCTGACGATACTGGAGGACTGAGGAAGGGAGGCCGGCTGGGGCCGGCTGGTGGGAT  
AGACCTGCGTCCGGACACTGAGCGCCTGATTAGGGCCCTCTCTAGGATGCCAGCCCT  
ACCCCTAACGACTATTGCCGGAGGATTCCACACTTCCGCTCTTGGGATAAACCTATTAA  
TTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATTCTGAAGAGGGCATGACTGC  
TTTCTCAGCCCCAACGCTCTAGCTGGGTGTACGGAGGGCTAGCCTGGGTGTACGGA  
GGGTCTAGCCTGGGTGAGTACGGAGGGCTAGCCTGGGTGAGTACGGAGGGCTAGCCTGGGT  
GAGTACGGAGGGCTAGCCTGGGTGTGATGGAGGATCTAGCCTGGGTGAGTATGGAGGGCT  
AGCCTGGGTGAGTATGGAGGGCTAGCCTGGGTGTGATGGAGGCTAGCCTGGGTGAGTAT  
GGAGGGCTAGCCTGGGTGTGATGGAGGGCTAGCCTGGGTGAGTATGGAGGGCTAGCCTG  
GGTGTACGGAGGGCTAGCTGAGTGCCTGGGACCTCAGAACACTGTGACCTTAGCCC  
AGCAAGCCAGGCCCTCATGAAGGCCAAGAACGGCTGCCACCATCCCTGCCAGCCAAAGAACT  
CCAGCTCCCCACTGCCTCTGTGTGCCCTTGCCTGTGAAGGCCATTGAGAAATGCCA  
GTGTGCCCTGGAAAGGCACGCCCTGTGCTCTGACACGGGCTGTGCTTGCCACAGAAC  
CACCCAGCGTCTCCCTGCTGTCCACGTCAGTTCATGAGGCAACGTCGCGTGGTCTCAGA  
CGTGGAGCAGCCAGCGCAGCTCAGAGCAGGGCACTGTGCTGGCGAGCCAAGTCCACTTG  
GGGGAGCTCTGGGGGACCAACGGGCCACTGCTACCCACTGGCCCCGAGGGGGGTGTAGACG  
CCAAGACTCACGCATGTGTGACATCCGGAGTCCTGGAGGGTGTCCAGTGGCACCAACTAG  
GTGCCTGCTGCCCTCACAGTGGGGTTCACACCCAGGGCTCTGGTCCCCAACACCTGCC  
GGCCAGGCCCTGCAGACCCAGACTCCAGCCAGACCTGCCTCACCCACCAATGCAGCCGGGCTG  
GCGACACCAGCCAGGTGCTGGTCTTGGGCCAGTCTCCACGACGGCTCACCTCCCTCCAT  
CTGCGTTGATGCTCAGAATCGCCTACCTGTGCCCTGCGTAAACCACAGCCTCAGACCAGCTA  
TGGGGAGAGGACAACACGGAGGATATCCAGCTTCCCCTGGGTGAGGAATGTGGGGAGC  
TTGGGCATCCTCCAGCCTCCAGCCCCCAGGCAGTGCCTACCTGTGGTGCCAGAAA  
AGTGCCCTAGGTTGGTGGCTACAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGCC  
CTGCCTCACCAAGGAAATAAGACTCAAGCCATAAAAAAAA

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**FIGURE 484**

MRPGAPGPLWPLPWGALAWAVGFVSSMGSGNPAPGGVCWLQQQEATCSLVLQTDVTRAECCA  
SGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGVECGPGKACRMLGGRPRCEAPDCS  
GLPARLQVCGSDGATYRDECRLAARCRGHPDLSVMYRGRCRKSCHEVVCPRPQSCVVDDQTGS  
AHCVVCRAAPCPVPSSPGQELCGNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPEEPPG  
GESAEEEENFV

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 73-77, 215-219

**Osteonectin domain proteins.**

amino acids 97-130, 169-202

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**FIGURE 485**

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCTCGTAGCGGGGCCGGATCCCC  
GAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTGAGATGAATGGCTGGGA  
AACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGTGGCGCCCTGGTGGCCTGCATCATC  
GTCTTGGCTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGATCATG  
GAGCTGGAAGGCAGGGTCCGCAGGGCGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGAAGAAC  
GAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGGCCAAC  
TTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCAGTTGGTGAATAACATC  
ACCACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCCTGCAGAGGAATTAC  
GGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAAAGAACAGACCAACCTGGAGAGGAAGTTC  
TCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTGTGAGGAGCGA  
ATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTCCAGAGACCTGAGTGAAAACAAC  
GACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAGGCAGCAGGCC  
CCACACACAGAGGTGCCACAAGGGAAAGGAAACGTGCTTGGTAACAGCAAGTCCCAGACACCA  
GCCCCAGTTCCGAAGTGGTTGGATTCAAAGAGACAAGTTGAGAAAGAGGAACCAATGAG  
ATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAGGCCAGGCCGGAGCAG  
GTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGAGCCGGAGAACTGGCCAGACC  
CCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGATGGAGGGCCCTGAGCGA  
GACCAGCTTGTCACTCCCCGACGGACAGGAGGAGGAGCAGGAAGCTGCCGGGAAGGGAGAAC  
CAGCAGAAAATGAGAGGAGAAGATGACTACAACATGGATGAAAATGAAGCAGAATCTGAGACA  
GACAAGCAAGCAGCCCTGGCAGGGAAATGACAGAAAACATAGATGTTTAATGTTGAAGATCAG  
AAAAGAGACACCATAAATTACTTGATCAGCGTGAAGAGGAAATCATAACTTGAATTGAA  
CTGGAATCACATATTCACAAACAGGGCGAAGAGAGTGAATGACTATAAAATGTTCATGAGGGACTGA  
ATACTGAAAATGTGAAATGTACTAAATAAAATGTACATCTGA

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**FIGURE 486**

MMGLGNRGRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGAV  
ELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQLKT  
LQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVASRD  
LSENNDQRQQLQALSEPQPRLQQAAGLPHTEPQPGKGNVLGNSKSQT PAPSSEVVLD SKRQVEK  
EETNEIQVVNEEPQRDR LPQE PGRE QVVEDRPVGGRGFGGAGELGQTPQVQA ALSVSQENPEM  
EGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGNDRNIDVF  
NVEDQKRDTINLLDQREKRNHTL

**Important features:**

**Signal peptide:**

amino acids 1-29

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**FIGURE 487**

AACTCAAACCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCGGAGTGGCCTGGCAGGG  
TGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTCCCTCATGTAT  
GGCAAGAGCTACTCGTGC GGTC TTCTCCCTGGCATA CAGCTCACAGCTCTTGGCCT  
ATAGCAGCTGTGGAATT TACCTCCC GG GTGCTGGAGGCTGTTAATGGGACAGATGCTCGG  
TTAAAATGCACTTCTCCAGCTTGGCCCTGTGGGTGATGCTCTAACAGTGACCTGGAATTT  
CGTCCTCTAGACGGGGGACCTGAGCAGTTGATTCTACTAACACATAGATCCCTCCAACCC  
ATGAGTGGCGGGTTAAGGACCGGGTGTCTTGGATGGGAATCCTGAGCGGTACGATGCCCTCC  
ATCCTCTCTGGAAACTGCAGTTGACGACAATGGGACATACACCTGCCAGGTGAAGAACCCA  
CCTGATGTTGATGGGTGATAGGGAGATCCGGCTCAGCGTCGTGCACACTGTACGCTCT  
GAGATCCACTCCTGGCTCTGGCATTGGCTCTGCCTGTGCACTGATGATCATAATAGTAATT  
GTAGGGCCTCTCCAGCATTACGGAAAAGCGATGGCCGAAAGAGCTCATAAAGGGTG  
GAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCTGTTATTTAGAA  
GACACAGACTAACAAATTAGATGGAAGCTGAGATGATTCCAAGAACAAAGAACCCCTAGTATT  
TCTTGAGTTAATGGAACCTTTCTTGGCTTTCCAGTTGACCCGTTCCAACCAGTTC  
TGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCACAGTGCTCCTCCATAT  
CACCAAGTCATACACAGCCTCATTATTAAGGTCTTATTAATTCAGAGTGTAAATTTTCAA  
GTGCTCATTAGGTTTATAAACAAAGAAGCTACATTTGCCCTTAAGACACTACTTACAGTGT  
TATGACTTGTATAACATATATTGGTATCAAAGGGATAAAAGCCAATTGTCGTTACATTT  
CCTTCACGTATTCTTTAGCAGCATTGCTACTAAAGTTAATGTGTTACTCTCTTCC  
TTCCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTGTTCTGATTAACAGTAAATC  
CTAAATTCAAACGTAAATGACATTTTATTTATGTCTCTCCTTAACATATGAGACACATC  
TTGTTTACTGAATTCTTCATATTCCAGGTGATAGATTTTGTG

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**FIGURE 488**

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTWT  
NFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSDGNPERYDASILLWKLQFDDNGTYTCQVK  
NPPDVGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLFQHYRKKRWAERAHK  
VVEIKSKKEERLNQEKKVSVYLEDTD

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**FIGURE 489**

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**FIGURE 490**

MLLWVSVVAALALAVLAPGAGEQRRAAKAPNVVLVVSDSFGRLTFHPGSQVVKLPFINFM  
KTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQKF  
GKLDYTSGHSISNRVEAWTRDVAFLLRQEGRPMVNLRNRTKVRVMERDWQNTDKAVNWLRK  
EAINYTEPFVIALGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLSEMHP  
VDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIYSSDHG  
ELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNNVSLVDIYPTMLDIAGIPLPQNLSG  
YSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGASILPQLFD  
LSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIGQNYNSVIA  
NLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

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**FIGURE 491**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA  
GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATGGC**  
CTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACTGGT  
TGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGT  
TGGCTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAGTGTGA  
CATCTATAGCACCCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGAC  
ATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTGTGGTGGCATGAGATGCACAGTCTT  
CTGCCAGGAATCCCAGCAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTTGG  
AGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTCATGGGATCCTACGGACTTCTACTC  
ACCACCTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTCTTACTTGGCATTATTC  
TTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCCCAGAGAAATCG  
CTCCAACTAACGATGCCTACCAAGCCAACCTCTGCCACAAGGAGCTCTCCAAGGCCTGG  
TCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGTATGTG**TGA**AGAAC  
CAGGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAGCACCCGAGGCCA  
CAGGTGAGGGACACTACCACCTGGATCGTGTAGAAGGTGCTGCTGAGGATAGACTGACTTGG  
CCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATGCAGGTTGAATTGCCAA  
GGATGCTGCCATGCCAGCCTTCTGTTTCTCACCTGCTGCTCCCTGCCCTAAGTCCCC  
AACCTCAACTTGAAACCCATTCCCTAACGCCAGGACTCAGAGGATCCCTTGCCTCTGGT  
TTACCTGGGACTCCATCCCCAACCCACTAATCACATCCCACTGACTGACCCCTGTGATCAA  
AGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATTGCTGGGATGGGAAGGAGAAGCAGT  
GGCTTTGTGGCATTGCTTAACCTACTTCTCAAGCTTCCCTCAAAGAAACTGATTGCC  
TGGAACCTCCATCCCACTCTGTTATGACTCCACAGTGTCCAGACTAATTGTGCATGAAC  
AAATAAAACCATCCTACGGTATCCAGGAAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAA  
GGCAGCCTGGGACATTAAAAAAATA

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**FIGURE 492**

MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSYVGASIVTAVGFSKGLWMECATHSTGITQ  
CDIYSTLLGLPADIQAAQAMMVTSAASSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFI  
LGGLLGFIPVAWLHGISLDFYSPLVPDSMKEIGEALYLGISSLFSLIAGIILCFSCSSQR  
NRSNYDAYQAQPLATRSSPRPGQPPKVSEFNSYSLTGYV

**Important features:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

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**FIGURE 493**

GCAC TGCTGCTGCCATCAGCTGCTGAAGCTCCATGGTGCCCAGAATCTCGCTCCTGCT  
TATGTGTCAGTCTGTCTCCTCCTTTGTGTCAGGGAAAGTCATCGCTCCGCTGGCTCAGAA  
CCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAGTGC  
TGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCAATGTGGTCCCCCTGCACCTTC  
TGGCCCTGCTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAAACGATTTGTTGTGAAG  
CTGAAGGTTCAAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGTGAAAGC  
AGAACGACGTTTCCCTGAGAAGACATAGAAAGAAAATCAACTTCAACTAAGGCATCTCAGAAA  
CATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTACAAAATGATGCAGCT  
CCAAGCCATTGTATGGCCATGTGGGAGACTGATGGGACATGGAGAATGACAGTAGATTATCA  
GGAAATAAAATAAGTGGTTTCCAATGTACACACCTGTAAAA

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**FIGURE 494**

MVPRIFAPAYVSVCLLLLCPREVIAPAGSEPWLQPAPRCGDKIYNPLEQCCYNDIAIVSLSET  
RQCGPPCTFWPCFELCCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

**Important features:**

**Signal peptide:**

amino acids 1-25

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**FIGURE 495**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT  
TCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCTGA  
TGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTTGCT  
ATGATGATGCCGTCGTGCCCTGGCCAGGACCCAGACGTGTGAAACTGCACCTTCAGAGTCT  
GCTTGAGCAGTGCTGCCCTGGACCTTCATGGTAAGCTGATAAACAGAACTGCGACTCAG  
CCCAGACCTCGGATGACAGGCTTGTGCAGTCAGCTAATGGAACATCAGGGAACGATGA  
CTCCTGGATTCTCCTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGATCTGGGA  
TGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATTCTGTGACC  
TGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCTCTAGAATTCTGGA  
CAGCATGAGATGCGTGTGCTGATGGGGCCAGGGACTCTGAACCCCTCTGATGACCCCTATG  
GCCAACATCAACCCGGCACCAACCCAAAGGCTGGCTGGGAACCCCTCACCCCTCTGTGAGATT  
TTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAATAAATTATGTA  
CTTTATAAATGAAAA

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**FIGURE 496**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVPL  
ARTQTCGNCTFRVC FEQCCPWT FMVKL INQN CDSARTS DDL RCRSVS

**Important features:**

**Signal peptide:**

amino acids 1-24

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**FIGURE 497**

TGAAGGACTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTCAGCTGAAGGGAGGCACTC  
CTTGGCCTCCGAGCCGATCACATGAAAGGTGGTGCCTAAGTCTCCTGCTCTCCGTCCTGGC  
ACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCCCTCA  
GAACCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGGCCAG  
CGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGCCAGGCAGCAGCTTGCCTA  
GGAGACTTCAAACCTCGGATTCAAGCCTGCTGCAGAACAGATCTCCATGAGGCACGATGGCAACAT  
GGTCTCTCTCCATTGGCATGTCCTGGCCATGACAGGCTTGATGCTGGGGCCACAGGGCC  
GACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAAGGCCCTGAAGCCCACCAAGCCGGCT  
CCTGCCTTCCCTTTAAGGGACTCAGAGAGACCCCTCTCCGCAACCTGGAACTGGGCCTCTC  
ACAGGGGAGTTTGCTTCATCCACAAGGATTGATGTCAGAACAGACTTCTCAATTATC  
CAAGAGGTATTTGATACAGAGTGCCTGCTATGAATTTCGCAATGCCTCACAGGCCAAAG  
GCTCATGAATCATTACATAACAAAGAGACTCGGGGAAATTCCCAAACGTTGAGATGAGAT  
TAATCCTGAAACCAAATTAAATTCTTGATTACATCTTGTCAAAGGGAAATGGTTGACCC  
ATTTGACCCCTGTCTTCACCGAAGTCGACACTTCCACCTGGACAAGTACAAGACCATTAAGGT  
GCCCATGATGTACGGTGCAGGCAAGTTGCTCCACCTTGACAAGAACGTTGTTGTCATGT  
CCTCAAACCTGCCCTACCAAGGAATGCCACCATGCTGGTGCCTCATGGAGAAAATGGTGA  
CCACCTCGCCCTGAAGACTACCTGACCACAGACTTGGTGGAGACATGGCTCAGAAACATGAA  
AACAGAAACATGGAAGTTCTTCCGAAGTCAAGCTAGATCAGAACGATGAGATGATGA  
GCTGCTTAGGCAGATGGGAATCAGAAGAACGTTCTCACCCCTTGCTGACCTTAGTGAACCTC  
AGCTACTGGAAGAAATCTCAAGTATCCAGGGTTTACGAAGAACAGTGATTGAAGTTGATGA  
AAGGGCACTGAGGCAGTGGCAGGAATCTGTCAGAAATTACTGCTATTCCATGCCTCTGT  
CATCAAAGTGGACCGGCCATTTCATTGATCTATGAAGAACCTCTGGAATGCTTCTGTT  
TCTGGCAGGGTGGTGAATCCGACTCCCTATAATTCAAGGACATGCATAAGCACTCGTCTG  
TAGTAGATGCTGAATCTGAGGTATCAAACACACAGGATACCAGCAATGGATGGCAGGGAG  
AGTGTCTTTGTTCTTAACTAGTTAGGGTGTCTCAAATAAAATACAGTAGTCCCCACTTA  
TCTGAGGGGGATACATTCAAAGACCCCAAGCAGATGCCTGAAACGGTGGACAGTGCTGAACCT  
TATATATATTTTCTCACACATACACATGATAAAAGTTAATTATAAAATTAGGCACAG  
TAAGAGATTAACAATAAAACAACATTAAGTAAATGAGTTACTTGAACGCAAGCACTGCAAT  
ACCATAACAGTCAAACTGATTATAGAGAAGGCTACTAAGTGACTCATGGCGAGGAGCATAGA  
CAGTGTGGAGACATTGGCAGGGGAGAATTACATCCTGGTGGACAGAGCAGGAGCATGC  
AAGATTCCATCCCACTACTCAGAATGGCATGCTGCTTAAGACTTTAGATTGTTATTCG  
AATTTTCATTTAATGTTTGGACCATGGTTGACCATGGTTAAGTGAACGACTGCAGAAAGCAA  
AACCATGGATAAGGGAGGACTACTACAAAGCATTAAATTGATACATATTTAAAAAAA  
AAAAAAA

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**FIGURE 498**

MKVVPSLLSVLLAQVWLVPGLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGEE  
EKAWLMASRQQLAKETSNGFSLLRKISMHDGNMVFSPFGMSLAMTGLMLGATGPTETQIKR  
GLHLQALKPTKPGLLPSLFKGLRETLISRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYFDTE  
CVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTPEDPVFTE  
VDTFHLDKYKTICKVPMGYAGKFASFTFDKNFRCHVLKLPYQGNATMLVVLMEKGMDHCALEDY  
LTSDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIFSPFADLSELSATGRNLQ  
VSRVLRRTVIEWDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLFLGRVVNP  
TLL

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**FIGURE 499**

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGCAACAGCTTGCCTGCAGGGAGCTCCCG  
TGGCGCTCCGCTGGCTGTGCAGGCCA**ATGGATT**CCTTGCAGAAATGCTGATCTCAGTCG  
CAATGCTGGGCGCAGGGCTGGCTACCGCTCCTCGTTATCGTGACCCGGAGAGC  
GGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAGGC  
CCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCACCACGCAAGGAGAACGTGG  
CCTGGAGGAAGAACTGGATGGTTGGCGCGAAGGCAGGCCAGCAGGGAGGTACCG**TGAG**ACC  
GGACTTGCCTCCGTGGCGCCGGACCTTGGCTGGCGCAGGAATCGAGGCAGCCTTCTCC  
TTCGTGGGCCAGCGGAGAGTCCGGACCGAGATAACCATGCCAGGACTCTCGGGGTCTGTGA  
GCTGCCGTGGTGAGCACGTTCCCCAAACCCCTGGACTGACTGCTTAAGGTCCGCAAGGC  
GGGCCAGGGCCGAGACGCCAGTCGGATGTGGTAAGTAAAGAACCAATAAAATCATGTTCCCT  
CCAAAAAAA

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**FIGURE 500**

MDSLRKMLISVAMLGAGAGVGYALLIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLAT  
LQEAAATTQENVAWRKNWMVGEGGASGRSP

**Important features:**

**Signal peptide:**

amino acids 1-18

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**FIGURE 501**

CAGGAGAGAAGGCACCGCCCCACCCGCCTCAAAGCTAACCTCGGGCTTGAGGGAAAGAG  
GCTGACTGTACGTTCTTCTACTCTGGCACCACTCTCCAGGCTGCCATGGGCCAGCACCCC  
TCTCCTCATCTGTTCTTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCCACCTTGT  
GGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCCAGGACCAGAG  
TAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAAGATGCTGCCACTGCTGGAGGTGGC  
AGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCACACCATCTCCGGAGAGTGGATCGTCT  
GGAGCAGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTGCCCTGTGTAGAGTTGATGA  
GAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAAGAAGGAATGAGAAGTACGATATGGT  
GACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCGATTGGTGG  
CCCAGCTGGTCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACGTGTTAGATGG  
GACACAGAACATGACACAGCCTTGTCTTCCAAAGGCTGCCGACTTCACCCCTGCCATGGCTGC  
CCGGAAAAGCTTCCGAGTCCGGTGCCCTCCCTGGTAGGCACAGGGCAGCTGGTATATGG  
TGGCTTCTTATTTGCTCGGAGGCCCTCTGGAAGACCTGGTGGAGGTGGTGGAGATGGAGAA  
CACTTGCAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGACAGCTCAGTATTCCC  
AGCAGAGGGCTGATCCCCCTACGGCTTGACAGCAGAACCTACATGACCTGGTAGCTGA  
TGAGGAAGGTCTTGGGCTGTCTATGCCACCCGGAGGATGACAGGCACCTGTGTCTGCCAA  
GTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCAGTCCAGAGAACATGC  
TGAGGCTGCCTTGTCTGTGGACCCCTATGTCGTCTATAACACCCGCTGCCAGTCG  
GGCCCGCATCCAGTGCTCTTGTGATGCCAGCGGCACCCCTGACCCCTGAACGGCAGCAGCTCC  
TTATTTCCCCCAGATATGGTGCCCATGCCAGCCTCCGTATAACCCCCGAGAACGCCAGCT  
CTATGCCCTGGATGATGGCTACCAGATTGTCTATAAGCTGGAGATGAGGAAGAAAGAGGAGGA  
GGTTTGAGGAGCTAGCCTGTTTGCATCTTCTCACCCCACATTTATATTATATCCC  
CACTAAATTCTGTTCTCATTCTCAAATGTGGCCAGTTGTGGCTCAAATCCTCTATATT  
TTTAGCCAATGCCAATCAAATTCTTCAGCTCCTTGTTCATACGGAACCTCAGATCCTGAG  
TAATCCTTTAGAGCCGAAGAGTCAAAACCTCAATGTCCTCCTGCTCTCCTGCCCATG  
TCAACAAATTTCAGGCTAAGGATGCCAGACCCAGGGCTCTAACCTGTATGCCAGGCC  
CAGGGAGCAGGCAGCAGTGTCTCCCTCAGAGTGACTTGGGAGGGAGAAATAGGAGGAGA  
CGTCCAGCTGTCCCTCTCCCTCACCTCCCTCAGTGCTGAGGAACAGGACTTCTC  
CACATTGTTGTATTGCAACATTTGCATTAAAGAAAATCCACAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 502**

MGPSPLLILFLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAAELRDFKNKML  
PLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKKGRRN  
EKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDTQNDTAFVFPLRDF  
TLAMAARKASRVRVFPFWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLANRTVV  
DSSVFPAAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQQWDTP  
CPRENAEAAVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPERRYGAHASLRYN  
PRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

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**FIGURE 503**

TGCGGCCAGTGTAGACCTGGGAGGAATGGCGGCTGCTGGCTGCTGGCTTTCTGGCTTG  
CTCGGTGCCAGGGCCAGGCCGTGGTGGAAAGACTGGACCTGAGCAGCTTGGGCC  
CTGGTACGTGCTTGGCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAAGAA  
CGTCGTGGGGTGGTGGTACCTCACTCCAGAAAACAACCTGCGGACGCTGCCTCTCAGCA  
CGGGCTGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAAGCGAAACTCCGGATGGGTGTT  
TGAGAATCCCTCAATAGGCGTGCTGGAGCTGGGTGCTGGCCACCAACTTCAGAGACTATGC  
CATCATCTTCACTCAGCTGGAGTTGGGACGAGCCCTAACACCCGTGGAGCTGTACAGTCT  
GACGGAGACAGCCAGCCAGGAGGCCATGGGCTCTCACCAAGTGGAGCAGGAGCCTGGCTT  
CCTGTACAGTAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGATCCTCTGTG  
AGTGTGCGTCCCAGTAGGGATGGCGCCACAGGGTCTGTGACCTCGGCCAGTGTCCACCC  
ACCTCGCTCAGGGCTCCCCGGGCCAGCACAGCTCAGAATAAGCGATTCCACAGCA

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**FIGURE 504**

MGGLLAAFLALVSVPRAQAVWLGRLDPEQLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
TPENNLR~~T~~LSSQHGLGGCDQSVM~~D~~LIKRN~~S~~GWVFENPSIGVLELWVLATNFRDYAIIFTQLEF  
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Important features:**

**Signal peptide:**

amino acids 1-20

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**FIGURE 505**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGGCAGAGGTCTCACA  
GCAGCCAAGGAACCTGGGGCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC  
CTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGTTCGAGTGC  
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTCGAGAACGCGGCTACTCTGTGGGCG  
ACGCTCATCGCCCCCAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACATAGTT  
CACCTGGGCAGCACAAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG  
TCCTTCCCCCACCCGGCTCAACAAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG  
CTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCTCTCCTCA  
CGCTGTGTCAGTGTGGCACAGCTGCCATTCCGGCTGGGAGCAGTCCAGCCCCAG  
TTACGCCCTGCCACACCTTGCATGCCAACATCACCATATTGAGCACCGAGAAAGTGTGAG  
AACGCCCTACCCGGCAACATCACAGACACCATGGTGTGCCAGCGTGCAGGAAGGGGCAAG  
GACTCCTGCCAGGGTGACTIONGGGGCCCTCTGGTCTGTAACCAGTCTTCAAGGCATTATC  
TCCTGGGCCAGGATCCGTGTGCGATCACCGAAAGCCTGGTCTACACGAAAGTCTGCAA  
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATAGACTGGACCCACCCACAGCCCA  
TCACCCCTCCATTCCACTTGGTTGGTCTGTCACTCTGTTAATAAGAACCTAAGCC  
AAGACCCCTCTACGAACATTCTTGGGCTCCTGGACTACAGGAGATGCTGTCACCTAATAATC  
AACCTGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTGAAATATTGTGACTCTG  
GGAATGACAACACCTGGTTGTTCTGTTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT  
ATATCAAGGTTCAATAATATTGCTAAATGAAAAAAA  
AAAAAAA

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**FIGURE 506**

MRILQLILLALATGLVGGETRIIKGFECKPHSQWPQAALFEKTRLLCGATLIAPRWLLAAHC  
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSIWTAV  
RPLTLSSRCVTAGTSCLISWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTMVCA  
SVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

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**FIGURE 507**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTACAGAGACGCCGACCCAGACATGAGG  
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA  
CCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC  
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCCTGTC  
CAGAACGCCAAACTCTTGACCACCGAGGAGAACCCACGAGGTCAAGGCAGGGCAGGGCCCCCATCCTT  
CCAGGCACCAAGGCCTGGATGGAGACCGAGGGACACCCTGGCCGTGCTGAGTCCCAGGCC  
GACCATGACAGCCTGTACCACCCCTCCGCTGAGGAGGACCAAGGGCGAGGAGAGGCCCGGTTG  
TGGGTGATGCCAAATCACCAAGGTGCTCCTGGGACCGGGAGGAAGACCAAGACCACATCTACCAC  
CCCCAGTAGGGCTCCAGGGCCATCACTGCCCGCCCTGTCCCAAGGCCAGGCTGTTGGGA  
CTGGGACCCCTCCCTACCCCTGCCAGCTAGACAAATAACCCAGCAGGCAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 508**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKA  
WGVVEPPEKDDQLVVLF  
PVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSL  
YHPPPEEDQGEERP  
RLWVMPNHQVLLGPEEDQDH<sup>I</sup>YHPQ

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**FIGURE 509**

GC GG AG CC GG CG CC GG CT GC GC AG AG GG AG CC GG CT CG CC GG CC AC CT CG CT GGG AG CC  
AC GAGG CT GC CG CA TC CT GC CC CT CG GA AC A **AT** GG ACT CG GCG CG AG GT GCT TGG CG CG  
CT GCT C CT TGG GAC G CT GC AG GT GCT AG CG CT GCT TGG GCG CC AT GAA AG CG CAG CC AT G  
GC GG CAT CT GCA AAC AT AG AGA ATT CT TGG CT CC AC AC A CT CC AG T GCT A ACT CA AC AG AG  
ACT CT CC AAC AT GT GC CT TGT ACC AT AAC AT GAA ACT TCC AAC AG T ACT GT GAA ACC ACCA  
ACT T CAG TT GC CT CAG ACT CC CAG TA AT ACA AC GG TC ACC ACC AT GAA AC CT AC AG CG G CAT CT  
AAT ACA AAC ACC AG GG AT GG T CT CA AC AA AT GACT TCT ACC ACC TT AA AG T CT AC ACC  
AAA ACA AAC AG T GTT CAC AG A AC AC AT CT CAG AT AT CA AC AT CC ACA AT GAC CG TA ACC CAC  
AAT AG TT CAG T GAC AT CT GCT GCT T CAT CAG TA ACA AT CACA AC AT AT G CATT CT G AAG CA  
AAG AA AGG AT CAA A AT TT GAT ACT TGG AG CTT GT TGG GT ATT GT ATT ACG CT GGG AG TT  
TT AT CT ATT CT TAC ATT GG AT G CAA A AT GT ATT ACT CA AG A AG GGG CATT CG GT AT CG A ACC  
A T A G AT G A A C AT G AT G C C AT C ATT **TA** AG G A A AT CC AT GG ACC A AG G AT GG A AT C A G AT TG AT  
G C T G C C C T AT CA AT TA AT TT GG TT ATT A AT AG TT AAA AC A AT ATT CT CTT TT G AAA ATA  
G T AT AA AC AGG C C AT G C AT AT A AT GT AC AGT GT ATT AC G T AA AT AT G T AA AG AT T CTT C A AGG  
TA AC A AGG TT GG TT GG T GAA A AT AA AC AT CT GG AT CT T AT AG AC CG TT C AT AC A AT GG TT  
AG CA AG TT C AT AG TA AG AC A A AC A AG T C CT AT CTT TTT TGG CT GGG GT GGG G CATT GG  
TC AC AT AT G ACC AG T A AT G A A AG A C G T C AT C ACT G A A AG A C A G A AT G C C AT CT GGG C AT A CA  
A AT A A G A AG TT G T C AC AG C ACT C AG G AT TT GG GT AT CTT GT AG C T C AC AT AA AG A ACT T  
C AG T G C T T T CAG AG G C T GG AT AT C TTA AT T A CT A AT G C C AC AC AG A A AT T A C A AT C A A A  
CT AG AT CT G A A G C AT A AT T A AG A A A AC AT C A AC AT T T T G C T T A A C T G T A G T A G T  
GG T C T A G A A A C A A A A T C T C C

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**FIGURE 510**

MGLGARGAWAALLLGTIQLVALLGAAGHESAAMAASANIENSGLPHNNSANSTETLQHVPSDHT  
NETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTPGMVSTNMTSTTLKSTPKTTSQNTS  
QISTSTMVTNHNSVTSAASSVTITTMHSEAKGSKFDTGSFVGIVLTLGVLSILYIGCKM  
YYSSRRGIRYRTIDEHDAAI

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**FIGURE 511**

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**FIGURE 512**

MARMSFVIAACQLVLGLLMTSLTESSIQNSECQLCVCEIRPWFTPQSTYREATTVDCNDLRL  
TRIPSNLSSDTQVLLQSNNIAKTVDELQQLFNLTELEDFSQNNFTNIKEVGLANLTQLTTLHL  
EENQITEMTDYCLQDLSNLQELYINHNQISTISAHAFAGLKNNRLHLNSNKLVIDSRWFDS  
TPNLEILMIGENPVIGILDMMNFKPPLANLRSVLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV  
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSDRYALDNLPELT  
KLEATNNPKLSYIHLRAFRSVPALESMLNNNALNAYQKTVESLPNLREISIHSNPLRCDCV  
IHWINSNKTNIRFMPLSMFCAMPPEYKGHQVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT  
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV  
QGADTRVATIKVNGLLDTQVLKIYVKQTESHSILVSWKVNSVMTSNLKSSATMKIDNPH  
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTKNAAFAVDISDQETST  
ALAAMGSMFAVISLASIAVYFAKRFKRKNYHSLKKYMQKTSSIPLNELYPPLINLWEGDSE  
DKDGSAADTKPTQVDTSRSYMW

**Important features:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 508-530

**N-glycosylation sites:**Amino acids 69-73; 96-100; 106-110; 117-121; 385-389; 517-521;  
582-586; 611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

**N-myristoylation sites:**

Amino acids 16-22; 224-230; 464-470; 637-643; 698-704

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**FIGURE 513**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTGCATCCTCCGACCTTCC  
CAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGCCACACCGCAAGGA  
GTTGGACAAAGGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAAACGCTGCTGG  
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCACCAGGCTGG  
GAAGGAAAGCAGAGAAA**ACTTGGCCAAGGGTCAACC**ATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCACC**ATGCTGCTGGCCAGGCCGGGAAGGAGCTG**CAGAATGC  
TCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAAC**AGCTGCTGAATGGCAACC**ATCAAAG  
CGGATCTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGCTCAGTCAA  
CACGCC**TTT**CATCAACCTCCGCC**CTGTGGAGGAGCGTCGCCAAC**ATCATGCCTAAACTGG  
CATCCGGCTTGTGGAGAATAATGTCGCCGTGTCACATCAGCTGACATGACCTGGAGGG  
TTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGTTGTACTGGGATTGTGAATAAA  
CTTGATACACCA

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**FIGURE 514**

MHLARLVGSCSLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSITHAGR  
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA  
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN  
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

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**FIGURE 515**

CCACCGCGTCCGCCAACCGGTCCGGTGCCACTCGCGCCGGCGCTCCGGCTTCTCTT  
TTCCCTCCGACCGGCCACGGCTGCCAGACATTCCGGCTGCCGGTCTGGAGAGCTCCCCGAA  
CCCCTCCGCGGAGAGGAGCGAGGCAGGGTGGCCCCGGGGCGCCTGGTCTCGGAG  
AAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGACTGACCGAGTTGGG  
CCGCGACTACCGCAGCTGACAGCGCATGAGCGACTCCCCAGAGACGCCCTAGCCGGTGTG  
CGCCAGGCAGGGCAGGTGGGCTGGCTGTTAGTGGTCCCCCCACGCCGGTCGCCG  
GCCGCCAGGATGGCGCTGGCAACCCGGGCCGCGCCCGCCGCTGCTACCCCTGCCGCCG  
TGCGAGCCGGCGTCCGGCCCGCCCTGCGCTCATGGACGGCGGCTCCGGCTGGCGGCCG  
GCGCCCCGGGCTGTGAATGCGACTGCCCTCGGCCGCGCTCCCGCCGCCGCCGG  
GACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCCTCTCCAGTTCCCTCCT  
GGTCACCTGCTGCCGTGGCTGTCAGTCCGAGCATCCGCTGGAGAACGCTGGCCA  
GGCACCAAGAGCAGCCGGCCAGGAGAACGCGTGGAGCACGCCACTGGGACGCCGGGG  
GAACGAGCTCGGGCGCCCGCGAGGGACGAGGGCGAGCGGGCGGACTGGAAGAGCAAGAG  
CGCCGTGGCTGCCGGCGTGGAGCAAGCTGAAGCAGGCCCTGGCTCCAGGG  
CGGGGGCGCCAAGGCCGGGATCTGCAGGTCCGCCCGGGACACCCCGCAGGCCAGG  
CCTGGCGCAGCCGCCAGGACGCGATTGGCCCGGAACTCGGCCACGCCAGGCCACCGA  
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGAGCACGAGAGCGGCTCGTGTACGC  
GATCGGGGAGAACGTTCGGCCGGCCCTCGGCCTGCCGTGCCTGTGCACCGAGGG  
GCTGTGGCGCAGCCCGAGTGGCGAGGCTGCACCCGCGCTGCATCCACGTCGACACGAGCCA  
GTGCTGCCCGCAGTGAAGGAGAGGAAGAACACTGCGAGTTCCGGGCAAGACCTATCAGAC  
TTGGAGGAGTTCGTGGTCTCCATGCGAGAGGTGTCGCTGTGAAGCCAACGGTGAGGTGCT  
ATGCACAGTGTACCGTGTCCCCAGACGGAGTGTGTGGACCCGTGTACGAGCCTGATCAGTG  
CTGTCCCATCTGAAAAATGGTCAAACGTCTTGCAGAAACCGCGGTGATCCCTGCTGGCAG  
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAA  
CGAGCGCAGGCCATGTGCACGAGACATGAATGCAGGCAAATGTAGACGCTTCCAGAACACA  
AACTCTGACTTTCTAGAACATTTACTGATGTGAACATTCTAGATGACTCTGGAACTATC  
AGTCAAAGAAGACTTTGATGAGGAATAATGGAAAATTGTTGGTACTTTCTCTTCTTGATA  
ACAGTTACTACAACAGAAGGAAATGGATATATTCAAAACATCAACAAGAACCTTGGCATAA  
AATCCTCTCTAAATAATGTGCTATTTCACAGTAAGTACACAAAAGTACACTATTATAT  
CAAATGTATTCATAATCCCTCATTAGAGAGCTTATATAAGTGTCTATAGATGCAGAT  
TAAAAATGCTGTGTTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 516**

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKRHATRDGPGRVNELG  
RPARDEGGSGRDWKSRSRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAEALAAA  
AQDAIGPELAPTPEPPEEYVYPDYRGKGCVDESGFVYAIKEKFAPGPSACPCLCTEEGPLCAQ  
PECPRHLPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVLCTVS  
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWRIERQA  
MCTRHECRQM

**Important features:****Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 11-30

**Glycosaminoglycan attachment site.**

amino acids 80-83

**N-myristylation sites.**

amino acids 10-15, 102-107, 103-108

**Cell attachment sequence.**

amino acids 114-117

**EGF-like domain cysteine pattern signature.**

amino acids 176-187

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**FIGURE 517**

GGACAACC GTT GCT GGG TGT CCC AGGC C T GAGG CAGG AC GG TACT CCG CT GAC AC CCTT CC CT  
TTCGGC CT T GAGG TT CCC AGC CT GG TGG CCCC AGG AC GTT CG C T GC AT GG CAG AGT GCT AC  
GGAC GAC GC CT ATGAAGCC CT TAGT C CT T C T AGTT GCG CTT T GCT AT GG C CT T CG T CT GT GC  
CGG CTT ATCC GAG C AT AACT GT GAC AC CT GAT GAAG AG CAAA ACT TGA AT CATT ATATA CAAG  
TTT TAGAGA ACCT AGT AC GAAG T GTT CC CT TGGG AGCC AGGT CGT GAG AAAA ATCT AACT  
CTCC AAAA CAT GTT ATT CT ATAG C ATCAA AGG GAT CAAA ATT AAGG AGC T AGTT ACAC ATG  
GAGAC GCT TCA ACT GAGA AT GAT GTT TA ACCA AT CCT AT CAGT GAAG AA ACT ACA AC TTCC  
CTAC AGG AGG CTT CAC ACCG GAA ATAGG AAAG AAAA ACAC AGG CACCA AGA AT GTT GCC AG TTG  
CGAT CAA ACCA AA CAAT GTT CC ATT GTT GC ATG CAG AGG AAC CT T AT ATT GAAA ATGA AG  
AGCC AGAG CCAG AGC CCG AGC CAG CT GCAA AAAA CAA ACT GAGG CACCA AGA AT GTT GCC AG TTG  
TTACT GAAT CAT CAC AGT CC AT AT GTT ACCT C ATAC AAGT CAC CT GT C ACCA CTT AGATA  
AGAG CACT GG CATT GAG AT CT C TAC AGA AT CAGA AG AT GTT CCT CAG CT C T CAG GT GAA ACT G  
CGAT AGAAA ACCG AAG AGT TGG AAG CACCC AGAG AGT TGG AATA AT GAT GAC AT TTG A  
AAAAA ATT T TAG AT ATT CACA AGT GCA AC AGG CACT T CT TAGT GAC ACC AGC A ACCAG  
CATATAGAGA AGAT ATT GAAG C CT TAA AGAT CAC CT AAA AC GAAG C CT T GCT C T AG CAG CAG  
CAG CAG A ACATA AATT AAAA CAAT GT TATA AGT CCC AGT T ATTGCC AGTAGG AGC AACA AGTA  
AT AAAA ATT GAT GAC AT CGAA ACT GTT ATTAC ATG CT GT G T AATT C T AAGT C TAA ACT CT ATG  
AAT ATT TAG AT ATT AA AT GT GTT CC ACCAG AGA GT GAG AG AAAA AGC T GCT ACAG T ATTCA ATA  
CAT TAAA AAAA AT AT GT GTAG AT CAAG GAG AGT CAC AGC CT T ATT AAA AGT TT ATT TAA ACA ATA  
TAT AAAA ATT TAA ACCT ACT TGT AT ATT CC AT AACA AGC T GAT TT AAG CAA ACT G CATT TTT  
TCAC AGG AGA AAT AAT C AT ATT CGT AATT CAAA AGT GT AT AAAA ATT TT CT ATT GTAG T  
TCAA AT GTGCC A ACAT CTT AT GT GT C AT GT GT T AT G AACA ATT TC AT AT G C ACT AAA ACC  
TA ATT TAA AAT AAA ATT TT GG TT CAGG AAAA

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**FIGURE 518**

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKNSPKH  
VYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKKTESTPFWSIKP  
NNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSTPSYKSPVTTLDKSTG  
IEISTESEDVPQLSGETAIEKPEEFGKHPEWNNDDILKKILDINSQQQALLSDTSNPAYRE  
DIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD  
IKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Important features:****Signal peptide:**

amino acids 1-19

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**FIGURE 519**

CGGCTCGAGTCAGCTGTGGGAGATTCAGTGCATTGCCCTGGTGCTTCATCTTG  
GATTGAAAGTTGAGAGCAGCATGTTGCCACTGAAACTCATCCTGCTGCCAGTGTACTG  
GATTATTCCCTGGCCTGAATGACTTGAATGTTCCCCGCCTGAGCTAACAGTCCATGTGGGT  
GATTCAAGCTCTGATGGGATGTGTTCCAGAGCACAGAAGACAAATGTATATTCAAGATAGAC  
TGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC  
AGTGTGCCTATTGGCGCTTCCAGAACCGCGTACACTTGATGGGGACATCTATGCAATGAT  
GGCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC  
CTCAAAGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC  
AAAGAGCTCATGGTCCATGTGGTGGATTGATTGAGATGGGATGTGTTCCAGAGCACAGAA  
GTGAAACACGTGACCAAGGTAGAATGGATATTTCAAGGACGGCGCGCAAAGGAGGAGATTGTA  
TTTCGTTACTACCACAAACTCAGGATGTCTGGAGTACTCCCAGAGCTGGGCCACTCCAG  
AATCGTGTGAACCTGGTGGGGACATTTCCGCAATGACGGTCCATCATGCTTCAAGGAGTG  
AGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGAAACCTGGTGTCAAGAAA  
ACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGAACCCGGCAGCCCTGAGG  
CCTCTGGTCTTGGTGGTAATCAGTTGGTATCATTGTGGAATTGTCTGTGCCACAATCCTG  
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAAGAGTTCAAGTGAATTCT  
ACAGTCTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCCCTGCCATT  
GAAAGATGTGAAGGGGAGAAACACATTACTCCCCAATAATTGTACGGGAGGTGATCGAGGAA  
GAAGAACCAAGTAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTGGCCTCTG  
AGGTCAAGATCGAACAACTCACTTGAAAAAAAGTCAGGTGGGGAAATGCCAAAAACACAGCAA  
GCCTTTTGAAGAAGAATGGAGAGTCCCTCATCTCAGCAGCGGTGGAGACTCTCCTGTGT  
GTCCTGGCCACTCTACCACTGATTCAGACTCCCGCTCTCCAGCTGTCTCCTGTCTCATT  
GTTTGGTCAATACACTGAAGATGGAGAATTGGAGCCTGGCAGAGAGACTGGACAGCTGGA  
GGAACAGGCCCTGCTGAGGGGAGGGAGCATGGACTTGGCCTCTGGAGTGGACACTGGCCCTG  
GGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTTGGATCAGACCTCCTGTGGCAGGG  
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

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**FIGURE 520**

MFCPLKLILLPVLLDYSLGLNDLNVSPPPELTVHVGDSALMGCVFQSTEDKCIKFIDWTLSPGE  
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV  
FKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL  
RMSVEYSQSWSGHFQNRVNLVDIFRNDGSIMLQGVRESDGNYTCIHLGNLVFKKTIVLHVS  
PEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNT  
KKTNPETKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPWPSLRSDRNNS  
LEKKSGGGMPKTQQAF

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**FIGURE 521**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAACAAATGTGTCCCCTCACATGG  
TTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA  
ACTACATTTGCAAAGTCATTGAACACTCTGAGCTCAGTTGCAGTACTCGGGAAAGCCATGCCAGGA  
TGAAGATGGATACATCACCTTAAATATTAAAACCTGGAAACCAGCTCTCGTCTCCGTTGCC  
TGCATCCTCCTCTGGTGGCGTGTGATGGCTTGATTCTGCTGATCCTGTGCGTGGGATGGT  
TGTGGGCTGGTGGCTCTGGGATTGGTCTGTCAATGCAGCGCAATTACCTACAAGATGAGAA  
TGAAAATCGCACAGGAACACTCTGCAACAATTAGCAAAGCGCTCTGTCATATGTGGTAAAACA  
ATCAGAACTAAAGGGCACTTCAAAGGTCAATAATGCAGCCCCCTGTGACACAAACTGGAGATA  
TTATGGAGATAGCTGCTATGGGTCTTCAGGCACAACATTAACATGGGAAGAGAGTAAGCAGTA  
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA  
AGCCAGGACTCATTAATTGTTGGTCGGATTATCTGCCAGAAGTCGAATGAGGTCTGGAA  
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTGGAAGATGGAAAAGGAAA  
TATGAATTGTGCTTATTTCATAATGGGAAAATGCACCCACCTCTGTGAGAACAAACATTA  
TTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT  
GGACAGGATAACACAGATAAGGGCTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA  
GCTGAAAAA

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**FIGURE 522**

MQDEDGYITLNKTRKPALSVGPASSSWRVMALILLILCVGMVVLVALGIWSVMQRNYLQ  
DENENRTGTLQQLAKRFCQYVVVKQSELKGTFKGHKCSPCDTNWRYYGDSCYGFRRHNLTEES  
KQYCTDMNATLLKIDNRNIVEYIKARTHЛИRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDG  
KGNMNCAYFHNGKMHPTFCENKHLMCERKAGMTKVDQLP

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**FIGURE 523**

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGACTGTGTGCTGAGAGACCATGGC  
AAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCCAA  
GAAAATATGTAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACCTAAAT  
TGTCTGTTGGGGAGCAAGCACCTCTGCCGGAGGTACCCAAAAAGCCTATGACATGGA  
GCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTGACCAG  
AACTGAAATATTAGAAGCGGAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA  
CGGATACACTGGCATCTACTCGTGGGTCTTCAAAAATGTTTATCAAAACTCAGATTAAAGT  
GATT CCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCAACTTT  
CTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTCTTAA  
AAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATCCACTCTAAT  
ATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGAAGATCTTCACTTCCGCCAACGA  
AAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG  
TCACGCCAGACAAGCAAGTGAGGAAGAACTCCAATAATGACTATACTGAAAATGGAATAGA  
ATTGATCCCAGCTGGATGAGAGAGGTTATTGTTGATTTACTGCCGTGAGGCAACCGCTA  
TTGCCGCCGCTGTGAACCTTACTAGGCTACTACCCATATCCACTGCTACCAAGGAGG  
ACGAGTCATCTGTCGTGTCATCATGCCGTGTAACTGGTGGTGGCCCGCATGCTGGGAGGGT  
CTAAATAGGAGGTTGAGCTAAATGCTAAACTGCTGGCAACATATAATAATGATGCTATT  
CAATGAATTCTGCCTATGAGGCATCTGCCCTGGTAGCCAGCTCCAGAATTACTGTAG  
GTAATT CCTCTTCATGTTCTAATAAAACTTCTACATTACCAAAAAAAAAAAAAAAA

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**FIGURE 524**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYD  
MEHTFYNSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQI  
KVIPEFSEPEEEIDENEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPT  
LISVSELQDFEEEEDLHF PAN EKKGIEQNEQWVVPQVKVEKTRHARQASEEEELPINDYTENG  
IEFDPMELDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

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**FIGURE 525**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGCATGAAGATCACTGGGGTC  
TCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA  
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCACAT  
ACCTACCAGTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACCGAGA  
GCTTGAAGAAGTAATGGAAGAGTTCAGTTCTCACGATGGAAGTTGCTAAATTCTCCATGGAC  
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC  
TTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGAGTAATCTTACTGAAT  
GGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTT  
TAACACGTCAATAAAAAATAATCTCCCAGA

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**FIGURE 526**

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE  
CHLCTESLKSNGRVQFLHDGSC

**Important features:**

**Signal peptide:**

amino acids 1-19

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**FIGURE 527**

CGACG**A**TGCTACGCGGCCGGCTGCCTCCTCCGTAGCGCTGCCGCCCTGG  
CTGCGCGCTGCTCTCGCTTGCCTGCTCTCTTAGAGCCGAGGGACCCGGTGGCCT  
CGTCGCTCAGCCCCATTTCGGCACCAAGACTCGTACGAGGATGTCACCCCGTGCTATTGT  
CGGGCCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGACCTGCACCCGGTGAGC  
TGGTCGCCCTCATCGCCACGGCACCCGCTACCCACGGTCAAACAGATCGCAAGCTGAGGC  
AGCTGCACGGGTTGCTGCAGGCCGCCGGTCCAGGGATGGCGGGCTAGTAGTACCGGCAGCC  
GCGACCTGGGTGCAGCGCTGGCCGACTGGCTTGTGGTACCGGACTGGATGGACGGGAGC  
TAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCTCGCTCTCCGG  
CCCTTTCAAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAAGCACCCTGCA  
TGGATAGCAGGCCGCCCTCCTGCAGGGCTGTGGCAGCACTACCAACCCCTGGCTGCCGC  
CGGACGTGCGAGATATGGAGTTGGACCTCAACAGTTAATGATAACTAATGAGATTTTG  
ATCAGTGTGAGAAGTTTAACTGAAGTAGAAAAAAATGCTACAGCTTTATCACGTGAAAG  
CCTTCAAAACTGGACCAAGAACATTAAAGGTTGAGCTACTTTGCAAGTGC  
CAGTAAATGATTAAATGCAAGATTAATTCAAGTAGCCTTTCACCTGTTGACATAGTGTGAAAG  
CAATTAAAGGTGTTAAATCTCCTGGTGTGATGTTTGACATAGTGTGAAAGGTATTAG  
AATATTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGTATACTATTAAACAGTCAT  
CCAGCTGCACCTGTTCAAGGATATCTTCAGCACTGGACAAAGCAGTGAACAGAAACAAA  
GGTCTCAGCCAATTCTCTCCAGTCATCCTCCAGTTGGTGTGATGTTGACATAGTGTGAAAG  
TGCTTCTCTCATGGCTACTCAAGACAAGGAACCCCTAACAGCGTACAATTACAAAAAC  
AAATGCATCGGAAGTCCGAAGTGGTCTCATTGACCTTATGCCTCGAACCTGATATTGTC  
TTTACCACTGTGAAATGCTAAGACTCCTAAAGAACAAATTCCGAGTGCAGATGTTATTAAATG  
AAAAGGTGTTACCTTGGCTACTCACAAGAAACTGTTGACATAGTGTGAAAGACTGAAGAAC  
ACTACAAGGACATCCTCAGAGTTGTCAAACCAAGTGAAGAATGTGAATTAGCAAGGGCTAAC  
GTACATCTGATGAACT**A**TGTAACTGAAGAACATTAAATTCTTAGGAATCTGCAATGAG  
TGATTACATGCTGTAATAGGTAGGCAATTCTGATTACAGGAAGCTTATATTACTTGAG  
TATTCTGTCTTTCACAGAAAACATTGGTTCTCTCTGGGTTGGACATGAAATGTAAGA  
AAAGATTTCACTGGAGCAGCTCTTAAGGAGAAACAAATCTATTAGAGAAACAGCTGGC  
CCTGCAAATGTTACAGAAATGAAATCTCCTACTTATATAAGAAATCTCACACTGAGATAG  
AATTGTGATTCTATAAAACACTTGAAAAGTGTGGAGTAACAAATATCTCAGTTGGACCAT  
CCTTAACTTGATTGAACTGTCTAGGAACCTTACAGATTGTTGTCAGTCTCTCTTCC  
TCAGGTAGGACAGCTCTAGCATTCTTAATCAGGAATTGTTGAGCTGGGAGTACT  
CTGGAAGAAAGTAACATCTCAGATGAGAATTGAAACAAAGAAACAGAGTGTGAAAGGAC  
ACCTTCACTGAAGCAAGTCGGAAAGTACAATGAAAATAATTGTTGGTATTATGAA  
ATATTGAAACATTTCATAATTCTTTACTCTAGGAAGTCTCAAAGACCATCTAA  
ATTATTATATGTTGGACAATTGCAACAAGTCAGATAGTTAGAATCGAAGTTTCAAATCC  
ATTGCTTAGCTAACTTTTCAATTCTGTCATTGGCTTCGATTGTTATATTCTTCTATTATG  
AAATGTATCTTGGTTGTTGATTCTTCTTCTTGTAAATAGTTCTGAGTTCTGTCA  
AATGCCGTGAAAGTATTGCTATAAAAGAAAATTCTTGTGACTTAAAAAA

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**FIGURE 528**

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLSG  
PEAPWRDPELLEGTCPTVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGASSTGSRD  
LGAALADWPLWYADWMMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD  
SSAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFITEVEKNATALYHVEAF  
KTGPEMQNILKKVAATLQVPVNLDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFIDDDAKVLEY  
LNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL  
SLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRVQMLLNEK  
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

**Important features:****Signal sequence**

amino acids 1-30

**N-glycosylation sites.**

amino acids 242-246, 481-485

**N-myristoylation sites.**

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

**Endoplasmic reticulum targeting sequence.**

amino acids 484-489

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**FIGURE 529**

GGAGAGCCGCGGCTGGGACCGGAGTGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTGG  
CGGAGAGATCAGAACGCTCTCCCCAAGCCGAGCCAACCTCAGCAGGGGACCCGGGCTCAGGGA  
CGCGCCGGCGCGGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCGAGCCGGGCG  
GTGATTGCAGCCCCAGACAGCGGCGCTGGCTGGTCGGCTGGCGGGCGCTGGGCTC  
TTGACAGCTGGAGTATCAGCCTTGGAAAGTATATAACGCCAAAAGAAATCTCGTGGCAAATGGT  
ACACAAGGGAAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGGGGTTGACCTCAGTC  
TCCTGGAGCTTCCAGCCAGAGGGGGCGACACTACTGTGCGTTTCCACTACTCCCAGGG  
CAAGTGTACCTTGGGATTATCCACCATTTAAAGACAGAACATCAGCTGGCTGGAGACCTTGAC  
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTATACACAATGGCACCTATATCTGT  
GATGTCAAAACCCCTCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTATGTCGTAGAA  
AAAGAGAATTGCGCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTGCTGTGGTCTA  
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTATAGAAGAAAAACTCTAACCGG  
GATTACACTGGCTGCAGTACATCAGAGAGTTGTCAACCAGTTAACGAGGCTCTCGGAAGTCC  
CCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTCTGGATCTCACCAAGGGCCAGTCATA  
TATGCACAGTTAGACCACTCCGGCGAACATCACAGTGACAAGATTAAAGTCAGAGTCGTG  
GTGTATGCGGATATCCGAAAGAATTAAAGAATACCTAGAACATATCCTCAGCAAGAAACAAA  
ACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACACATGTAGCCTTGGAGACCCAGG  
CAAGGACAAGTACACGTACTCACAGAGGGAGAGAAAAGATGTGTACAAAGGATATGTATAAA  
TATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGATGATGAAAAGATGGTATGATT  
TACATATGTACCATTTGTCTGTTGTACTTCTTTCAAGGTCAATTACAATTGGGAG  
ATTCAGAAACATTCTTCAACCATTAGAAAATGGTTGCCTTAATGGAGACAATAGCAG  
ATCCTGTAGTATTCAGTAGACATGGCCTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA  
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATAACCCAGGGTGGCCTTAC  
ACAGTATCAGTACCATTTATGTCTGCCGCTTTAAAAAATACCCATTGGCTATGCCACTTG  
AAAACAATTGAGAAGTTTTGAAGTTCTCACTAAAATATGGGGCAATTGTTAGCCTT  
ACATGTTGTAGACTTACTTAAGTTGCACCCCTGAAATGTGTATCTAATTCTGGATT  
CATATAGCAAGATTAGCAAAGGATAATGCCGAAGGTCACTCATTCTGGACACAGTTGGAT  
CAATACTGATTAAGTAGAAAATCCAAGCTTGCTTGAGAACTTTGTAACGTGGAGAGTAAAA  
AGTATCGGTTTA

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**FIGURE 530**

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST  
STTGGLTSVWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINENMQ  
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLISMILAV  
LYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLSLPSGSHQGPVIYAQLDHSGGHHS  
DKINKSESVVYADIRKN

**Important features:**

**Signal peptide:**

amino acids 1-37.

**Transmembrane domain:**

amino acids 161-183

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**FIGURE 531**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCGA  
GGCTGGTGGAAAGAAGCCGAGATGGCGCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGCTC  
TTGCTGATGGCGGTAGCAGGCCAGTCGAGCCGGGAGCGGCTGCCGGGACTGGT  
GCGCGAGGGCTGGGCGGAAGGTGAGAGGGGAGGCCTGTGGCACGGTGGGCTGCTGCTG  
GAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAAGCGGGCTCACTGCTCTGGAAC  
CAGCAGGATGGTACCTTGTCCCTGTACAGCGCAGCTCAGCAGGAGGAGCGGGGCCACTC  
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAGGCGACCCGGGCGCTG  
GATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGTCCCTGGTGGAGTCG  
CACCTGTCGGACCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGCGTGTGGT  
GTGACGCACCCCCGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTAAC  
ACCTCGGTGCAGCTGCAGCCGCCCACACAGCCCCAGGCCCTGAGACGGCGGCCATTGAG  
CGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAGTCCTTCTCGCC  
AAATACTGGATGTACATCATTCCGTCGTCTGTTCTCATGATGTCAGGAGCGCCAGACACC  
GGGGGCCAGGGTGGGGTGGGGTGGGGTAGTGGCCTTGCTGTGCCA  
CCCTCCCTGTAAGTCTATTAAAAACATCGACGATACTGAAATGTGTGAACGTTTGAAAAA  
GCTACAGCTTCCAGCAGCAAAGCAACTGTTTTGGCAAGACGGCCTGATGTACAAGCT  
TGATTGAAATTCACTGCTCACTGATACTGTTATTCAAGAAACCCAAGGAATGGCTGTCCCCATC  
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGGCAGTTATTAAACTGTCCCCAGATC  
GACACGCAAAAAAAA

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**FIGURE 532**

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAFTGARGAGAEGREGEACGTVGLLLEHSEID  
DSANFRKRGSSLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEAGG  
YVSSFVPACSLVESHLSDQTLHVVDAGNVGVSVTHPGGCRGHEVEDVDLELFNTSVQLQP  
PTTAPGPETAAFIERLEMEQAQKAKNPQEQQKSEFAKYWMYIIPVVLFLMMMSGAPDTGGQQGGG  
GGGGGGGGSGLCCVPPSL

**Important features:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

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**FIGURE 533**

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGGCTGGTGGTGAT  
GGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTGAC  
TGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAGAGG  
CCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACCTGAA  
GACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCATACTTGTATGGATTATC  
TCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTCCGATA  
AAAAGCTATTACTAWTTAA  
AA

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**FIGURE 534**

MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHCGLGGRGQPKDATDWC  
CQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

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**FIGURE 535**

GCTGAGCGTGTGCGCGGTACGGGCTCTCCTGCCCTCTGGGCTCCAACGCAGCTCTGTGGCTG  
AACTGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC  
CCAAATTGCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGTAGGATCCAGTTTT  
TTTTAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCAT  
GAAGATCCTATTACCTAGGAAGATTGATGTTGCTGCGAATGCGGTGTTGGATTATTT  
GTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTCAAAATCGGTCCATCTCCAAG  
GGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGG  
CTGTCATGCAACTGGCCCCAAGCAGCTAAGGACGACCTTGAACAATACAA  
**AGGATGGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCC**  
ACTGTCCTACTGACAATGCTTCTCTGCCAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA  
GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGT  
TGCTTAGGTTGCCCCCTCGCTATAACAGCCTCAAAAACCTTAAGTATAATCAATTAAAGGG  
CTCAACCAGCTCACCTGGCTATAACCTTGACCATACCATATCAGCAATATTGACGAAAATGCT  
TTAATGGAATACGCAGACTCAAAGAGCTGATCTTAGTCCAAATAGAATCTCCTATTTCCTT  
AACAAATACCTTCAGACCTGTGACAAATTACGGAACTTGGATCTGCTCTATAATCAGCTGCAT  
TCTCTGGGATCTGAACAGTTGGGGCTTGCGGAAGCTGCTGAGTTACATTACGGCTAAC  
TCCCTGAGAACCATCCCTGCGAATATTCAAAGACTGCCGCAACCTGGAACCTTGGACCTG  
GGATATAACGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGCATGATCAGACTCAAAGAA  
CTTCACCTGGAGCACAATCAATTTCAGCTCAACCTGCCCTTTCCAAGGTTGGTCAGC  
CTTCAGAACCTTACTTGCACTGGAATAAAATCAGTGTCACTAGGACAGACCATGTCCTGGACC  
TGGAGCTCCTTACAAGGCTTGATTATCAGGCAATGAGATCGAAGCTTCAGTGGACCCAGT  
GTTTCCAGTGTGTCGGAAATCTGCAGCGCTCAACCTGATTCCAACAAGCTCACATTATT  
GGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAGTCTGCTGGAAATATATGG  
GAATGCAGCAGAAATATTGCTCCCTGTAACCTGGCTGAAAGTTAAAGGTCTAAGGGAG  
AATACAATTATCTGTGCCAGTCCAAAGAGCTGCAAGGAGTAAATGTGATCGATGCAGTGAAG  
AACTACAGCATCTGTGGAAAAGTACTACAGAGAGGTTGATCTGCCAGGGCTCTCCAAAG  
CCGACGTTAACGCCAAGCTCCCCAGGCCAGCATGAGAGCAAACCCCTTGCCCCGACG  
GTGGGAGCCACAGAGCCCAGAGACCGATGCTGACGCCAGACATCTCTTCCATAAA  
ATCATCGGGCGAGCGTGGCTTTCTGTCCTGCTCGTCATCTGCTGGTTATCTACGTG  
TCATGGAAGCGGTACCCCTGCGAGCATGAAAGCAGCTGCGAGCGCTCCCTCATGCAAGGCAC  
AGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTATGTAGAT  
TATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTAT  
AACAAATGGGCTCCAGGGAGTGTGAGGTAT**TGA**ACCATTGTGATAAAAAGAGCTTAAAGC  
TGGGAATAAGTGGTGTATTGAACTCTGGTACTATCAAGGAAACGCAGTGCCTTCTGCTGGTT  
CCCTTCCCTCTCCCTCACTTGGTGGCAAGATCCTCTGCTGGTCTTGTGATTCTCATA  
ATACTGGTCATTTCTCATAACATAATCAACCCATTGAAATTAAATACCAATCAATGT  
GAAGCTGAACCTGGTTAATATAATACCTATTGTATAAGACCTTACTGATTCCATTAAAT  
GTCGCAATTGTTAAGATAAAACTTCTTCATAGGTAAAAAAAAAA

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**FIGURE 536**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGRCCEGKMVYCESQKLQEIPSSISAGC  
LGLSLRYNSQLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRALKELILSSNRISYFLN  
NTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLG  
YNRIRSLARNVFAGMIRLKELHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTMSWTW  
SSLQRLLSGNEIEAFSGPSVFQCVNLQRLNLDNSNKLFIGQEILDWSIISNDISLAGNIWE  
CSRNICSLVNWLKSFKGLRENTIICASPKELOQGVNVIDAVKNYSICGKSTTERFDLARALPKP  
TFKPKLPRPKHESKPLPPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVS  
WKRYPASMKQLQQRSLMRRKKRQSLKQMTPSTQE FYVDYKPTNTETSEMLLN GTGPCTYN  
KSGSRECEV

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

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**FIGURE 537**

GGGACTACAAGCCGCAGCGCTGCCGTGGCCCTCAGCAACCCTCGACATGGCGCTGAGGCCGCCACCGCGAC  
 TCCGGCTCTGCCTCGCTGCCGTACTTCTCTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGCTGTAATC  
 TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGCG  
 AGACAAGTGAACCCCAGGATCGAGTGGAAAGAAAATTCAAGAACACAAACCATATGTGTTTTGACAACAAAA  
 TTCAGGGAGACTTGGCGGGTCGTGAGAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
 ACTCAGCCCTTATCGCTGTGGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
 CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGGCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
 ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGTATCGCAATGATGTACCAACTGCCACGGATT  
 CCAGAGCCAATCCCAGATTGCGAACATTCTCTTCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG  
 TTCACAAGGAGACTTGGCGACTACTGCAATTGCTTCAATGACCGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
 AGATGGAAGTCTATGACCTGAACATTGGCGAATTATTGGGGGTTCTGGTTCTGCTGTTACTGGCCCTGA  
 TCACGTTGGGCATCTGCTGTGATCACAGACGGTGGTACTCTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
 ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTCAAGACACAAGTCATCGTTG  
 TGATCTGAGACCCCGGGTGTGGCTGAGAGCCACAGAGCGCACGTGACATACCTCTGCTGAGAAACTCCGTCAA  
 GGCAGCAGAGACTGATGCACTCGGACAGAGCTAGACACTCATTCAAAGCTTCTGTTGGCAAAGTTGACCA  
 CTACTCTTCTACTCTAACAAAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCAA  
 GGAAGCGAAACTGGGTGGCTACTGAGTTGGTCTTAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG  
 GTGATCTAAAGAGTTGGCTCACGTAACAGCCCGTGTGGCCCTGTGAAGGCCAGCATGTTACCCACTGGTGT  
 CAGCAGCCACGACAGCACCATGTGAGATGCCAGGTGGGACAGCACCCGAGCTTCTTAAAGGCTCTGC  
 GAAAAGGCTTCTAACACAGCAGCTTACTCTCATGGGCCACAGACACCACCCGAGCTTCTTAAAGGCTCTGC  
 TGATCGGTGGTGTGCACTGTCATTGTGGAGAAAGCTTTTGATCAGCATTTGTAACACAAACCAAATCAGGAAG  
 GTAAATTGGTTGCTGGAAGAGGGATCTGGCTGAGGAACCTGTTGTCCAACAGGGTGTCAAGGATTAAAGGAAA  
 ACCTTCGCTCTAGGCTAAGTGTGAAATGGTACTGAAATATGTTCTATGGGTCTTGTGTTATTAAATT  
 TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAGAAAATTCTATTAAACTGTAATATATTG  
 CATACAATGTTAAATAACCTATTGGTAAAGGAAACTTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT  
 TGGAAAATATCAATAATTAGAGTATTGACCTTACCAAGGAACCTCTCATGGAAAGTTACTGTGATGTTCTTTCT  
 CACACAAGTTTAGCCTTTTCAAGGGAAACTCATGTCATCTACACATCAGACCATAGTGTGCTTAGGAAACCTT  
 TAAAATTCCAGTTAACGCAATGTGAAATCAGTTGATCTCTCAGGTTAGGTAGCTTGTGAACT  
 GCCTCTCTGAGATGACTAGGACAGTCTGACCCAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG  
 CCAGTCAGCTCTGGGTTGCGCCAGGCGCCCCGCTAGCTACTGTTGCTCGCTGTCTGCCAGGGCCCT  
 GCCATCTCTGGGCCACTGCAAGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTGGCTCTCATCCAGCACAGC  
 TCTCAGGTTGGGACTGCAGGGACTGGTGTCTTCCATGTAGCGTCCAGCTTGGCTCTGTAAACAGACCT  
 TTTGGTTATGGATGGCTCAAAATAGGGCCCCAATGCTTAAAGTTTTAAGTTGTTAATTATTGTT  
 AAGATTGCTAAGGCCAAGGCAATTGCGAAATCAAGTCTGTCAAGTCAATAACATTGTTAAAGAAAATGGAT  
 CCCACTGTTCTCTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCTGCAATTCAAAACAAACCATGAT  
 GGAGTGGCGGCCAGTCCAGCCTTAAAGAACGTCAGGGAGCAGGCCAGGTGAAAGGCCCTGGGGGGAGGAAAG  
 TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCAGACACTGCTCCATT  
 TGTGGGGGAGATTGCAACATCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
 GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTG  
 GAATGGCTCTACTACTCACCTTGCTTTCAGCTTCAAGTGTGCTTGTGTTATGAAACACTTGTGCTGCC  
 AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGTGCTGCCAGGCGCTGGCAGAGGCA  
 GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGATGGCATGGCTTGGGATGCTTACGCTCAAGGTC  
 CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCACCCACCTCAGCGTTGGGATTCACGCTCCAGCCT  
 TCTTGGTTGTCACTAGTGTAGGGTAGCTTATTGCCCCCTTCTTATACCCCTAAACACTTCTACACTAGTGC  
 TGGGAACCCAGGTCTGAAAAAGTAGAGAGAGAAGTGAAGAGTCTGGGAAGTAGCTGCTTACACTAGTGC  
 CGGAAAAGGAATACTCGTGATTAAAGATATGAATGTGACTCAAGACTCGAGGGCGATACGAGGCTGTGAT  
 GCCTTGGATGGATGGTGTGTAACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC  
 CTCATTATAAAAGCTCAAAAACCCA

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**FIGURE 538**

MALRRPPRLRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDP  
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSKIKWNVTRRDSALYRCEVVARNDRKEI  
DEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPR  
FRNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVV  
LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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**FIGURE 539**

CCAGGACCAGGGCGACCGGCTCAGCCTCTCACTTGTCAAGAGGCCGGGAAGAGAAGCAAAGC  
GCAACGGTGTGGCCAAGCCGGGCTTCTGCTCGCCTCTAGGACATACACGGGACCCCTAA  
CTTCAGTCCCCAAACGCACCCCTCGAAGTCTGAACCTCAGCCCCCACATCCACGCCGG  
CACAGGCCGGCAGGCCAGGTCCCAGGAAGGCATGCCAGGGGGTCGGGAGCTGG  
GCTCGGGCGGGAGTAGGGCCGCAGGGAGGCAGGGAGGCTGCATATTCAAGATGCCGG  
CTGCGCCCTGGGAGAGGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGGCCGA**A**  
**T**GAGCCGCGTGGCTCGCTGCTGGCGCCGCTGCTCTGCGGCCACGGAGCCTTGCC  
GCCCGTGGTCAAGGGAAAAGGTGTGTTGACTCAAGCATCCCTGCTACAAAATGG  
CCTACTTCCATGAACCTGTCAGCCGAGTGAGCTTCAGGAGGCACGCCCTGGCTTGAGAGTG  
AGGGAGGAGTCCTCTCAGCCTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGC  
AAAACCTGACAAAACCCGGACAGGGATTCTGATGGTGATTCTGATAGGGCTTGGAGGA  
ATGGAGATGGCAAAACATCTGGTGCCTGCCAGATCTTACCACTGCTGATGGAAGCAATT  
CCCACTACCGAAACTGGTACACAGATGAACCTTCCTGCCAGTGAAAGTGAAGATGTTGATGT  
ATCACCAACCAACTGCCAACCTGGCCTTGGGGTCCCTACCTTACCACTGGAATGATGACA  
GGTGTAACTGAAGCACAAATTATATTGCAAGTATGAACCAAGAGATAATCCAACAGCCCTG  
TAGAAAAGCCTTATCTAACAAATCAACCAGGAGACACCCATCAGAATGTGGTTACTGAAG  
CAGGTATAATTCCAATCTAATTATGTTGTTACCAACAATACCCCTGCTCTTACTGATAC  
TGGTTGCTTTGAAACCTGTTGCTGCAAGTAAAGGAAGAACAAAAGTA  
GTCCAAACCAGTCTACACTGTGGATTCAAAGAGTACCAAGAAAAGAAAGTGGCATGGAAGT**A**  
**A**AAACTCATTGACTTGGTCCAGAATTGTAAATTCTGGATCTGTATAAGGAATGGCATCAG  
AACAAATAGCTTGAATGGCTTGAATCACAAGGATCTGCAAGATGAACCTGTAAGCTCCCT  
TGAGGCAAATATTAAAGTAATTCTTATATGTTCTATTATTCATTAAAGAATATGCTGTGCTA  
ATAATGGAGTGAAGACATGCTTATTTGCTAAAGGATGCACCCAACTTCAAACCTCAAGCAAA  
TGAAATGGACAATGCAGATAAGTTGTTATCAACACGTCGGGAGTATGTGTAGAAGCAAT  
TCCCTTATTCTTCACCTTCATAAGTTGTTATCTAGTCATGTAATGTATATTGTTGATTA  
AATTTCACAGTGTGCAAAAGTATTTCACCTTGCTATAAGTGTGTTGATAAAATGAACCTGTTCTA  
ATATTATTGTCATCTCATTTCAATACATGCTCTTTGATTAAAGAAACTTATTAC  
TGTGTCACTGAATTCAACACACAAATATGTCACCATAGAAAAAGTTGTTCTCGAA  
ATAATTCACTTCAAGCTCTGCTTGGTCATGTCAGGAAATCTCTCAGAAATAAGA  
AGCTATTCAATTAGTGTGATATAAACCTCTCAAACATTACTTAGAGGCAAGGATTGTCT  
AATTCAATTGTGCAAGACATGTCCTATAATTATTAGCTTAAATTAAACAGATTG  
TAATAATGTAATTGTTAATAGGTGCTAAACACTAATGCACTGAGTCATTTGAACAAAAGAAGT  
GACATACACAATATAACATATGTCCTCACACGCTGCTTATATAATGAGAACAGCTCTG  
AGGGTCTGAAATCAATGTCCTCTCTGCCCCACTAAACAAAGATGGTTGCTGGGGTT  
GGGATTGACACTGGAGGCAGATAGTTGCAAAAGTTAGTCAGGTTCCCTAGCTGTATTAGC  
CTCTGACTATTAGTATAACAAAGAGGTCTGAGGAGACCAGGTGAATAGTCACATTCAG  
TGTGGAGACAAGCACAGCACAGACATTAGGAAGGAAAGGAACATCGAAATCGTGTGAAA  
ATGGGTTGGAACCCATCAGTGATCGCATATTGATGAGGGTTGCTTGAGATAGAAAATG  
GTGGCTCTTCTGCTTATCTCCTAGTTCTCAATGCTTACGCCTGCTCTCAAGAGA  
AAGTTGTAACTCTCTGGTCTCATATGTCCTGTGCTCCTTTAACCAAATAAGAGTTCTG  
TTCTGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 540**

MSRVVSSLGAALLCGHGFRRVSGQKVCADFKHPCYKMAFHELSSRVSFQEARLACES  
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDGSN  
SQYRNWTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAP  
VEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKT  
SPNQSTLWISKSTRKESGMEV

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89 and 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

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**FIGURE 541**

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGTCTGGTCGGGTGGTCTGCTCTGGCATGCCCTG  
CCACAGCCACTGGGCCCGAAGTTGCTCAGCTGAAGTAGACACCACCTGGGTGGTGTGCGAGGCCGGCAGGTGG  
GCGTGAAGGGCACAGACCGCCTTGTAATGCTTTCTGGCATTCCATTGCCCCAGCGCCACTGGGCCCTGACC  
GGTTCTCAGCCCCAACCCCAGCACAGGCCCTGGGAGGGTGTGCGGGATGCCAGCAGTGCGCCCAATGTGCCCTAC  
AAGACGTGGAGGACATGAACACAGCAGATTTGCTCAACGGAAAACAGCAGATCTTCTCCCTTCAGAGGACT  
GCCTGGTCTCAACGCTATAGCCAGCTGAGGTCCCCCAGGGTCCGGTAGGCCGGTATGGTATGGGTCCATG  
GAGGCCTCTGATAACTGGCGCTGCCACCTCTACGATGGATCAGCTCTGGCTGCCATGGGATGTGGTGTGG  
TTACAGTCCAGTACCGCCTGGGTCTTGCTTCTCAGCACTGGAGATGAGCATGCACCTGCCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTGCCTGGGTGCAAGAAAACATGCCCTTCGGGGTGCACCTCAACTGTGTCA  
CTGTCTTGGTGGATCTGCCGGTGGGAGCATCATCTGGCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC  
ACAGAGCCATCACACAGAGTGGGTATGCCACCCAGGGATCATGACTCTCACCCCTGCCCTAGCTCAGA  
AAATCGAAACACCTGGCTCAGCTCCAGCTCCCGCTGAGATGGTGTGGCAGTGCCTCAGCAGAAAGAAGGG  
AAGAGCTGGCTTGAAGAAAGCTGAAAAAAACTATCTATCCTCTCACCGTTGATGGGACTGTCTTCCCCAAAA  
GCCCAAGGAACCTCTGAAGGAGAAGCCCTTCAACTGTGCCCCCTCTCATGGGTGTCACAAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGCTGGGTCTCTGGATACAATGGAGCAGATGAGCCGGAGGACATGCTGGCATCT  
CAACACCCTTGTGACCAGTCTGGATGTGCCCTGAGATGATGCCACCGTATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAATGCCAGGCCTCCAGGAATTATGGGTGACGTATTATCAATGTTCCACCGTCA  
GTTTTCAAGATACCTTGAGATTCTGAAGCCCTGTTTCTATGAGTTCCAGCATGACCCAGTTCTTTG  
CGAAGATCAAACCTGGCTGGGTGAAGGCTGATCATGGGCCAGGGCTCTTGTGTTGGAGGTCCCTCTCA  
TGGACGAGAGCTCCCGCTGGCTTCCAGGGCCACAGGGAGGAGAACAGCAGTAAGGCTCACCACATGATGGCC  
AGTGGACCCACTTGCCCGACAGGGGACCCAATAGCAAGGCTGCTCTGGCCCTGGCCAATTCACCGGG  
AACAAATATCTGGAGATCAACCCAGTGCCACGGCCGGACAGAATTCAAGGGAGGGCTGGATGCACTGGTCA  
AGACGCTCCCCAGCAAGATAAACAGTGGCACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAG  
AGGCCTGAACCTTCTGGCTGGGCAAACCAACTCTCAAGTGGTGGCAGAGTCCCAGCACGGCAGGCCCTC  
CCCCCTGCTGAGACTTAATCTCACCAGCCCTAAAGTGTGCCGCTCTGACTGGAGTTATGCTTTTGAA  
ATGTCACAAGGCCCTCCACCTCTGGGCTTGTACAAGTTCTCCCTCTCCCTGAAGTGCCTTCTGCTT  
CTTCGTGGTAGGTTAGCACATTCTCTAGGACTCACCCCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCT  
TGGGTGTGCGGCCCGAGCTGCTGCTCATTAGACACAGTCCACCCAGGGCTAGCACCTGCTGTCTGCT  
CCCCCTCAGAGGAGCTCTCAAATGGGATTAGCTAACCCACTCTGTCACCCACACCAGGATGGGGAGG  
CCTGGAGCTAGGGGGTGTGAGTGAGTGAGTGAACACAGAATATGGGAAATGGCAGCTGCTGAACCTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCACCCAGCACATTGTCACCCCTGGCAGAAGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCCAGGGGATCCAGCCTAGAGCAGACCTTACCCCTGAC  
TAAGGCCCTCAGACTAGGGGGAGGGTCTCTCTCTGCTGCCAGTCAGGCCCTGCACAAGACAAACAGA  
ATCCATCAGGGCATGAGTGTCAACCCAGACCTGAGCCCTCACCAATTCCAGGCCCTCAGGACGCTGGATG  
CCAGCTCCAGGCCCTAGTGCAGGGCTCCCTCCCTGGGCTTGGGAGACAGCTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGAGGGCATGGACAGGAGCTCCGTGGCTATTGTCACA  
GAGAAAAGAAGAGACCCACCCACTGGGTGCAAAAGGTGAAAAGCACCAAGAGGTTTCAAGATGGAAGTGA  
GTGACAGTGTGCTGCAGCCCTCACAGGCCCTGCTCTCCCTGCCGCTCTGCCCTGGCTCCACTTGGCA  
GCACCTGAGGAGCCCTCAACCCAGCCGCTGACTGTAGGAGCCCTTCTGGGCTGCCAAGGCCGGAGCCAGCT  
CCCTCAGCTTGCAGGGGGAGGTGGGGAGGGAGGGAGGGGGAGGGCTGCCAGGACCCGGGCTGGCAGCGCT  
AGTGAGTTCCGGGGGGGGCTGGGCTGG  
TAGCACCTGGGGCAGCAGCTGCTGCTCGTCAAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
GACCTGCAGGCCCTCCATGCCCTGCCCTCCCCCAGGCCCTGGGCTGGGCTGGGGGGGGGGGGGGGGGGGG  
CGCCGCCCTGCCAGGCCCTGG  
CTGGCAGGAGCTCCACCTGCTGCCCTGG  
GGACTTGGAGAACCTTATGTCTAGCTAAGGGATTGTAACATACCCGATGGGACTCTGTATCTAGCTCA  
TGTAACACACCAATCAGCACCCCTGTCAGCTCAGTGTGTTGTGAATGCAACCAACTCTGTATCTGGCT  
ACTCTGGTGGGGACTTGGAGAACCTTGTGTCACACTCTGTTATCTAGCTAATCTAGTGGGGATGTGGAGAAC  
TTGTGTCAGCTCAGGGATGTAACCGCACCAATCAGCACCCCTGTCACAAACAGACACTTGA  
GGACCAATCAGCAGGATGTGGTGGGGAGAACAGAGAACAGAACAGAACAGGGCTGCCAGCCAGTGACA  
CCCTCGGGTCCCCCTCCACGCCGTGGAAGCTTGTCTTCGCTCTTGCAATAATCTGCTACTGCCCAAAA

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**FIGURE 542**

MERA VRVESGV LVGVVCLLACPATATGPEVAQPEVD TTLGRVRGRQVGVKGTDR LVNVFLGI  
PFAQ PPLGPDRFSAPHPAQ PWEGRV DASTAPP MCLQD VESMNSSRFVLNGKQQIFS VSEDCLV  
LNVY SPAEV PAGSGR PVMVWVHGGALITGAATSYDG SALAAYGDVVVTVQYRLGVLGF STG  
DEHAPGNQGFLDVVAALRWVQENIA PFGGDLNCVTVFGGSAGGS IISGLV LSPVAAGLFHRAI  
TQSGVITTPGIIDSHPWPLAQKIANTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNTIYPLT  
VDGTVPKSPKELLKEKPFHSVPFLMGVNNHEFSWLIPRGWGLLDTMEQMSREDM LAISTPVL  
TS LDVPP EMMPPTVIDEYLGSNSDAQAKCQAFQEFM GDVF INVPTVSFSRYLRD SGSPVFFYEF  
QHRPSSFAKIKPAWKADHGAEGAFVFGGPFLMDESSRLAFPEATEEKQLSLTMMAQWTHFA  
RTGDPNSKALPPWPQFNQA EQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA  
QEDL

**Important features:**

**Signal peptide:**

amino acids 1-27

**Transmembrane domain:**

amino acids 226-245

**N-glycosylation site.**

amino acids 105-109

**N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

**Carboxylesterases type-B serine active site.**

amino acids 216-232

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**FIGURE 543**

TGTGCGCTGGCCCTGCCCATGAGACCCCCGGAGCGTCCCCCTCCCGGCCCTCTGCTTCGCTGCTGCTA  
CTGGGGGGCAGCCACGGCTCTTCTGAGGAGCCGGCCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC  
TATCCCCTGTTGTGGCAGCGGGCCGAGCGCTGACCCCGCAGAAAGGTGCTGAGCACCTAACATCCAGCGA  
GTCCCTGGGTCAACAGGACGCTGTTCATGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCACG  
TCCACGGAGCTGGCTACAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAACCTGTTGCGATGAAG  
GGCAAACAGGGGGGAGGTGCGAAACTCTCGTAAGGTGCTGCTCTCGGGAGGTCACGCTCTTGTGTC  
GGTTCACAGCCTCAACGGCTGCGCAACTACAGCATAGACACCCGTCAGGGAGAACATCACG  
GGTATGGCCGCTGCCGTACGACCCAAAGCAGCCAATGGTGCCTCTGTCAGGGATGCTCTCACAGCT  
ACTGTTACCGACTTCTAGCCATTGATGCTGTCATCTACCGCAGCCTGGGACAGGGCCACCCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTCAAAGAGCCTTACTTGTCCATGGGTGGAGTGGGGCAGCCATGTCCTACTTCTC  
TTCCGGGAGATTGCGATGGAGTTAACTACCTGGAGAAGGTGGTGTGCCCCGTTGGCCGAGGTGTCAGAAC  
GACGTGGAGGCTCCCCCGCTGCTGGAGAACAGTGGACGTCCTCTGAAGGCCGCTCAACTGCTCTGTA  
CCCCGGAGACTCCCTTACTTCAACCGTGTGCAAGGCTGTCACGGGCGTGGTCAGGCTCTGGGGCCGGCCGCGTG  
GTCTCGGGCTTTTCCAGCCCCAGCACAGCATCTGGCTGGCTGTCAGGCTTGGACACAGGTG  
GAGCTGTGTTGAAGGCCGCTTGGAGAGACAAGTCCCCCGATCTGGACGGGGTGGAGGATCAG  
GTGCTCGACCCGGGGGTGCTGGCGACCCCCGGGATGCACTGACATGCTCCAGGCCCTTGCCGGATGAC  
ATCCTCAACTTGTCAAGACCCACCCCTCTGATGGACGAGGGGGTGCCTCTGCTGGGCCATGCCCTGGATCTG  
CGGACCCGTAGGGCACAGCTGACTCGAGTGGCTGGACGTCAGGGCCCTGGGGCAACAGACCGTT  
GTCTTCCTGGGTTCTGAGGCGGGACGGTCTCAAGTTCCTGCTGGGCCAATGCCAGCACCTCAGGGACGTCT  
GGGCTCAGTGTCTCTGGAGGAGTTGAGACCTACCGGCCGACAGGTGTTGACGGGGGGGGTGGCGAGACA  
GGGAGGGCTGCTGAGCTTGGAGCTGGACGCGAGCTTGGGGGGCTGCTGGCTGCCCTTCCCCGCTGGTGTGTC  
CGAGTGGCTGTGGCTGCTGGAGCAGTACTCGGGGTGTAGAAGAACATGTCAGGCCAGTCAGGACCCCTACTG  
GGGTGGGCCCCCGACGGCTCTGCACTTCTGCAAGGGGGACCCCTGGGGCAACAGGGGGCTTGGACAGGAGTGG  
GCCAGCACCTCAGGTTAGGGACTGCACAGGACTCTGGGGCCAGCTCTCCGAGGGACGCCGGGGTGGTG  
TCGGTGAACCTGCTGTAACGTCCTGGCTGGCCCTTCTGTTGGGGGGCTGCTGGGGGGCTCAGCTGGG  
TGGTCTGTTGGGCTCCGTGAGCGGGGGAGCTGGCCGGCAAGGACAAGGGAGGCCATCTGGCGCACGGGCG  
GGCGAGGGGGTGTGAGCGTCAGCCGCTGGGGAGCGCACGGGCGCAGGGTCCCAGGGGGGGGGGGGGAGGGGGT  
GGCGGTGGCGCCGGGGTCCCCCGAGGCCCTGCTGGCGCCCTGATGCCAGAACGGCTGGGCCAACGGCACCGCTG  
CTGAGGG  
CTGGGCAACTCCGACCCGACCCCCACGCCCCCTGG  
TCCGCTTACCTCTCTCTGCTGCTGGCCGCCGG  
CCCGACGGCCGCTATGTCCTGG  
CCGGACCCGCCGG  
CCCTGGAGCCCGCCCCGACGGGAGCGCTGAGGGAGGCCACTGGGGCCCCACGCCCTGGGGGGGGGGGGGGGGGG  
CGCACCCACAGTCAACAGGGGAGGCCGG  
GACTTGGGGCACTCTCTCTATGG  
ATGGCTTGGCAGTGCACCCACGGGAACCGAGGAGCGAGAGACGGTGCAGAACGCCGGGGGGGGGGGGGGGGGG  
AGTGGGTGCTCAAGTCCCCCGGG  
CTGGGCTCTCCCCCTACCGGG  
GATTTGAGGTTGACCTTATGCGCTAGGTTGGTTGGTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
AATTGACAACCTCCGTTCTGG  
CTGCAGACCTAACGCCCTCCCCCACCCCTGGAAAGTCCCTCCCCAACCCAGGCCCTGGCGTGTGGGTGTGCG  
TGCCTGTCGTGCGTGTGCAAGGG  
TGGGCGTGTGTCAGTGGGGCACCGCGTGCAGGGTGTGTCACGAGGCCGACGATGTCGGTGGGCCAGGGGG  
TGGGCGTGTGGCTGAGGG  
CCCCCCCCACTCTGCAAGGGGAACGG  
AGTCACATCGGCAGCAGCTGTAAGGGCTTGG  
ATACGGCCCCAGGG  
CCATGCACTGCCAGCTGGCTGGCTGGCTCTGCGCTCTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
AAAACCTGTTAACACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAAACAAAAAA

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**FIGURE 544**

MQTPRASPPR PALLLLLLLGGAHGLFPEEPPPLSVAPRDYLNHYPFVGSGPGRLTPAEGAD  
DLNIQRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGER  
RNFVKVLLRDESTLFVCGSNAFPVCANYSIDTLQPVGDNISGMARCPYDPKHNVALFSDG  
MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHD SKWFKEPYFV HAVEWGSHVYFFFREIAMEF  
NYLEKVVVS RVARVCKNDVGGSPRVLEKQWTSFLKARLNCS VPGDSHFYFNVLQAVTGVVSLG  
GRPVVLAVFSTPSNSIPGS AVCAFDL TQVAAVFEGRFREQKSPESIWT PVPEDQVPRPRPGCC  
AAPGMQYNASSALPDDILMFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVADVGAGPWGN  
QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCCRGPGGETGQRLLSLELD  
AASGGLLA AF PRCVV RVP VARCQQYSGCMKNCIGSQDPYCGWADGSCI FLS PGTRAAFEQDV  
SGASTS GLGDCTG LRLRASL SEDRAGLVSVNLLVTSSVAAVFGAVVSGFSVGWFVGLRERREL  
ARRKDKEA ILAHGAGEA VLS VS RL GERRAQGP GRRGGGGAGVPE ALLA PLMQNGWAKAT  
LLQGGPHDLD SGLLPTPEQTPLPQKRLPTPHPHPHALG PRAWDHG HPLL PASASSSLLAP  
RAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPD RRRVVSAPTGPLDPASAADGLPR  
PWSPPP TGSLRRPLGPH APPAATLRRHTFNSGEARPGDRH RGCHARPGTD LAHLLPYGGADR  
TAPPVP

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 318-339, 598-617

**N-glycosylation sites:**amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466**Glycosaminoglycan attachment sites.**

amino acids 51-55, 573-577

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation sites.**amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885

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**FIGURE 545**

GATGGCGCAGCCACAGCTCTGTGAGATCGATTCTCCCAGTTCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTATATCGTCAATTCCCCAA  
ACAAGTTTGACATTCCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCCTAACCTGCTGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCACGGAG  
GCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCTTCAGCCTCTCTGCTGCGTTTATCTCCTATGGACTCCTTCACTGGACTGAAG  
ACACTCAATTGGGAAGCTGTGTGATGCCACAAACCTTCAGGAAATACGAAATGGATTTC  
GAGATACTGGGCAGTGTGCAAGCAAAGATGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCCATTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAAGATCAGC  
AGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCATGCCCATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACGCCAGATTCTGAGTCACTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTGGGAACTAGACATTCTCTGCAATGGATGGAG  
GAGACAGAATAGGAGGAAAGTGTGCTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGCCAAACCCACCATCTTTACTGTACTAGTCTGTGCT  
GGTCACAGTGTATCTTATTATGCATTACTTGCTCCTGCATGATTGCTTATGCATCCCC  
AATCTTAATTGAGACCATACTGTATAAGATTGTAATATCTTCTGCTATTGGATATATT  
TATTAGTTAATATATTATTATTGCTATTAATGTATTTATTTTACTTGGACATG  
AAACTTAAAAAAATTCACAGATTATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT  
ACAGTAAAAAAAAACCTTGAAATTCTAGAAGAGTGGCTAGGGGGTTATTCAATTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATTGCACATCTACCTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTCTACAAATAAGTTCTTGATACCAAAAAAAAAAAAAAA

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**FIGURE 546**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPE  
IFSSREAWQFFLLLWSPDFRPKMKA\$LAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE  
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDHY  
TLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI  
LLQWMEETE

**Important features:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

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**FIGURE 547**

AGCAACTCAAGTTCATCATTGCTCTGAGAGAGAGGAGCAGCGCGTTCTCGGCCGGGACAGCA  
GAACGCCAGGGGACCCTCACCTGGGCGCCGGGCACGGGCTTGATTGTCTGGGTCGCG  
GAGACCCGCGCGCCTGCCCTGCACGCCGGCGAACCTTGAGTCGCGTGGCTGCTGCGA  
TCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTCTGTCACCTCTTACACTTCTTCATT  
ATCGGTGGATCATTTGAGAGTCGCTTGTAATGTTGGACTTTGCTACTTTATTGCTTC  
TTTCTGGCGACAGTCCAGCACTCGCCGAGACCGGGAGAAAGGCAGCTGAGCCCAGAAG  
AGCGAAATATGGGGACCCGGCTAAAAGCAGACGTCGTCCTCCGCCGCTATTCTATATT  
CAGGCAGTGGATACATCAGGAATAAATTACATCTTCTCCAGGCAGAAAGGTCTCAGGTG  
AAAGTCTCAGCACCAAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTAGACCGAAAAGAT  
GGGTCTTCATAGTAAGATAACAGAAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTAAA  
TTCCAAGGGCAACATGTGCCAAATCCCCATATATTAAAAGGGCCGGTTACCATGAGAAC  
TGTGACTGTCCTCTGCAAGATAAGTAGTCAGCCTGGCTACGGGAGATGAACCTGCCCTGAAACCATT  
GCTCAGATTCAAGAGAGATCTGGCACATTCCCTGCTGTGGATCCAGAAAAGATTGCACTAGAA  
ATCCCAAAAGATTGGACAGAGGCAGAGCCTATGTCACTACACCTAAAGGATAACAAGGTT  
TATATCAAGACTCATGGTGAACATGTAGGTTAGAATTTCATGGATGCCATACTACTTTCT  
TTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTTTGTTAATTGGGAGACTGGCCTTG  
GAAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTCTGGTGTGGCTCCACAGATTCC  
AAGGATATCGTGATGCCTACGTACGATTGACTGATTCTGTTCTGGAAACCATGGCCGGGTA  
AGTCTGGATATGATGTCGTGCAAGCTAACACGGGCTCCCTGGAAAGCAAAAATTCCACT  
GCCGTCTGGAGAGGGCAGACAGCCGAAAGAGAGACTCGAGCTGGTAAACTCAGTAGAAAA  
CACCCAGAACTCATAGCGCTGTTACCAACTTTCTTTAAACACGATGAAAACCTG  
TATGGTCCCATTGTGAAACATATTCACTTTGATTCTCAAGCATAAGTATCAAATAAAT  
ATCGATGGCACTGTAGCAGCTTATGCCATATTGCTAGTTGGTGAAGTGTGCTG  
AAGCAGGATTCCATCTACTATGAACATTTCACATGAGCTGCAAGCTGGAAACACTACATT  
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACTTAAATGGCGAAAGATCACGATGAA  
GAGGCCAAAAGATAGCAAAGCAGGACAAGAATTGCAAGAAATAATCTATGGCGATGAC  
ATATTCTGTTATTATTCAAACATTCCAGGAATATGCCAATTACAAGTGAGTGAGCCCCAA  
ATCCGAGAGGGCATGAAAAGGTAGAACACCAGAGACTGAGGACGACCTCCCTGTACTTGC  
CATAGGAAAAGACCAAAGATGAACTGAATGCAAATAACTTCTATTAGAATAATGGTGC  
TCTGAAGACTCTTCTTAACAAAAAGAAGAATTTTTAAGTATTAATTCCATGGACAATATA  
AAATCTGTGTGATTGTTGCAGTATGAAGACACATTCTACTTATGCAGTATTCTCATGACTG  
TACTTTAAAGTACATTAGAATTATATAATAAAACCACCTTATTAAAGGAAAAAAA

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**FIGURE 548**

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPARFYIQAVENTSGNKFT  
SSPGEKVFQVKVSAPEEQFTRGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKSPY  
ILKGPVYHENCDCPLQDSAALREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRGQRQSL  
CHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTKVKMPDVELFVNLDWPLEKKKSNSNIHP  
IFSWCGSTDSDKDIVMPTYDLTDVLETMGRVSLDMMMSVQANTGPPWESKNSTAVWRGRDSRKE  
RLELVKLSRKHPELIDAFTNFFFFKHDENLYGPIVKHISFFDFKKHYQINIDGTVAAYRLP  
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKKIAKAGQE  
FARNNLMGDDIFCYYFKLFQEYANLQVSEPOIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

**Important features:****Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 302-306, 414-418

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

**Tyrosine kinase phosphorylation site.**

amino acids 341-348

**N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

**Endoplasmic reticulum targeting sequence.**

amino acids 499-504

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**FIGURE 549**

GGGTGATTGAAC TAAAC CTT CGCC GACCGAG TTT GCAGT ACGGCC GT CACCC GACC GCT GC  
CTGCTTGC GGTT GGAG AAATCA AGGCC CT ACCGGG CTCG TAGT CACCT CT ATAGT GGGC  
GTGGCC GAGGCC GGGGT GACCC TGCC GGAGC CTCC GCTGCC AGCGA C ATGTT CAAGGTA ATT C  
AGAGGTCC GTGGGG CCAGCC AGCCTGAGCTTGCTCACCTCAAAGTCTATGCAGCACCA AAAA  
AGGACTCACCTCC AAAA ATTCC GTGAAGGTTGATGAGCTTCACTCTACTCAGTT CCTGAGG  
GTCAATCGAAGTATGTGGAGGAGGCAAGGAGCCAGCTTGCTGAAGAAAGCATCTCACAGCTCCGAC  
ACTATTGCGAGCCATACACAACCTGGTGT CAGGAAACGTACTCCC AACTAACGCCAAGATGC  
AAAGTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCT CCTGGATT TT  
TTCCGAGACTTGGTGTATTGGTTTGCTGGCCTTATTGGACTCCTTTGGCTAGAGGTTCAA  
AAATAAAGAAGCTAGTGTATCCGCCTGGTTCATGGGATTAGCTGCCCTCCCTATTATCCAC  
AACAAAGCCATCGTGTGCCCCAGGTCA GTGGGAGAGATTATATGACTGGGTTACGAGGAT  
ATATAGTCATAGAAGATTGTGGAAGGAGAACTTCAAAAGCCAGGAAATGTGAAGAATT CAC  
CTGGAAC TAAGTAGAAA ACTCCATGCTCTGCCATCTTAATCAGTTAGGTAAACATTGGAAA  
CTCCATAGAATAAATCAGTATTCTACAGAAAATGGCATAGAAGTCAGTATTGAATGTATTA  
AATTGGCTTCTCTTCAGGAAA ACTAGACCAGACCTCTGTTATCTCTGTGAAATCATCCT  
ACAAGC AAAACTAACCTGGAATCCCTCACCTAGAGATAATGTACAAGCCTAGAACCTCCTCAT  
TCTCATGTTGCTATTATGTACCTAATTAAAACCCAAGTTAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

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**FIGURE 550**

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLLEES  
ISQLRHYPYTTWCQETYSQTPKPMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL  
LARGSKIKKLVYPPGMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG  
NVKNSPGTK

**Important features:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 111-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 26-30

**Tyrosine kinase phosphorylation site:**

Amino acids 36-44

**N-myristoylation sites:**

Amino acids 124-130;144-150;189-195

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